

CORRIGENDUM

Desolvation Barrier Effects Are a Likely Contributor to the Remarkable Diversity in the Folding Rates of Small Proteins [J. Mol. Biol. (2009) 389, 619–636]

Allison Ferguson, Zhirong Liu and Hue Sun Chan*

It has come to our attention that the no-desolvation-barrier (no-db) folding rates in Wallin and Chan¹ that we have used were given in a unit different from the with-desolvation-barrier (with-db) folding rates that we simulated.² This information should be noted. As a result, Fig. 3b and its legend should be replaced with the revised version below. As shown in the revised figure, the data are consistent with a single front factor $\mathcal{F} \approx 10^{-5}$ (in units of the reciprocal of the number of simulation time steps) for both the no-db models and the with-db models. If linear regression is performed separately on the two sets of models, the front factor for the no-db models becomes $\mathcal{F}^{(0)} \approx 9.0 \times 10^{-6}$, whereas the front factor for the with-db models remains unchanged at $\mathcal{F}^{\text{db}} \approx 1.7 \times 10^{-5}$. Other conclusions of our article² are not affected. We thank Dr. Stefan Wallin for discussion regarding the time unit used by Wallin and Chan.¹

References

1. Wallin, S. & Chan, H. S. (2006). Conformational entropic barriers in topology-dependent protein folding: perspectives from a simple native-centric polymer model. *J. Phys. Condens. Matter*, **18**, S307–S328; Corrigendum: **21**, 329801 (2009).
2. Ferguson, A., Liu, Z. & Chan, H. S. (2009). Desolvation barrier effects are a likely contributor to the remarkable diversity in the folding rates of small proteins. *J. Mol. Biol.* **389**, 619–636; Addendum: **392**, 242 (2009).

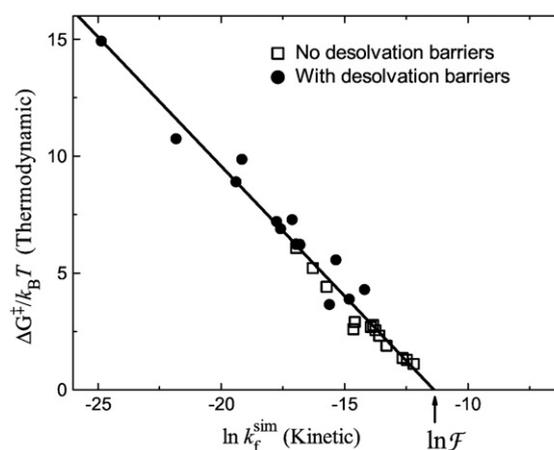


Fig. 3. (b) The free-energy barrier height ΔG^\ddagger (in units of $k_B T$) versus the logarithmic midpoint folding rate k_f^{sim} determined from simulations of the with-db models (filled circles) and no-db models (open squares) of the 13 proteins that we studied. The straight line was determined from a linear regression with correlation coefficient $r = -0.98$. The x -intercept of the straight line provides the preexponential (front) factor in Kramers theory, $\mathcal{F} \approx 10^{-5}$, for both the with-db models and the no-db models. Data for the no-db models were adapted from Fig. 4 of Wallin and Chan¹ (cited as Ref. 27 in Ferguson *et al.*²). The time unit used by Wallin and Chan¹ was 100 simulation time steps. For a comparison of the with-db and no-db models on equal footing, the time unit for folding rates in the present figure is given by the number of simulation time steps for both the with-db models and the no-db models.

*Corresponding author. E-mail address: chan@arrhenius.med.utoronto.ca.