Supporting Information

Javadi and Main 10.1073/pnas.0907455106

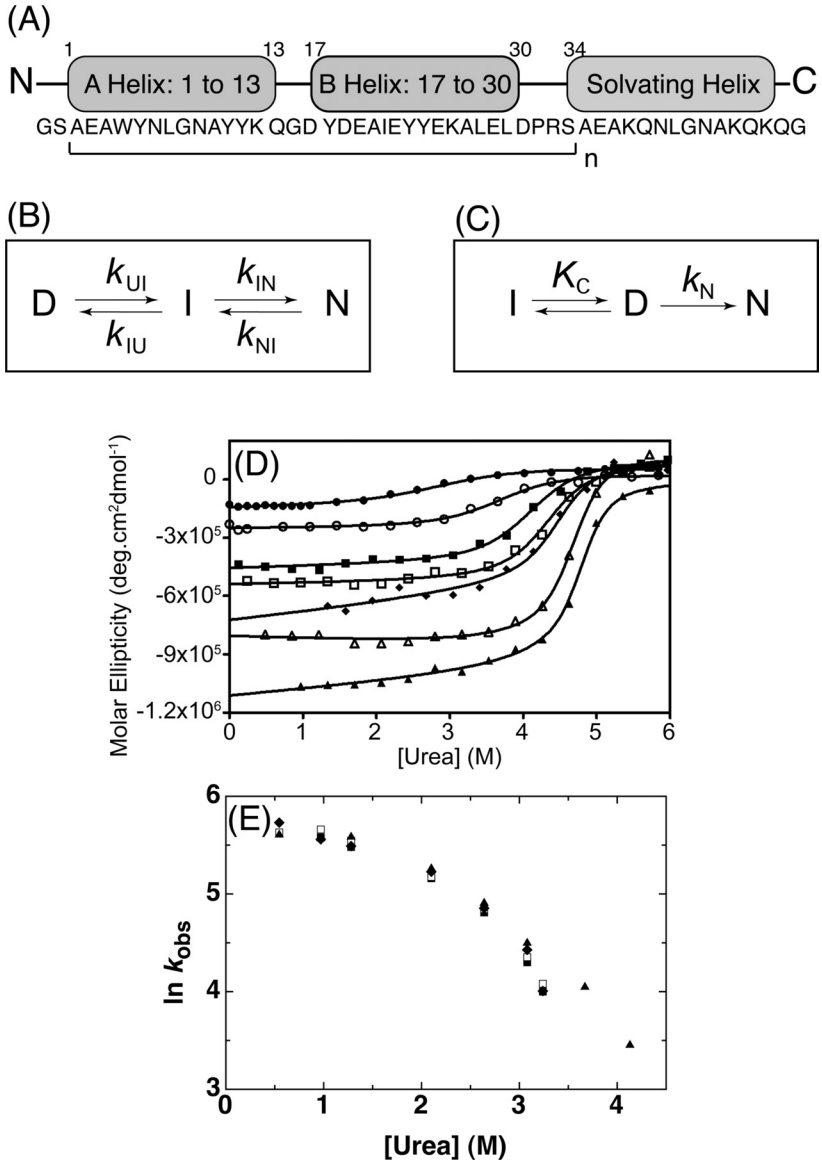

Fig. S1. (*A*) Schematic illustration of the amino acid sequence for the CTPR*an* proteins. Sequence commences at the N terminus with the residues G and S. The 34-aa sequence is repeated (*n*) and terminates with a solvating helix at the C terminus. (*B*) Folding Scheme 1, depicting a sequential, on-pathway, 3-state model for folding. (*C*) Folding Scheme 2, depicting a minimal dead-end scheme with a populated compact off-pathway intermediate species. (*D*) Urea-induced equilibrium unfolding experiments of the CTPRa proteins at 10 °C followed by ellipticity [CTPRa2 (●), CTPRa3 (○), CTPRa4 (■), CTPRa5 (□), CTPRa6 (◆), CTPRa8 (△), and CTPRa10 (▲)]. Solid lines correspond to the global best fits to the 1-dimensional Ising model (see *SI Appendix* for details on analysis) [Kajander T, Cortajarena AL, Main ERG, Mochrie SGJ, Regan L (2005) A new folding paradigm for repeat proteins. *J Am Chem Soc* 127(29):10188–10190]. (*E*) Representative refolding kinetics of CTPRa4 (■), CTPRa5 (□), CTPRa6 (◆), and CTPRa10 (▲) as a function of urea concentrations.

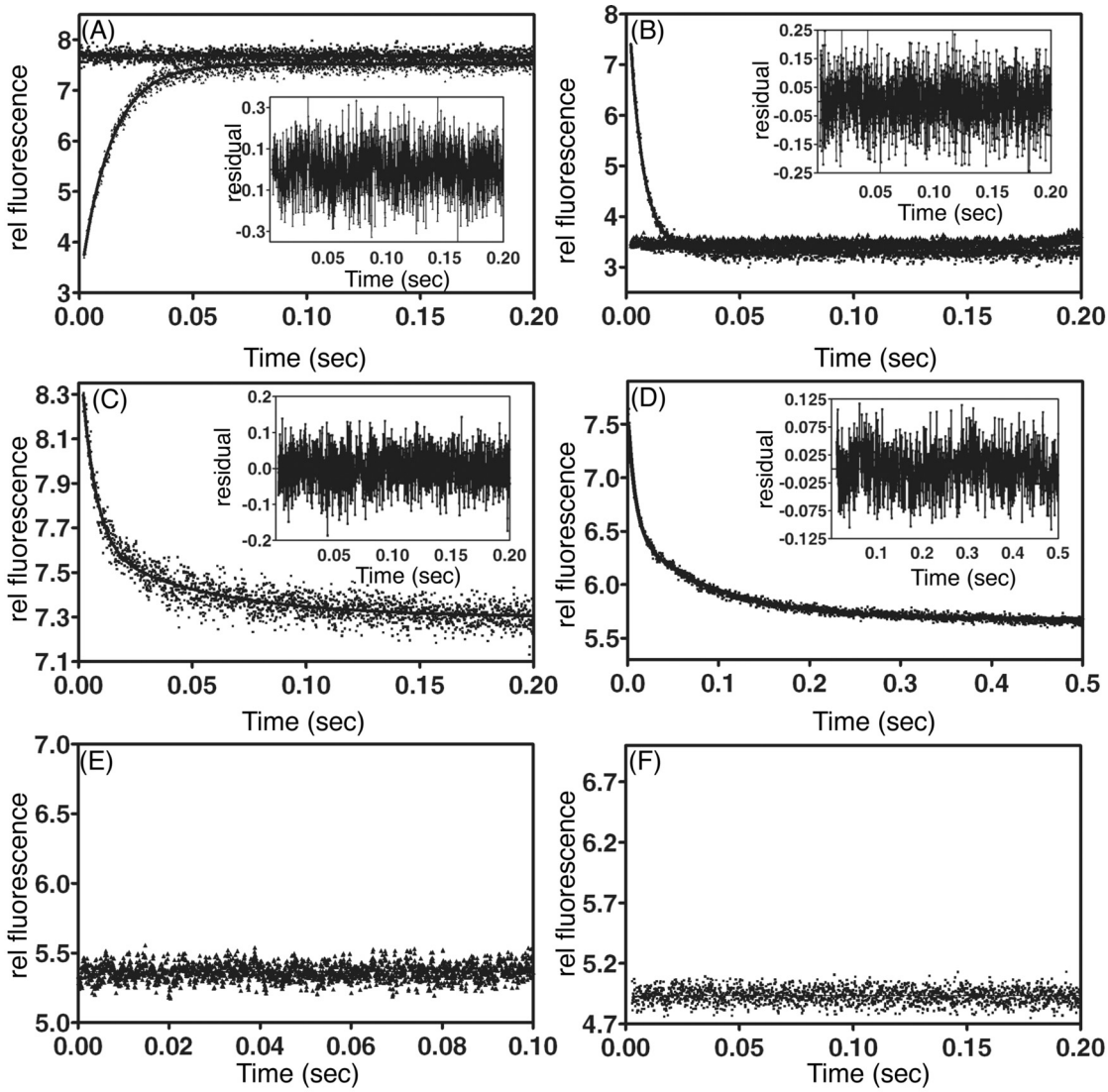

Fig. S2. (*A* and *B*) Representative refolding and unfolding traces of CTPRa4 to a final [GuHCl] of 2.35 M and CTPRa5 to a final [GuHCl] of 3.68 M, respectively, overlaid with the native or denatured baselines, which show the reaction has gone to completion. *Insets*: Respective residuals when fit to a single exponential. A dead-time of 2 ms was cut off, which accounts for ≈10–20% of the total amplitude. (*C* and *D*) Representative ANS refolding traces for CTPRa4 and CTPRa10, respectively, to a final [GuHCl] of 0.54 M. *Insets*: Respective residuals when fit to a double exponential. (*E* and *F*) Representative ANS refolding traces for the same proteins at a higher final [GuHCl] of 2.55 M for both proteins.

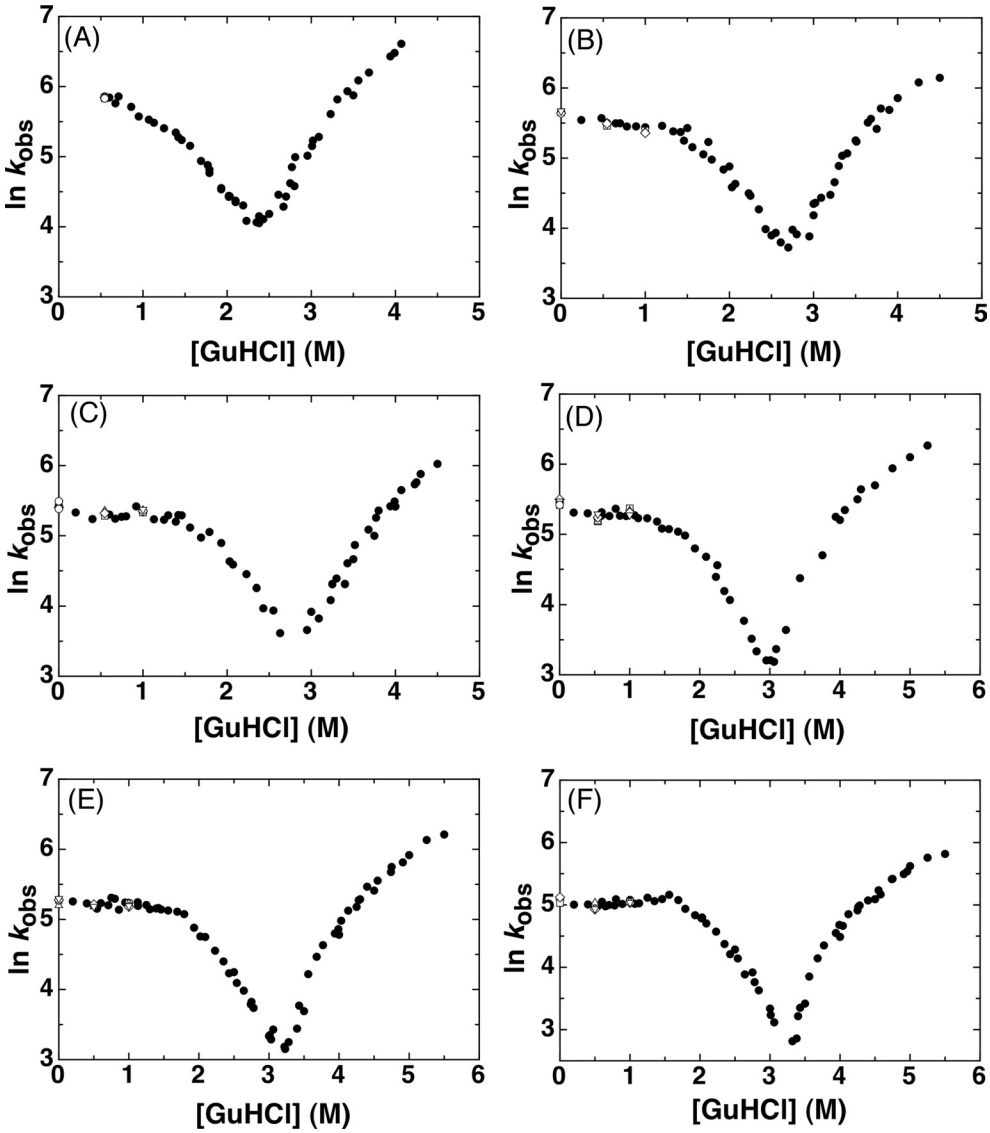

Fig. S3. Chevron plots of the CTPRa proteins (○) showing the dependence of ln k_{obs} when protein concentration was varied at specific denaturant concentrations. (*A*) CTPRa3 with the rate constant at 0.54 M [GuHCl] monitored at protein concentrations 0.5 μM (○), 1 μM (△), 5 μM (□), and 10 μM (◇). (*B*) CTPRa4 with the rate constants at 0 M, 0.54 M, and 1 M [GuHCl] monitored at protein concentrations of 0.25 μM (○), 1 μM (△), 2.5 μM (▽), and 7.5 μM (◇). (*C*) CTPRa5 with the rate constants at 0 M, 0.54 M, and 1 M [GuHCl] monitored at protein concentrations of 0.75 μM (○), 1 μM (△), 2.5 μM (□), and 5 μM (◇). (*D*) CTPRa6 with the rate constants at 0 M, 0.54 M, and 1 M [GuHCl] monitored at protein concentrations of 0.1 μM (○), 1 μM (△), 2.5 μM (▽), and 10 μM (◇). (*E*) CTPRa8 with the rate constants at 0 M, 0.54 M, and 1 M [GuHCl] monitored at protein concentrations of 0.5 μM (○), 1 μM (△), 2.5 μM (▽), and 5 μM (◇). (*F*) CTPRa10 with the rate constants at 0 M, 0.54 M, and 1 M [GuHCl] monitored at protein concentrations of 0.1 μM (▽), 1 μM (△), 5 μM (□), and 10 μM (◇).

Other Supporting Information Files

Table S1
Table S2
Table S3
Table S4
Table S5
SI Appendix