

ADDENDUM

Addendum to “Desolvation Barrier Effects Are a Likely Contributor to the Remarkable Diversity in the Folding Rates of Small Proteins”
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The authors wish to include a technical point that is important for the completeness of their work, especially for readers who may wish to reproduce their calculation:

Simulated folding rates in Figs. 3b, 5a, and 10 for the db models were computed by averaging over 40–200 trajectories for each protein. Most of the model folding rates were obtained by direct simulations. The folding rates of four slowest-folding db-model proteins (1aps, 1urn, 1wit, and 1ris) were estimated with the help of bias potentials for kinetics as described in Ref. 52 [Badasyan *et al.*; see Eq. (10) of this reference] cited in the paper.