

**Table 3****Size- and stability-normalized folding times and proximity to speed limit.**

Protein name (PDB code) and mutation	$\tau$ (normalized) ( $\mu\text{s}$ ) <sup>a</sup>	$\frac{\tau_{\text{(observed)}}}{\tau_{\text{(speed limit)}}}$ <sup>b</sup>
<b>From measured folding times</b>		
$\alpha_3\text{D}$ (2A3D)	1	4
Albumin binding domain (1PRB) K5I/K39V	2	2
$\lambda$ -repressor (1LMB) G46A/G48A/D14A	4	20
Villin headpiece subdomain (1VII) N68H/K65Nle	15	5
BBA5	20	30
Engrailed homeodomain (1ENH)	20	40
Tryptophan cage (1L2Y)	40	20
WW domain FBP28 (1E0L) W30F	60	50
Peripheral subunit binding domain (2PDD)	80	150
WW domain Pin (1PIN)	300	250
<b>From extrapolated folding times</b>		
Protein A, B domain (1BDC)	20	10
Cytochrome <i>b</i> <sub>562</sub> (1QQ3)	60	5

<sup>a</sup>Calculated from  $(50/N)^3 (K_{\text{eq}}/15)^{1/3} \tau_{\text{(observed)}}$ , where  $N$  is the number of residues,  $K_{\text{eq}} = \exp(-\Delta G_{\text{folding}}/k_B T)$  and  $\tau_{\text{(observed)}}$  is  $\tau_{\text{folding}}$ , as given in Table 2. The average size for the ten proteins with measured folding times is  $\sim 50$  and the average stability, calculated as  $\exp(-\langle \Delta G_{\text{folding}}/k_B T \rangle)$ , is  $\sim 15$ . <sup>b</sup>Calculated using  $\tau_{\text{(speed limit)}} = 0.01 N \mu\text{s}$  and the observed  $\tau_{\text{folding}}$  given in Table 2.