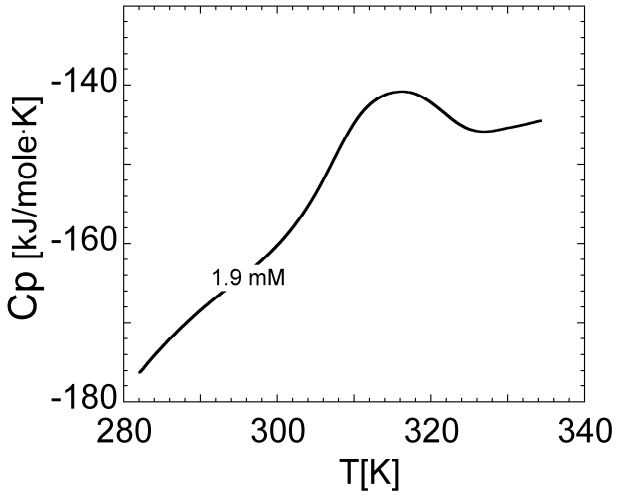
Supporting information:

Differential scanning calorimetry

To obtain an estimate for the molar enthalpy ΔH and the prefactor $K_{H,0}$ in equation 1 in the main text, we performed differential scanning calorimetry. A 1.9 mM solution of TR_4T was loaded into a Micro DSC III Setaram calorimeter at 50 ˚C and then cooled down to 20 ˚C. After 12 hours of equilibration (during which gel was formed), the temperature was decreased from 20 to 5 ˚C and equilibrated for next 4 hours to assure that all side blocks are involved in triple helices. After equilibration the temperature was increased at a scan rate of 0.2 K/min The resulting thermogram is shown below.



The enthalpy calculated from this thermogram is -166±12 kJ/mole of protein, which corresponds to ΔH=-250±20 kJ/mole triple helix, while the ΔC_p maximum occurs at a temperature of T_m=315K. These data are in good agreement with literature data for pure $(GlyProGly)_9$[18].If we consider this to be the temperature at which half of the helices have melted (i.e. $C_H=C_T/3$), we can calculate $K_{H,0}$ from

$$K_{H,0} = \frac{\exp\left[\frac{\Delta H}{R \cdot T_m}\right]}{3 \cdot C_T^{\,2}} \qquad \text{(S1)}$$

For ΔH=250 kJ/mole triple helix this gives $K_{H,0}$ $5 \cdot 10^{-37}$ $l^2/mole^2$.