

Supporting Information For: Effect of interactions with the chaperonin cavity on protein folding and misfolding[†]

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Table S1 Parameters for fit of phenomenological model to rates and stabilities. Cavity size is given below each protein name.

Protein:	NTL9	prb ₇₋₅₃	Protein G
Cavity:	2.4 nm	2.8 nm	2.6 nm
A_F	0.46	0.29	0.15
n_F^0	9.8	26	27
$\kappa_F / k_B T$	0.2	10	30
A_{\ddagger}	13	0.38	8.3
n_{\ddagger}^0	2.8	12	8.2
$\kappa_{\ddagger} / k_B T$	0.053	0.030	0.020
$B_U / k_B T$	14	34	58
Cavity:	2.8 nm	3.0 nm	2.8 nm
A_F	1.3	1.5	0.026
n_F^0	24	19	27
$\kappa_F / k_B T$	0.2	10	30
A_{\ddagger}	0.92	0.7	56
n_{\ddagger}^0	7.9	8.7	5
$\kappa_{\ddagger} / k_B T$	0.073	0.054	0.016
$B_U / k_B T$	20	23	40
Cavity:	3.2 nm	3.2 nm	3.0 nm
A_F	2.9	2.72	0.55
n_F^0	12	29	14
$\kappa_F / k_B T$	0.2	10	30
A_{\ddagger}	1.2	.37	2.8
n_{\ddagger}^0	9.6	12	0.29
$\kappa_{\ddagger} / k_B T$	0.086	0.027	0.0020
$B_U / k_B T$	24	38	40

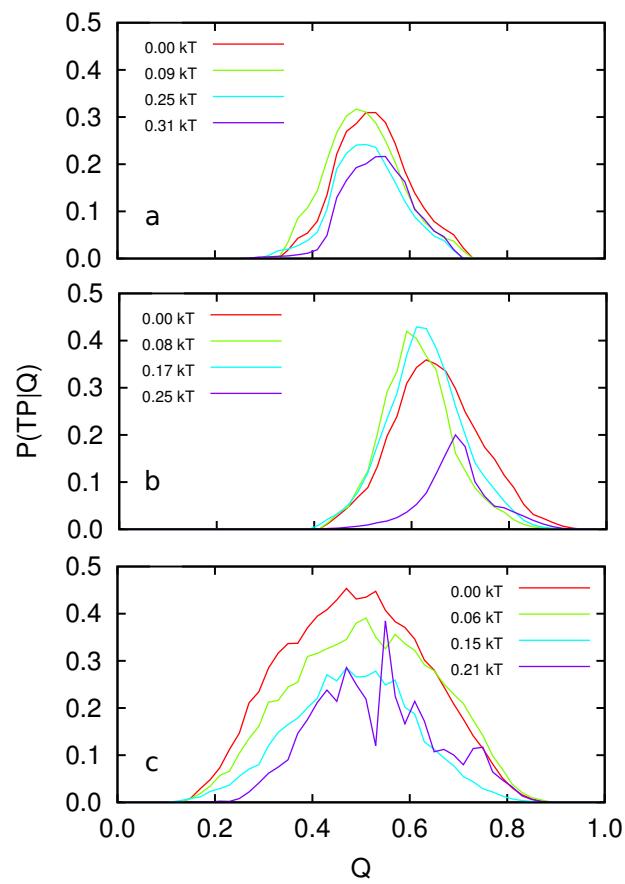


Fig. S1 Effects of confinement on the location of the folding barrier along Q , given by $P(TP|Q)$ for (a) 1div, (b) prb and (c) protein G.

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