Supporting information

for

For the sequence YKGQ the turn and extended conformational forms are separated by small barriers and the turn propensity persists even at high temperatures: Implications for protein folding

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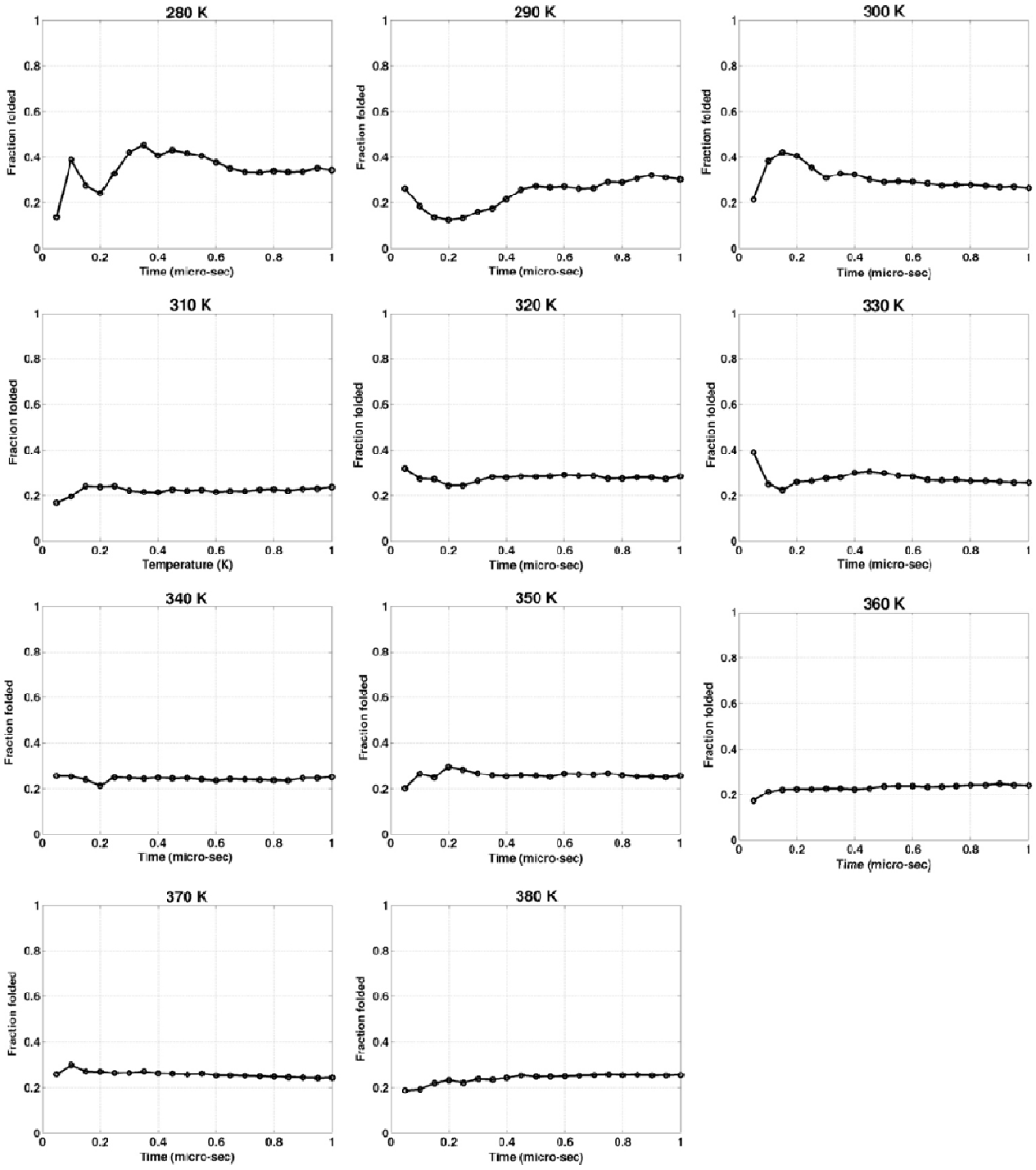

Figure S1 Fraction folded (end-to-end distance < 0.7 nm) with respect to simulation time, at all eleven simulation temperatures. All simulations reached convergence within 1μs of simulation time. At higher temperatures convergence is attained at earlier times than those at lower temperatures.

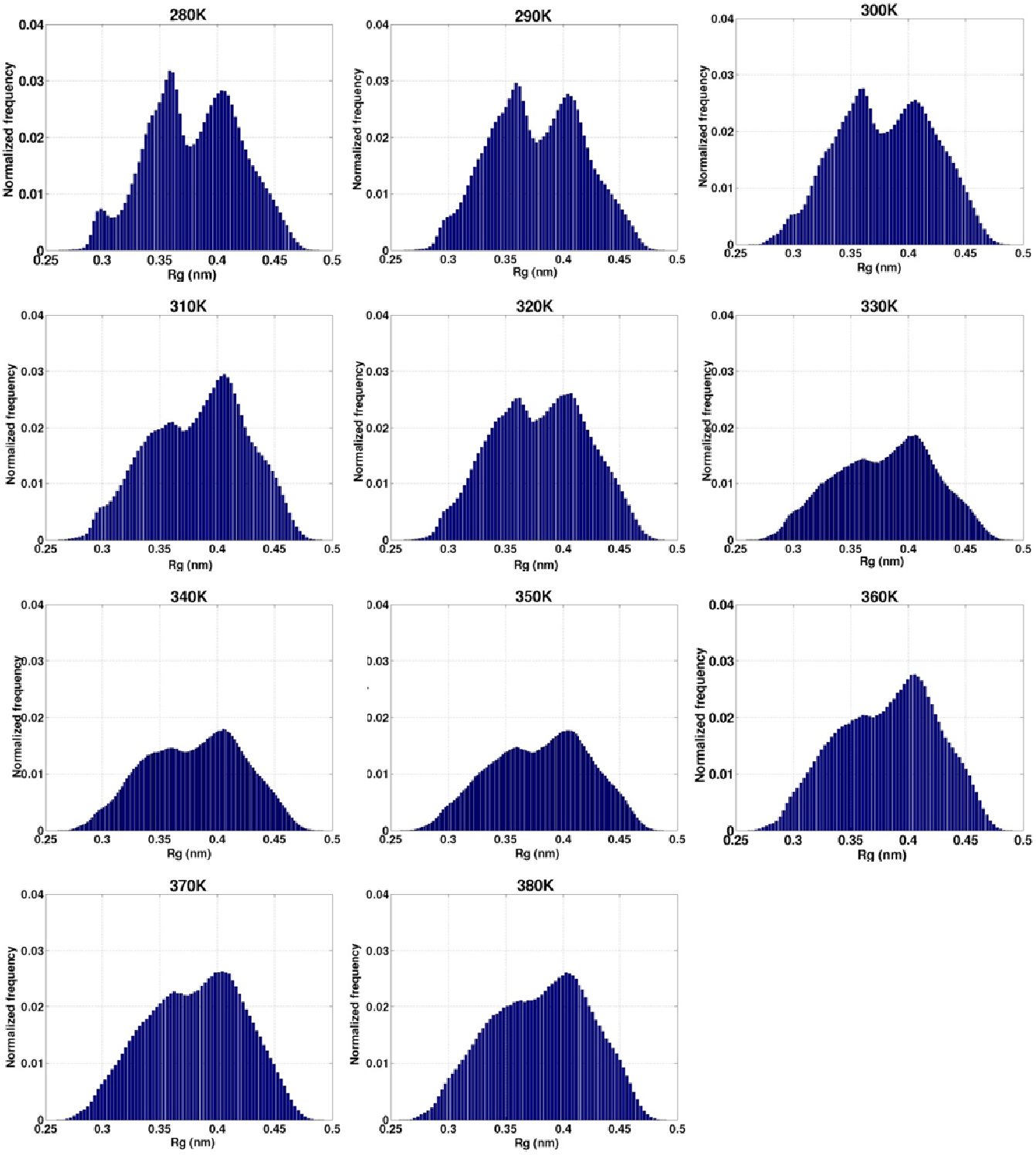

Figure S2 Normalized frequency distribution of radius of gyration (Rg) of peptide backbone at eleven simulation temperatures for the YKGQ peptide.

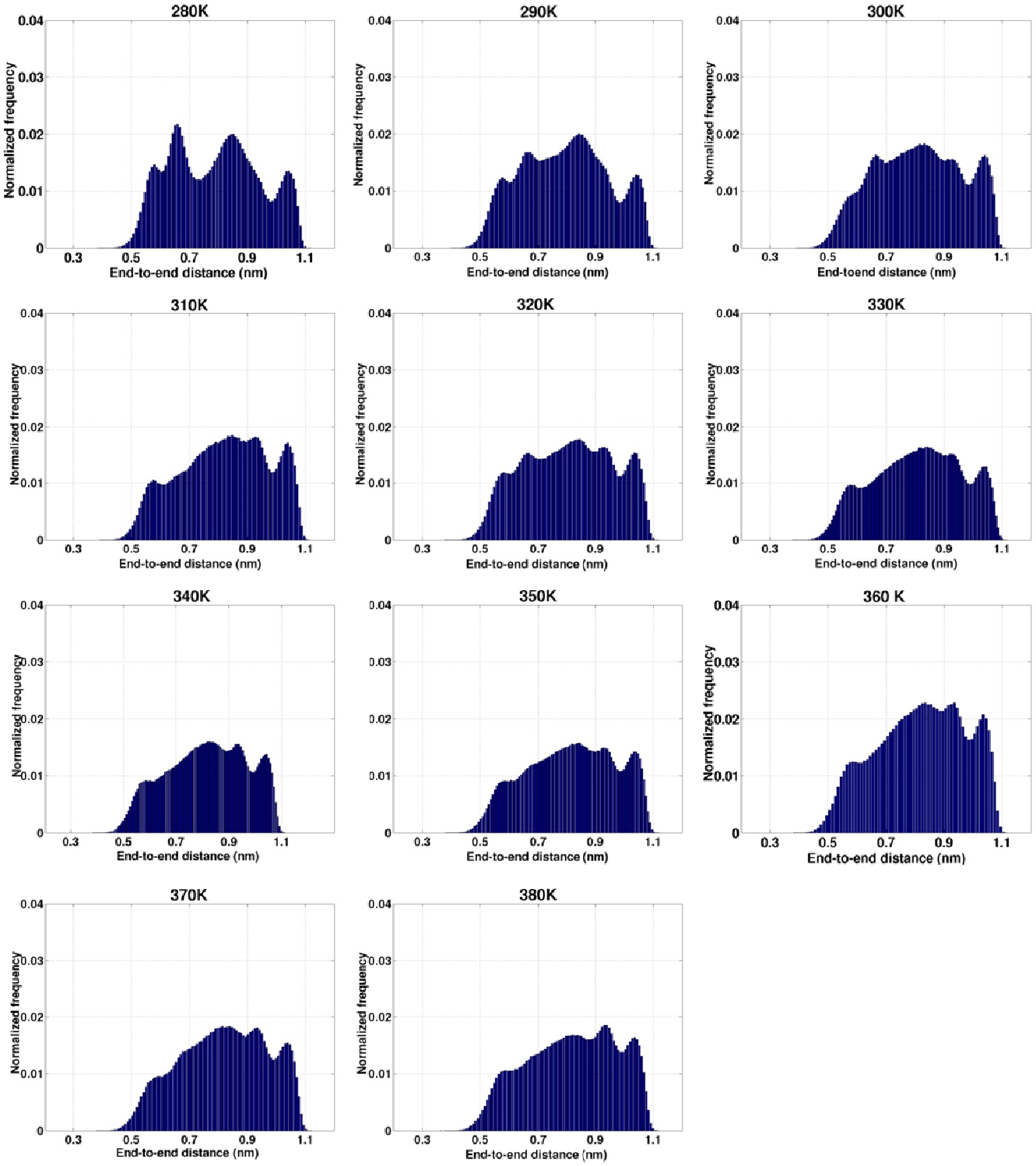

Figure S3 Normalized frequency distribution of end-to-end distance at eleven simulation temperatures for the YKGQ peptide.

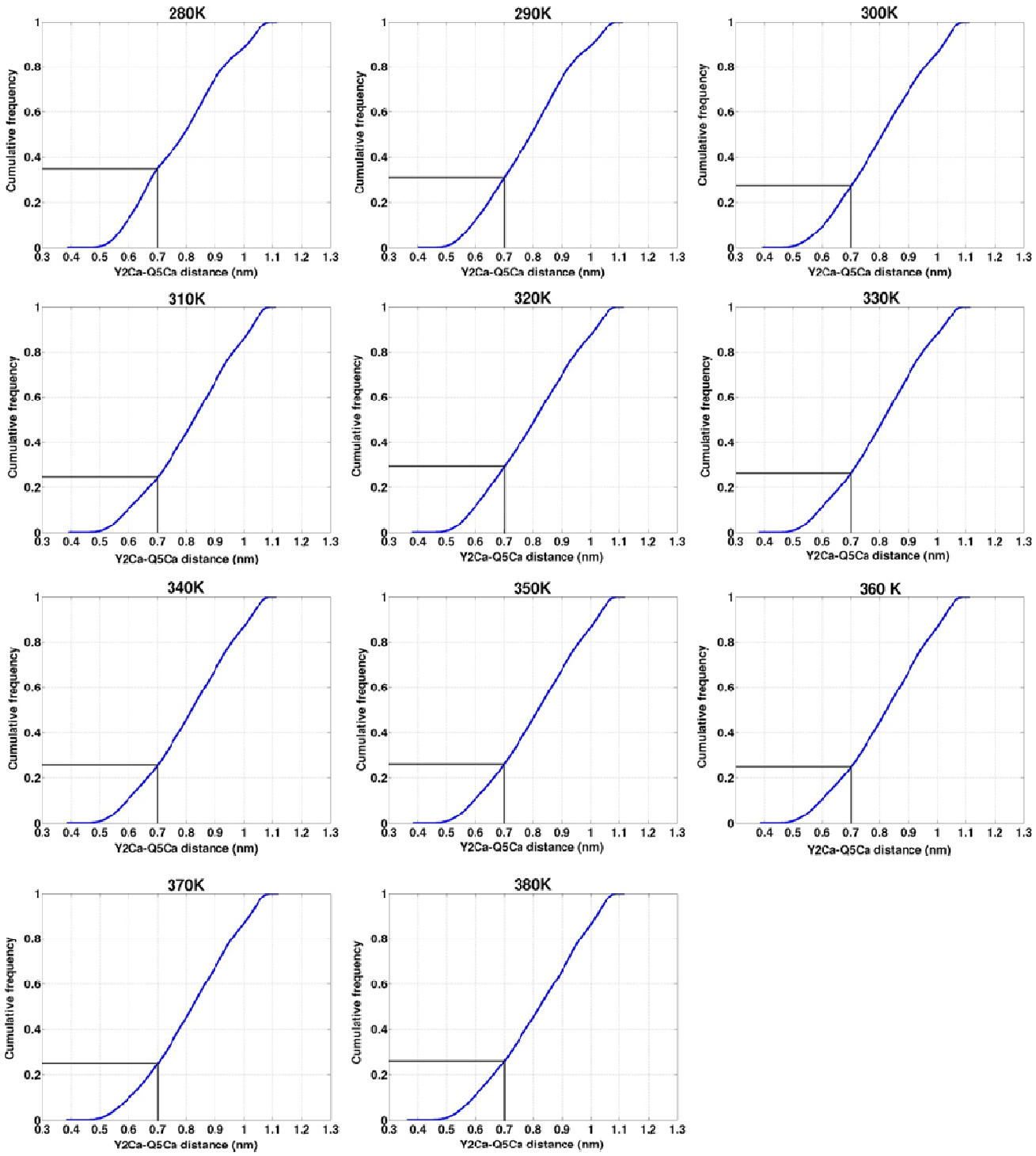

Figure S4 Cumulative frequency distribution of end-to-end distance at eleven simulation temperatures for the YKGQ peptide. Turn-like conformations (end-to-end distance < 0.7 nm) were observed to show relatively higher sampling at lower temperatures than at higher temperatures.

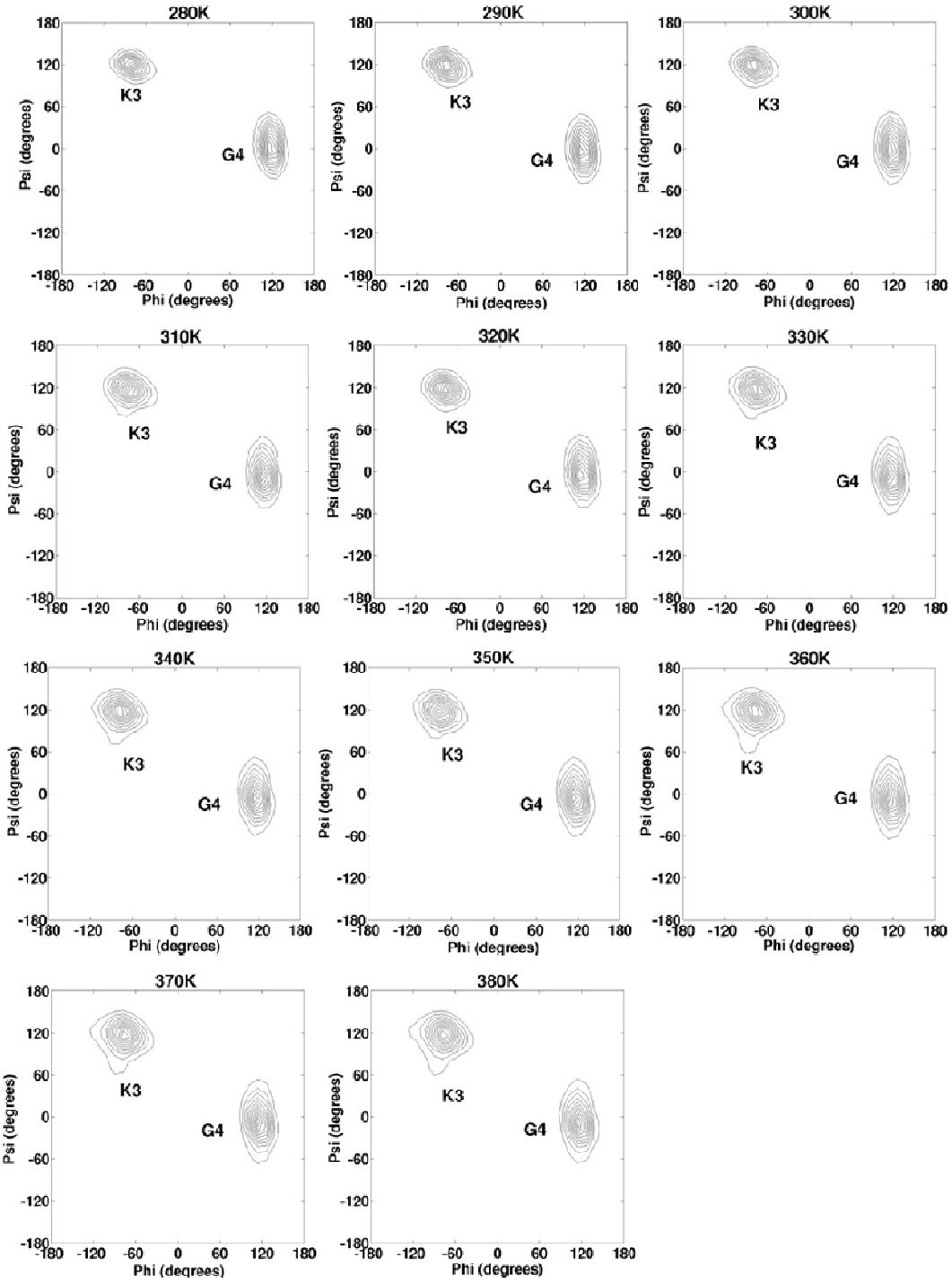

Figure S5 Probability contour plots (top ten contours shown exclusively for the turn ensemble) for backbone dihedral angles of corner residues, K3 and G4, at eleven simulation temperatures for the YKGQ peptide indicate a type II like β-turn formation.

Table S1 Observed fraction folded and calculated values of thermodynamic quantities $\Delta G_{U\rightarrow F}$, $\Delta S_{U\rightarrow F}$, $T\Delta S_{U\rightarrow F}$ and $\Delta H_{U\rightarrow F}$ at each corresponding temperature is listed below.

T (K)	**280**	**290**	**300**	**310**	**320**	**330**	**340**	**350**	**360**	**370**	**380**
Fraction folded	0.34	0.30	0.26	0.24	0.28	0.26	0.25	0.26	0.24	0.24	0.25
$\Delta G_{U\rightarrow F}$ (kJ/mol)	1.5	2.0	2.5	3.0	2.4	2.9	3.1	3.1	3.4	3.5	3.4
$\Delta S_{U\rightarrow F}$ (J/mol/K)	-35.0	-31.4	-27.9	-24.4	-20.8	-17.3	-13.7	-10.2	-6.7	-3.1	0.4
$T\Delta S_{U\rightarrow F}$ (kJ/mol)	-9.8	-9.1	-8.4	-7.5	-6.7	-5.7	-4.7	-3.5	-2.4	-1.2	0.1
$\Delta H_{U\rightarrow F}$ (kJ/mol)	-8.1	-7.1	-6.0	-5.0	-4.0	-2.7	-1.5	-0.3	0.9	2.2	3.6

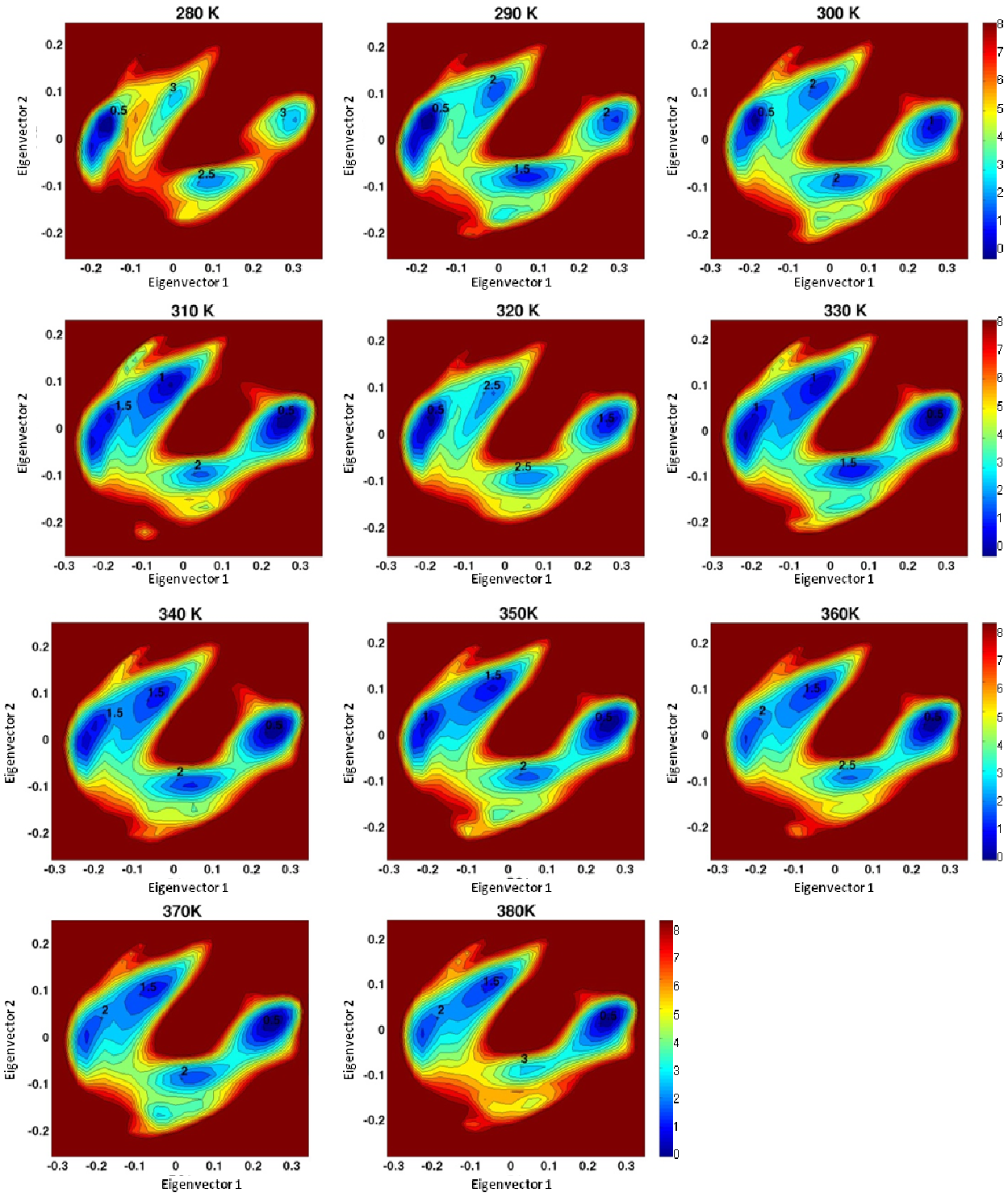

Figure S6 Free energy landscapes of the peptide YKGQ for all eleven simulations at different temperatures. Free energy is in kJ/mol in all the plots.

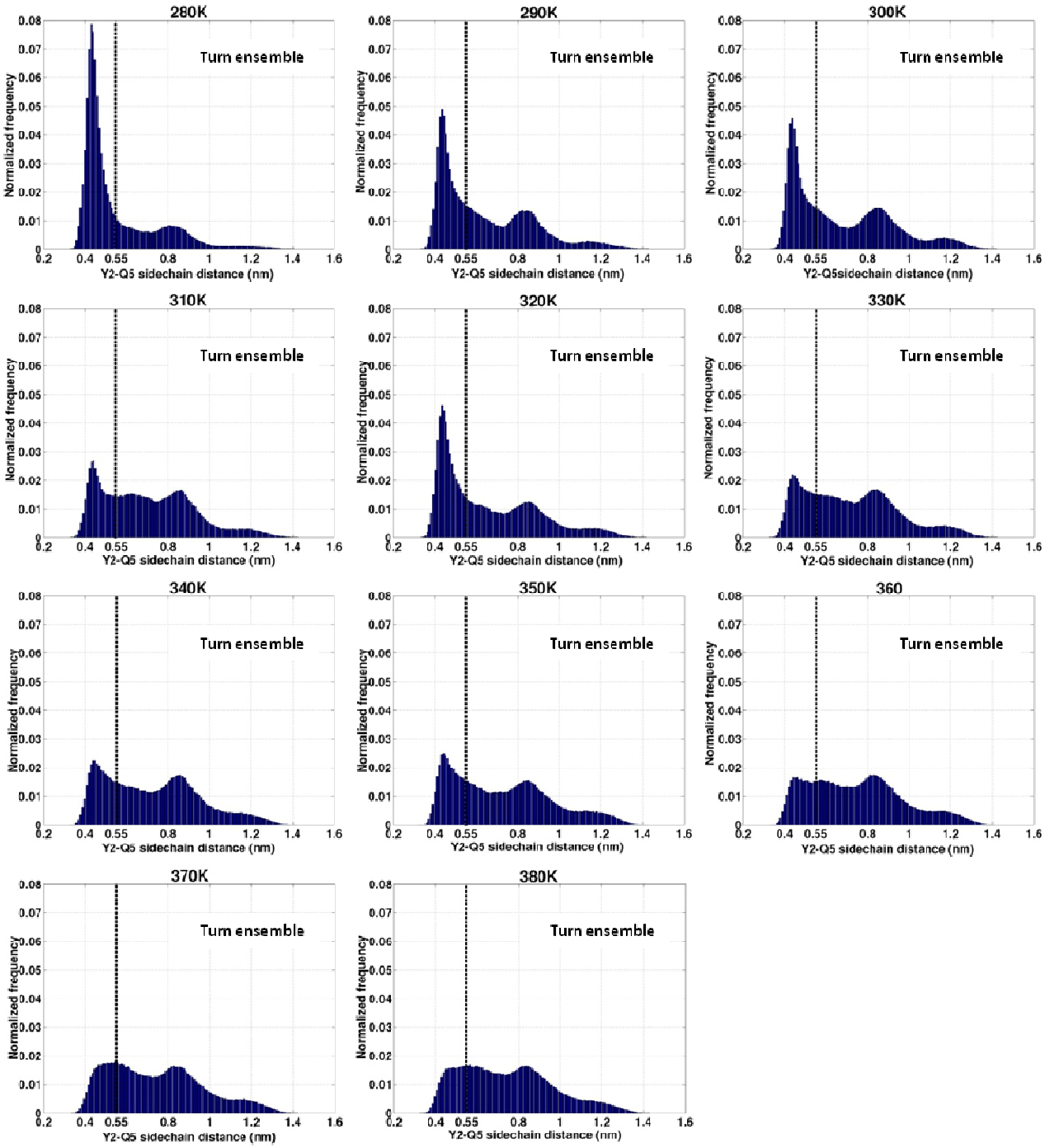

Figure S7 Y2-Q5 side-chain distance distribution in turn and unfolded ensemble at eleven simulation temperatures. Percentage of frames sampling Y-Q side-chain association (Y2-Q5 side-chain distance ≤ 0.55nm) is significantly smaller in unfolded ensemble than the turn ensemble, suggesting Y-Q side-chain association stabilizes turn formation in YKGQ.

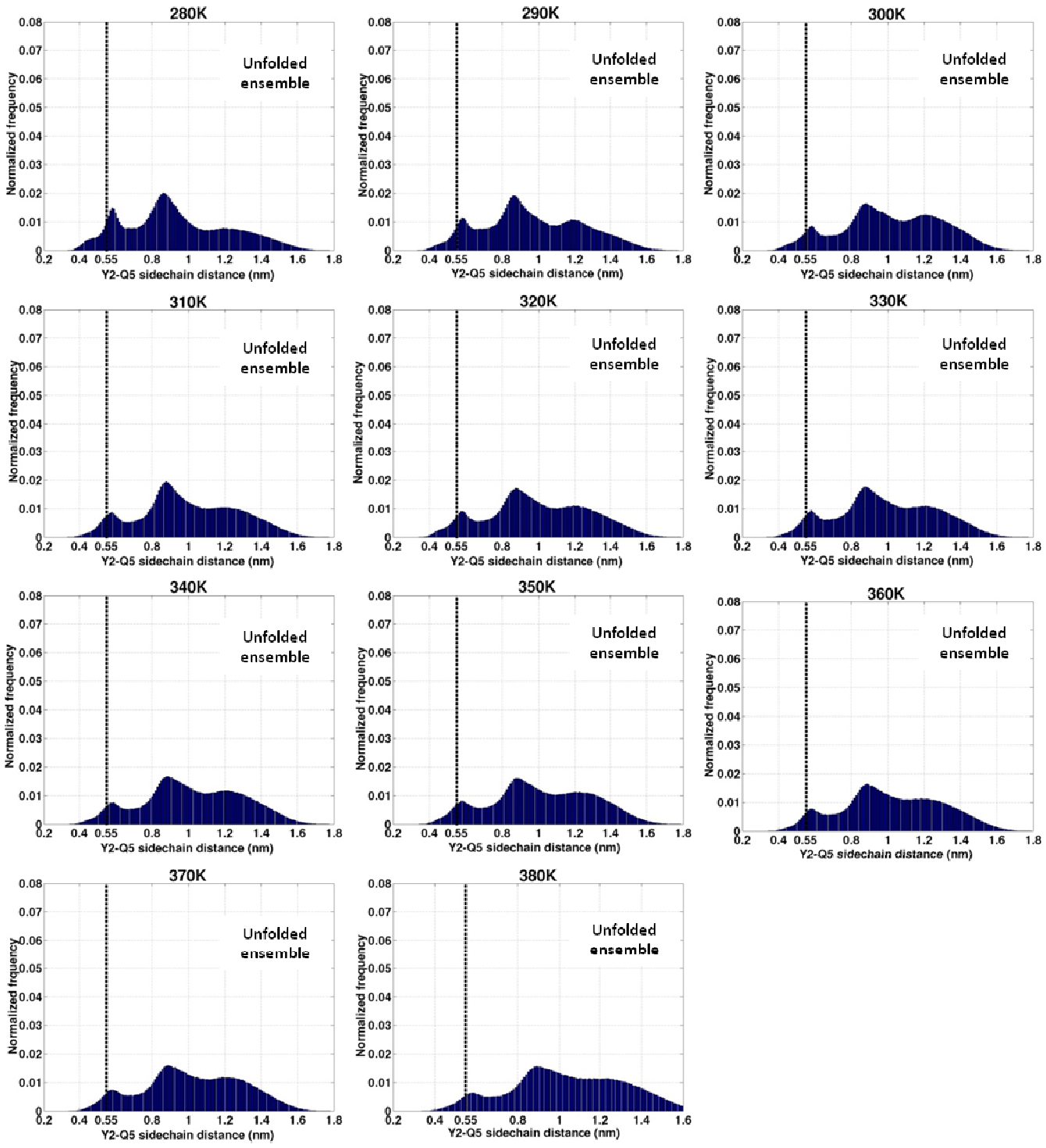

Figure S7 Contd…

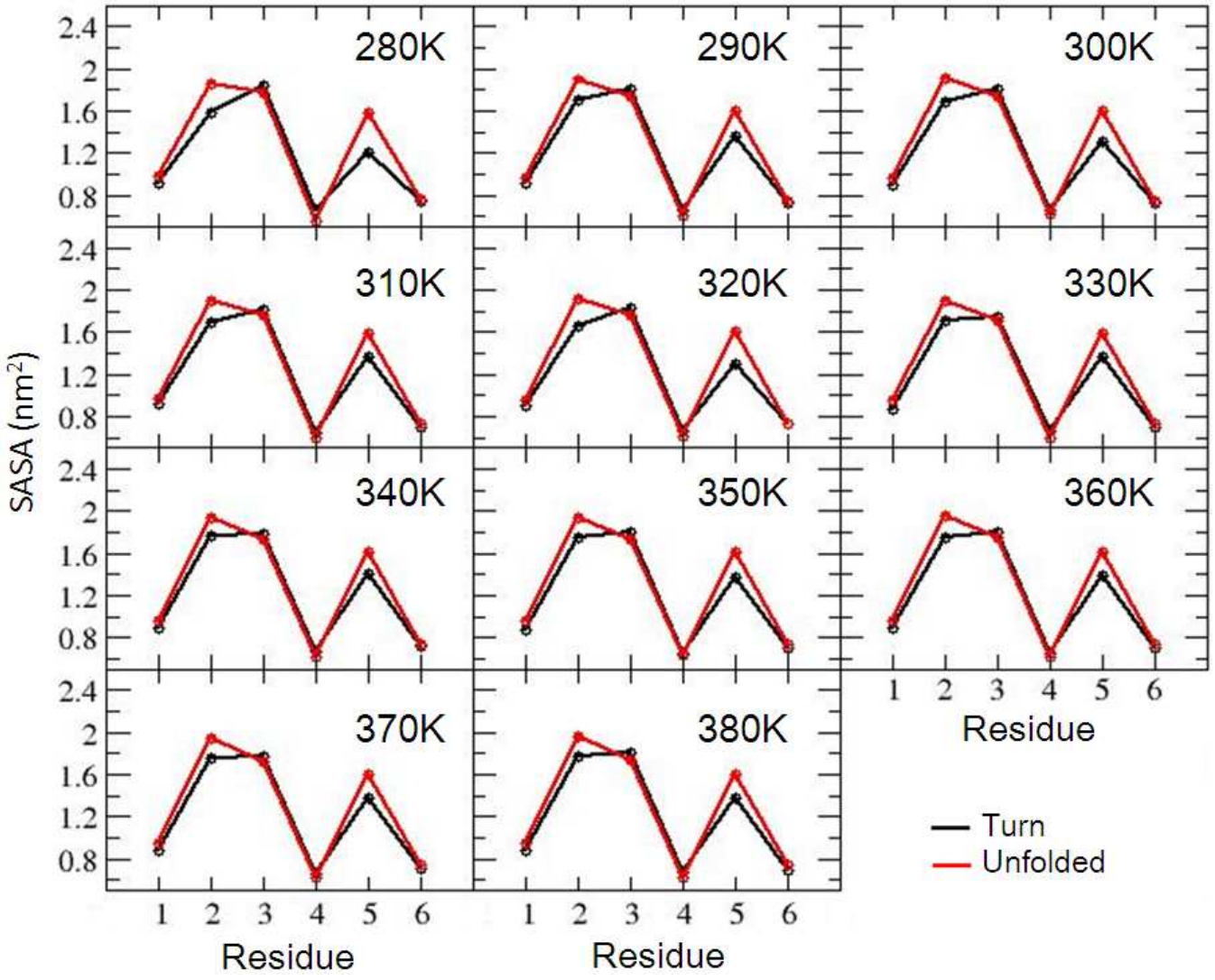

Figure S8 Solvent accessible surface area (SASA) of each residue in turn and unfolded ensembles at eleven simulation temperatures. Y2 andQ5 undergo relative burial upon turn formation. Change in SASA upon turn formation was observed to be higher at lower temperatures, in correspondence to stronger Y-Q association at lower temperatures. K3 remains solvent exposed at all temperatures, irrespective of the conformation sampled by the peptide.

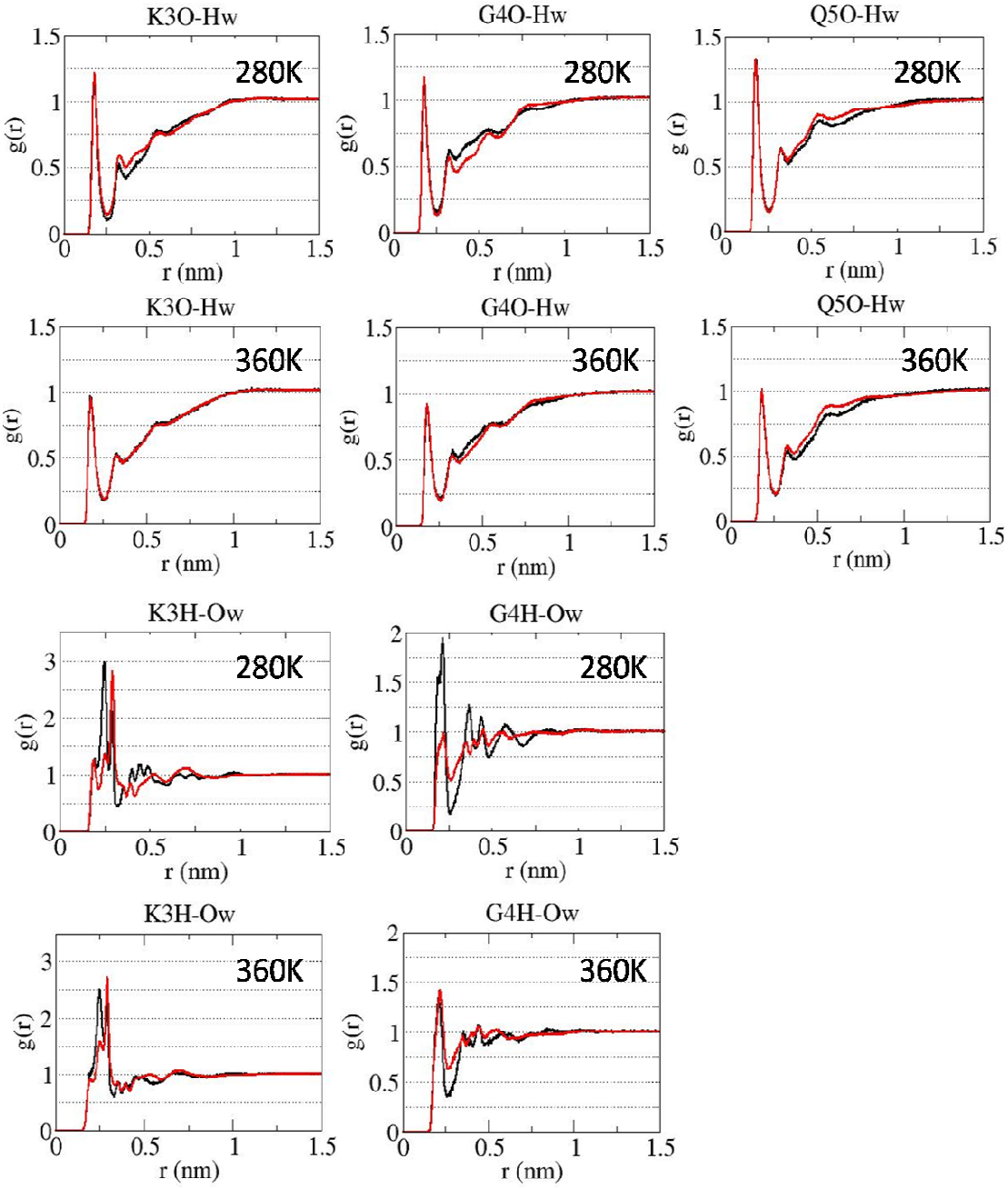

Figure S9 Radial distribution function (RDF) of the water atoms around YKGQ peptide backbone atoms atom 280 K and 360 K, respectively. RDF of the water hydrogen atoms around backbone carbonyl oxygen (CO-H_w) and water oxygen atoms around backbone amide hydrogen (NH-O_w) of K3, G4 and Q5 for the peptide YKGQ. Black and Red curve represent RFD for turn and unfolded conformational ensemble, respectively.

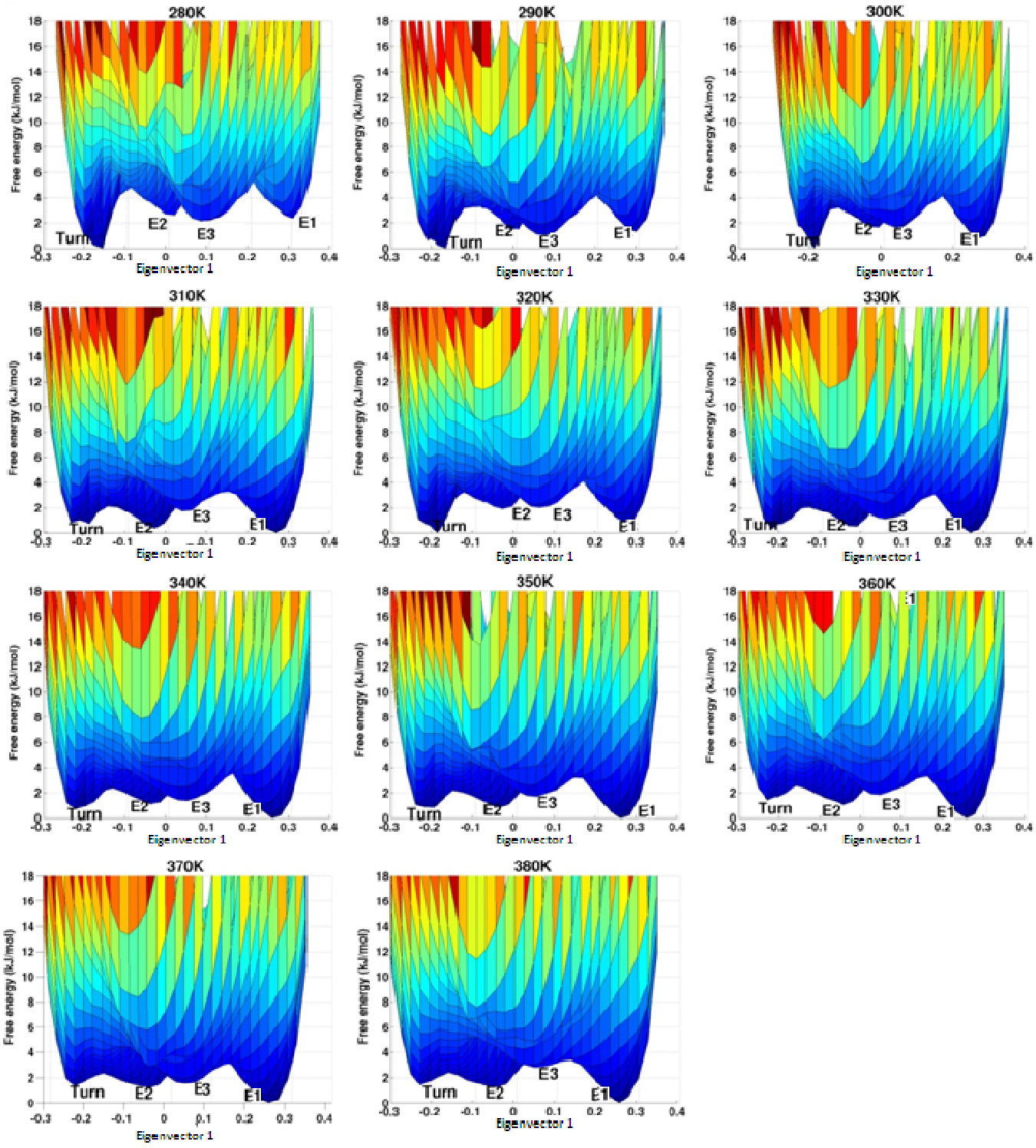

Figure S10 Projection of free energy surface on eigenvector 1 for all eleven temperature simulations for the peptide YKGQ.

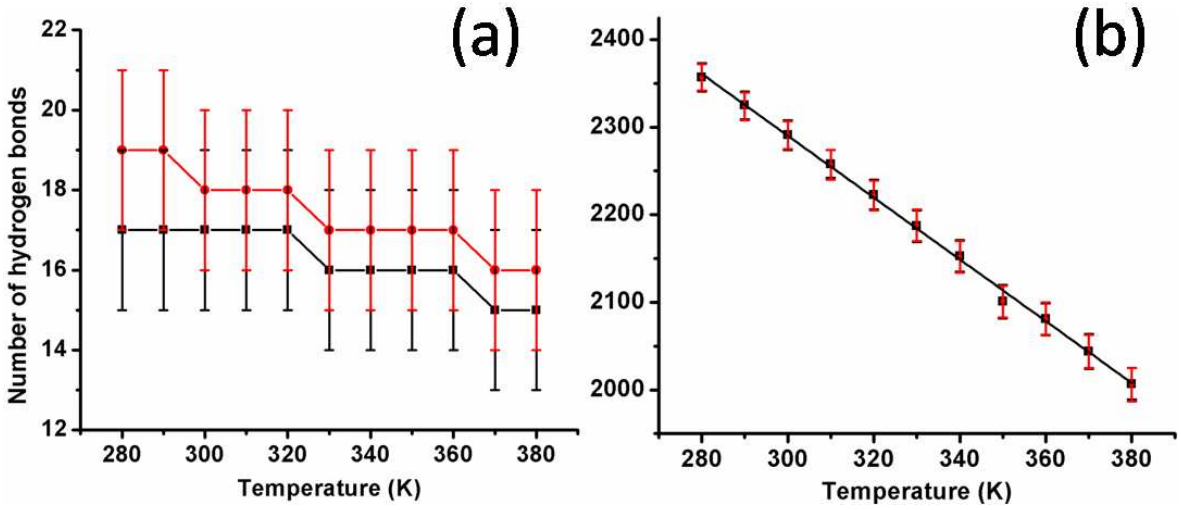

Figure 11 Variation of number of (a) peptide-water hydrogen bonds and (b) water-water hydrogen bonds, for folded (black) and unfolded (red) conformational ensembles, with change in temperature. Standard deviation at each temperature is shown as bars.