Table 3

Kinetic and thermodynamic parameters for the folding of dimeric proteins.

Protein	Reference	PDB code	Chain length	Structure	Denaturant	$\Delta G_{U-F}^{H_2O}$ (kcal mol^{-1} dimer^{-1})	m (kcal mol^{-1}M^{-1})	$[D]_{50\%}$ (M)	Temp. (°C)	$^{a}k_F^{H_2O}$ (M^{-1} s^{-1})	$k_F^{H_2O}$ (10 μM protein s^{-1})	$m^{\ddagger-U}$ (kcal mol^{-1} M^{-1})	$k_U^{H_2O}$ (s^{-1})	$m^{\ddagger-F}$ (kcal mol^{-1} M^{-1})	$^{b}\beta_T$
Arc repressor															
wild type	[78–80]	1ARQ	2 × 53	$(\beta\alpha_2)_2$	Urea	9.6	1.4		20	9.1×10^6	91		0.2		0.75
wild type	[81]	1ARR			GdnHCl	10.1	3.0		25	8.4×10^6	84	1.83	0.2	0.88	0.68
PL8					GdnHCl	12.7	3.1		25	7.4×10^6	74	2.10	0.002	1.14	0.65
MYL mutant					Urea	14.3	^{c}2.6		25	3.0×10^6	3000				0.4
^{d}ROP	[51]	1ROP													
wild type		1RPR	2 × 63	$(\alpha_2)_2$	GdnHCl	7.7	2.4	3.3	25	^{e}0.013	0.013		9.8×10^{-7}	0.47	0.8
Ala_2Leu_2 (1+8)						6.3	2.9	2.3	25	2.1	2.1	1.8×10^{-4}			
Ala_2Leu_2 –6						8.1	2.7	2.7	25	4.0	4.0	4.9×10^{-2}			
GCN-4	[82]	2ZTA 3DGC 1YSA	2 × 33	$(\alpha)_2$	GdnHCl	10.5	1.8		5	4.2×10^5	4.2	0.97	3.3×10^{-3}	0.88	0.52

[a]At low protein concentration the refolding of dimers often follows first-order kinetics with respect to the protein concentration such that $k_{obs} = k_F$[protein], as expected for a bimolecular reaction. For Arc repressor and GCN-4 the refolding rate constants are given as the first-order rate constant. For ROP the rate-limiting step is unimolecular and the rate corresponds to the rate observed and is independent of protein concentration. [b]Calculated from $1 - m^{\ddagger-F}/m$. [c]Average value. [d]Values for k_F^{H2O} and k_U^{H2O} are calculated from Table 1 of [51] using an average $m^{\ddagger-F}$ of 0.8 M^{-1} and an average value for $m^{\ddagger-U}$ of 1.5 M^{-1} and extrapolating the data to 0 M GdnHCl. [e]For wild-type ROP the refolding rates are strongly dependent on ionic strength – values given are in 100 mM Tris-HCl (pH 8), 0.2 mM EDTA and 0.1 M KCl.

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