Table 2

Kinetic and thermodynamic parameters for the folding of proteins that fold with three-state kinetics.

Protein	Reference	PDB code	Contact order	Chain length	Structure	Denaturant	$\Delta G_{U-F}^{H_2O}$ (kcal mol^{-1})	m (kcal mol^{-1}M^{-1})	$[D]_{50\%}$ (M)	Temp. (°C)	$k_F^{H_2O}$ (s^{-1})	ΔG_{U-I}^{H2O} (kcal mol^{-1})	$k_U^{H_2O}$ (s^{-1})	$m^{\ddagger-F}$ (kcal mol^{-1} M^{-1})	β_T
Ubiquitin															
wild type	[24]	1UBQ	15.1	67	α/β	GdnHCl	7.2	2.0	3.7	25	350	1.5	0.0012	0.82	0.59
wild type + 0.4 M Na_2SO_4							10.2	2.2	4.6		900	3.1	9×10^{-5}	1.05	0.52
Barstar	[54]	1BTA	12.2	89	α	Urea	4.8	1.3	3.9	25	31	1.9	0.068	0.17	0.87
[a]CD2, pH 7.0	[55]	1HNG	17.5	98	β-sandwich	GdnHCl				25	6.0	0.8	5.0×10^{-4}	1.60	[b]0.68
[a]CD2, pH 4.5						GdnHCl	8.7	5.0	1.7	25	14	1.8	1.0×10^{-4}	1.89	0.62
Barnase	[56]	1BNI	11.4	110	α/β	Urea	10.5	2.3	4.6	25	13	3.2	1.1×10^{-4}	0.27	0.88
[c]Suc 1				113	α/β	Urea	7.2	1.7	4.4	25	65	1.6	0.0001	0.78	0.54
Lysozyme (hen egg white)	[57]	1HEL	10.8	129	α/β	GdnHCl				20	4	2.7	6.2×10^{-7}	0.73	0.75
Lysozyme (hen egg white)	[58]	1HEL				GdnHCl	13.5	2.1	3.8	25	3.5	4.9	5.0 x 10-5	0.43	0.80
CheY	[59]	3CHY	9.0	129	α/β	Urea	5.2	1.6	3.3	25	2.7	[d]nd	0.012	0.47	0.71
[e]p16				148	α	Urea	3.1	1.7	1.9	25	33	1.5	1.4	0.08	0.95
GroEL apical domain (191-345)	[60]	1JON	15.7	154	α/β	Urea	[f]5.6	2.0	2.8	25	2.3	3.8	0.004	0.45	0.78
Ribonuclease H (*Escherichia coli*), pH 5.5	[61]	2RN2	12.4	155	α/β	Urea	[g]9.9	2.1	4.7	25	0.6	3.6	1.69×10^{-5}	0.42	0.80
Ribonuclease H (*E. coli*), pH 5.5	[62]	2RN2	12.4	155	α/β	GdnHCl	9.5	5.2	1.8	25	4.1	4.8	3.7×10^{-5}	1.91	0.63
N-terminal domain from PGK	[58]	1PHP	11.5	175	α/β	GdnHCl	8.4	7.6	1.1	25	9.5	5.2	0.03	1.24	0.84
[h]C-terminal domain from PGK	[63]	1PHP	8.0	219	α/β	GdnHCl	13.6	13	1.0	25	0.03	3.4	7.6×10^{-10}	7.1	0.45

[a]Some care must be taken in comparing these proteins as the values are calculated using denaturant activity not concentration of denaturant. [b]Calculated assuming the equilibrium m value does not vary significantly with pH. [c]F. Rousseau, J.W.H. Schymkowitz, M. Sánchez del Pino and L.S. Itzhaki, unpublished observations. [d]Not determined as it requires knowledge of the *cis–trans* isomerisation ratio in the unfolded state. [e]L. Itzhaki, personal communication. [f]Average of values obtained from CD and fluoresence experiments. [g]Calculated from the fit of the kinetic data to a three-state model. [h]The folding of the C-terminal domain of PGK is monitored in the presence of the N-terminal domain (fluorescence probe is only in C-terminal domain) – the domains act independently.

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