Table 2

Ultrafast folding proteins.

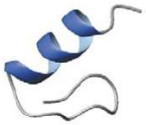
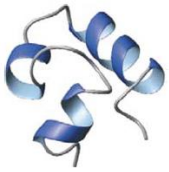
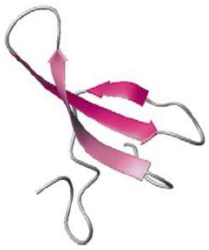
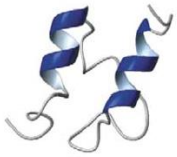
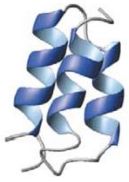
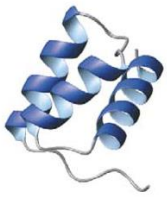
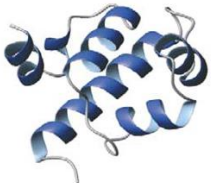
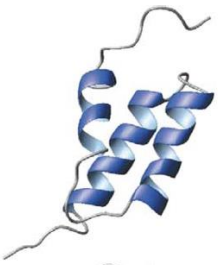
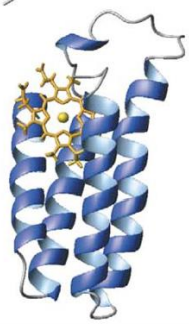
Protein name (PDB code) and mutation	Number residues (relative contact order)[a]	Structure	$\tau_{folding}$ (μs)	$\Delta G_{folding}$ (kcal/mol)	T (K)	Data reference	Simulation/theory references
Measured folding times							
Tryptophan cage (1L2Y)	20 (0.200)		**4.1**	−0.7	296	[15]	[13,23,101–106]
BBA5	23 (0.136)		**7.5**	+0.8	298	[21]	[21,107]
Villin headpiece subdomain (1VII)	35 (0.115)		**4.3**	−3.1	300	[16]	[22,91,108–119]
N68H/K65Nle	35		**1.7**	−3.6	300	b	
HP-36	36		**8**	−0.6	329	[18]	
WW domain Pin (1PIN)	34 (0.190)		**85**	−1.9	312	[11]	[120]
WW domain FBP28 (1E0L)	37 (0.170)		~**30**[c]	−1.7	298	[12]	[120–122]
W30A			**24**	−1.2	298	[12]	
W30A			**47**	−0.8	313	[19]	
W30F			**19**	−2.1	313	[19]	
Peripheral subunit binding domain (2PDD)	41 (0.105)		**62**	−1.1	314	[8]	[91]
Albumin binding domain (1PRB)	47 (0.123)						
K5I			**2.5**	−2.6	350	[89]	[88,123]
K5I/K39V			**1**	−2.8	347		

Table 2 Continued

Protein name (PDB code) and mutation	Number residues (relative contact order)[a]	Structure	$\tau_{folding}$ (μs)	$\Delta G_{folding}$ (kcal/mol)	T (K)	Data reference	Simulation/theory references
Engrailed homeodomain (1ENH)	61 (0.121)		**27**	−2.1	298	[10]	[10,17,91]
α_3D (2A3D)	73 (0.096)		**3**	−1.9	323	[20]	[20]
λ-repressor (1LMB)	80 (0.092)		**250**	−3.0	310	[124]	[62,63,88, 125,126]
A37G			**44**	−0.4	330	[14]	
G46A/G48A			**22**	−1.0	335		
G46A/G48A/D14A			**18**	−1.5	335		
Extrapolated folding times[d]							
Protein A, B domain (1BDC)	58 (0.092)		**8 (200)**[e]	−4.3	310	[127]	[91,119,128–146]
Cytochrome b_{652} (1QQ3)	106 (0.075)		**5 (670)**[f]	−10	298	[147]	[88]

[a]The relative contact order (RCO), which is the mean separation in sequence by contacting atoms, is defined by $\mathrm{RCO} \equiv \frac{1}{N\Lambda} \sum_{\text{contacts}} |i-j|$, where N is the number of residues in the protein, Λ is the total number of atomic contacts and $|i-j|$ is the separation in sequence between residues i and j with distance between atoms less than 0.6 nm. [b]J Kubelka *et al.*, unpublished. [c]Extrapolated from 2 M urea. [d]Measured folding time in parentheses. [e]In 2 M urea. [f]In 2.2 M GndHCl. Nle = norleucine (-HC^{α} -$(CH_2)_3$-CH_3).