

SI Table 2: Thermodynamic parameters for equilibrium unfolding of CTPRa proteins fit to the Ising Model.

Variables	^a m_1	^a x_c	^a J	^b H	^c $\Delta G_{0 \rightarrow 1}^{H_2O}$ (kcalmol ⁻¹) (Stability of a helix)	^c $\Delta G_{0 \rightarrow 2}^{H_2O}$ (kcalmol ⁻¹) (Stability of a repeat)	^c $\Delta G_{0 \rightarrow 3}^{H_2O}$ (kcalmol ⁻¹) (Stability of 1.5 repeats)
Fluorescence using GuHCl	0.7 ± 0.02	3.6 ± 0.02	1.7 ± 0.04	1.3 ± 0.04	-2.6 ± 0.1	-1.0 ± 0.1	0.5 ± 0.2
C.D. using GuHCl	0.8 ± 0.02	3.6 ± 0.02	1.9 ± 0.04	1.4 ± 0.04	-2.4 ± 0.1	-1.0 ± 0.1	0.5 ± 0.2
C.D. using Urea	0.4 ± 0.02	5.3 ± 0.05	1.5 ± 0.05	1.1 ± 0.05	-2.2 ± 0.1	-0.9 ± 0.2	0.3 ± 0.2
^d Average	-	-	1.7 ± ^d 0.2	1.3 ± ^d 0.2	-2.4 ± ^e 0.4	-1.0 ± ^e 0.5	0.4 ± ^e 0.6

The errors reported are from the fitting of the experimental data. ^aObtained from global fit of equilibrium data using SI equation 4. ^bCalculated from $H = 1/2 m_1(x - x_c)$. ^cCalculated from SI equation 5. ^dAverage obtained from CD (urea and GuHCl) and Fluorescence (GuHCl), errors are quoted as a standard deviation of all of the experiments. ^eErrors obtained through propagation of one standard deviation of the averaged H and J values.