Supporting Information

Mittal and Best 10.1073/pnas.0807742105

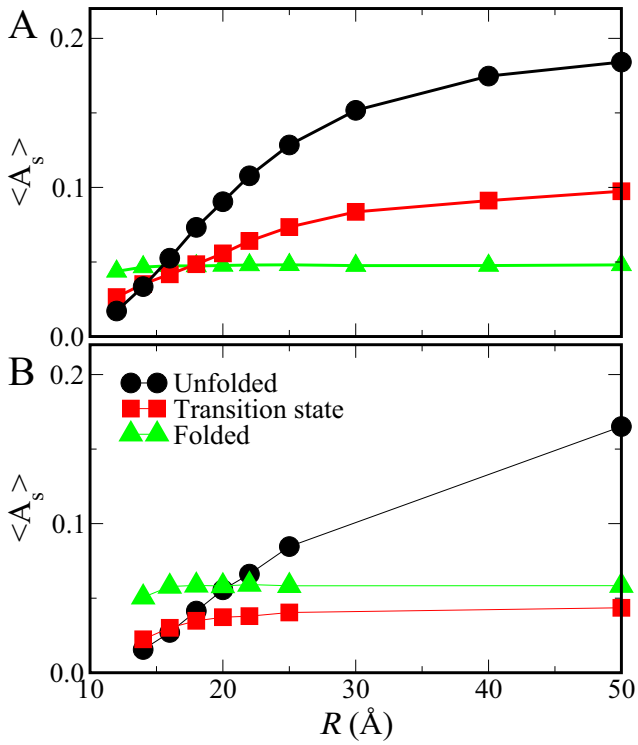

Fig. S1. Average asphericity parameter $\langle A_s \rangle$ as a function of cavity size R for prb (*A*) and protein G (*B*) for $d_c = 3$. We use

$$A_s = \frac{1}{2}\left(\sum_{i>j=1}^{3} (R_i^2 - R_j^2)^2 \right) / \left(\sum_{i=1}^{3} R_i^2 \right)^2 ,$$

where the R_i^2 are the principal radii of gyration [van Giessen AE and Szleifer I (1995) Monte Carlo simulations of chain molecules in confined environments. *J Chem Phys* 102:9069–9076]. This parameter is 0 for a spherical object and 1 for a rodlike object. We notice that with decreasing R, the unfolded structures become more spherical as expected, and there is no significant change in the shape of the folded structures. Confinement has an intermediate effect on the transition state asphericity. The larger change in transition state shape occurs for prb because the unconfined transition state is more aspherical for this protein than for protein G.

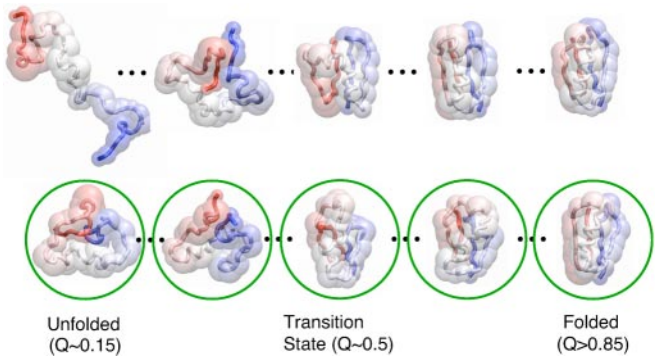

Fig. S2. System snapshots representing folding transition paths in bulk (*Upper*) and in a spherical cavity with $R = 22.5$ (*Lower*) for protein G. The circle in the lower path indicate the size of the cavity relative to the protein.

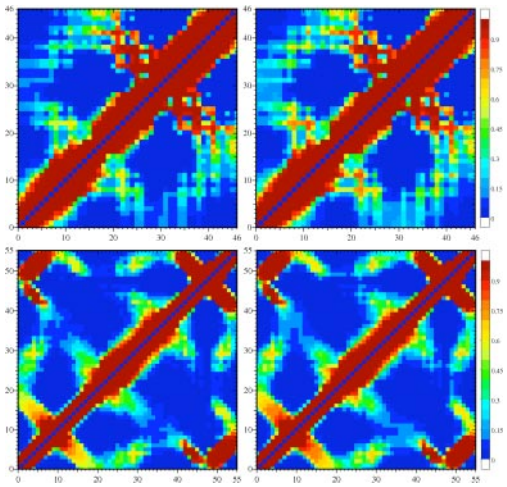

Fig. S3. Contact maps for prb in bulk (*Upper Left*) and enclosed in a spherical cavity of radius $R = 20$ Å (*Upper Right*) and protein G in bulk (*Lower Left*) and enclosed in a spherical cavity of radius $R = 20$ Å (*Lower Right*) in the transition state as calculated using a 12-Å cut-off.