	N_{res}	N_s	*Time* μs	N_f	N_u	T K	ΔG_f kcal mol^{-1}	ΔH_f kcal mol^{-1}	ΔCv_f kcal mol^{-1} K^{-1}	T_m K	τ_f μs	τ_u μs	τ_{tp} μs
Chignolin	10	1	106	39	38	340	−0.9	−6.1(1)	−0.1(2)	381.0 (361.0–393.0)	0.6(1)	2.2(4)	0.04(1)
Trp-cage	20	1	208	12	12	290	0.8	−2.1(2)	0.0(1)	206.0 (0.0–233.0)	14(4)	3(1)	0.22(5)
BBA	28	2	325	14	14	325	0.7	−2.9(2)	−0.2(2)	undefined	18(5)	5(1)	0.7(1)
Villin	35	1	125	34	34	360	0.8	−15(1)	0.2(3)	343.0 (339.0–346.0)	2.8(5)	0.9(2)	0.27(3)
WW domain	35	2	1137	12	11	360	−0.9	−26(3)	−0.1(2)	373.0 (365.0–376.0)	21(6)	80(24)	0.5(1)
NTL9	39	4	2936	17	14	355	−1.3	−26.3(3)	−0.5(1)	370.0 (367.0–371.0)	29(7)	175(47)	0.9(1)
BBL	47	2	429	12	11	298	0.8	−2(1)	0.1(5)	251.0 (0.0–267.0)	29(8)	7(2)	3.1(6)
Protein B	47	1	104	19	19	340	0.6	−8(1)	0.0(2)	317.0 (311.0–328.0)	3.9(9)	1.6(4)	0.7(1)
Homeodomain	52	2	327	27	28	360	−0.7	−7.2(8)	0.2(3)	> 360	3.1(6)	9(1)	1.1(1)
Protein G	56	4	1155	12	13	350	0.3	−22(1)	−0.5(1)	345.0 (339.0–348.0)	56(16)	37(10)	1.8(3)
α3D	73	2	707	12	12	370	−0.1	−38(1)	−0.6(2)	370.0 (367.0–372.0)	27(8)	31(9)	0.9(2)
λ-repressor	80	4	643	10	12	350	0.9	−11(1)	−0.7(2)	undefined	49(15)	13(4)	3.1(7)

Table S1. Summary of the thermodynamic and kinetic parameters of 12 proteins, calculated from simulations of reversible folding. N_{res} is the number of amino acid residues; N_s is the number of independent simulations performed; *Time* is the total simulation time; N_f and N_u are the total number of folding and unfolding events observed in the simulations; T is the simulation temperature; ΔG_f is the free energy for the folding reaction at the simulation temperature, calculated from the folding and unfolding rates; ΔH_f is the enthalpy of the folding reaction at the simulation temperature, calculated as the difference in potential energy between the unfolded and the folded state; ΔCv_f is the heat capacity change for the folding reaction, calculated from the difference in the potential energy fluctuations in the folded and unfolded states; T_m is the melting temperature (and 68% confidence interval) when it can be extrapolated from the calculated ΔG_f, ΔH_f, and ΔCv_f values; τ_f and τ_u are the mean folding and unfolding times; τ_{tp} is the mean transition path time. Times are in μs, temperatures are in K and energies are in kcal mol^{-1}. Standard errors are reported in parentheses. A comparison of some of these quantities with the experimental data is presented below in the sections describing the individual proteins.