Table 1

Rate of formation of structural elements of proteins.

Sequence	$\tau_{contact}$ (µs)		T (K)	References
Disordered loop				
Lip-$(AARAA)_4$-W-NH_2	0.09		293	[41]
C-$(AGQ)_n$-W-NH_2; n = 1–6	0.02–0.1		273	[40]
Xan-$(GS)_n$-NAla-GS; n = 1–28	0.007–0.16		296	[36]
Xan-S_n-NAla-GS; n = 2–11	0.012–0.03		296	[36]
W-X_6-DBO-NH_2; X = G,S,D,N,A,T,L,F,E,Q,H,R,K,V,I	0.03–0.4		Ambient (X=G) – (X=I)	[37]
Unfolded cytochrome c HTVEKGGKHKTGPNLH	0.25		295	[96]

Sequence	$\tau_{folding}$ (µs)[a]	$\Delta G_{folding}$ (kcal/mol)	T (K)	References
α Helix				
Ac-YG $(AKA_3)_2$ AG-NH_2	2.0	1.2	284	[97]
Ac-YGSPEA$_3$KA$_4$-^DR-NH_2	0.7	0.5	284	[97]
Ac-YGG $(KA_4)_3$ K-NH_2	0.7	0.2	290	[98]
Ac-YGSPEA$_3$ $(KA_4)_2$ ^DR-NH_2	0.6	0	288	[99]
Ac-WA$_3$H$^+$ $(A_3RA)_3$ A-NH_2	0.4	0	300	[46]
A$_5$ $(A_3RA)_3$ A	0.8	0.7	310	[100]
β Hairpin				
(GB1) GEWTYDDATKTFTVTE	6	0	297	[49]
(trpzip4) GEWTWDDATKTWTWTE	13		300	[51]
(peptide I) SESYINPDGTWTVTE	0.8	0	300	[51]
(ubiquitin) MQIWVKNPDGTITLEVK	~20	~−1	303	b

[a] Calculated assuming a two-state system from $\tau_{folding} = \tau_{obs}(1 + \exp(\Delta G_{folding}/k_B T))$, where τ_{obs} is the measured relaxation time. [b] V Muñoz et al., unpublished. DBO, 2,3-diazabicyclo[2,2,2]oct-2-ene; NAla, naphtylalanine; Xan, xanthone.

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