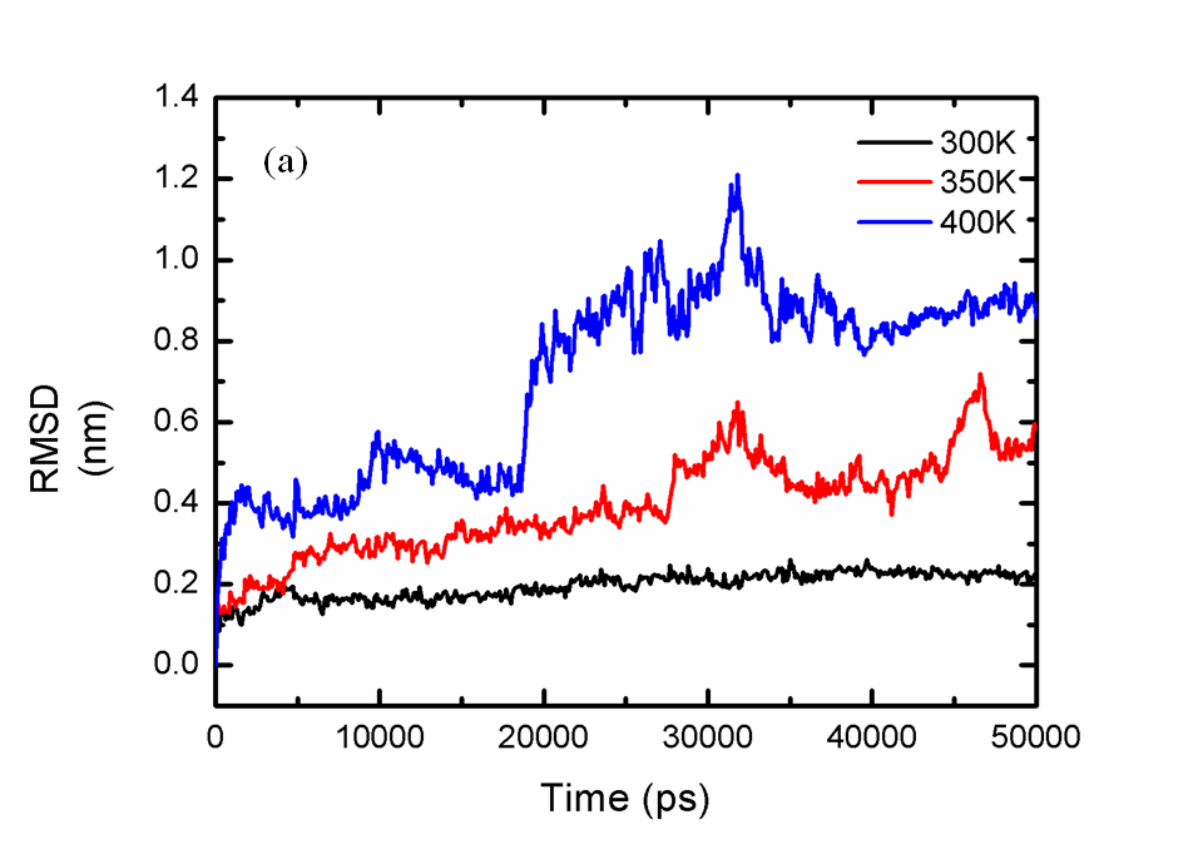
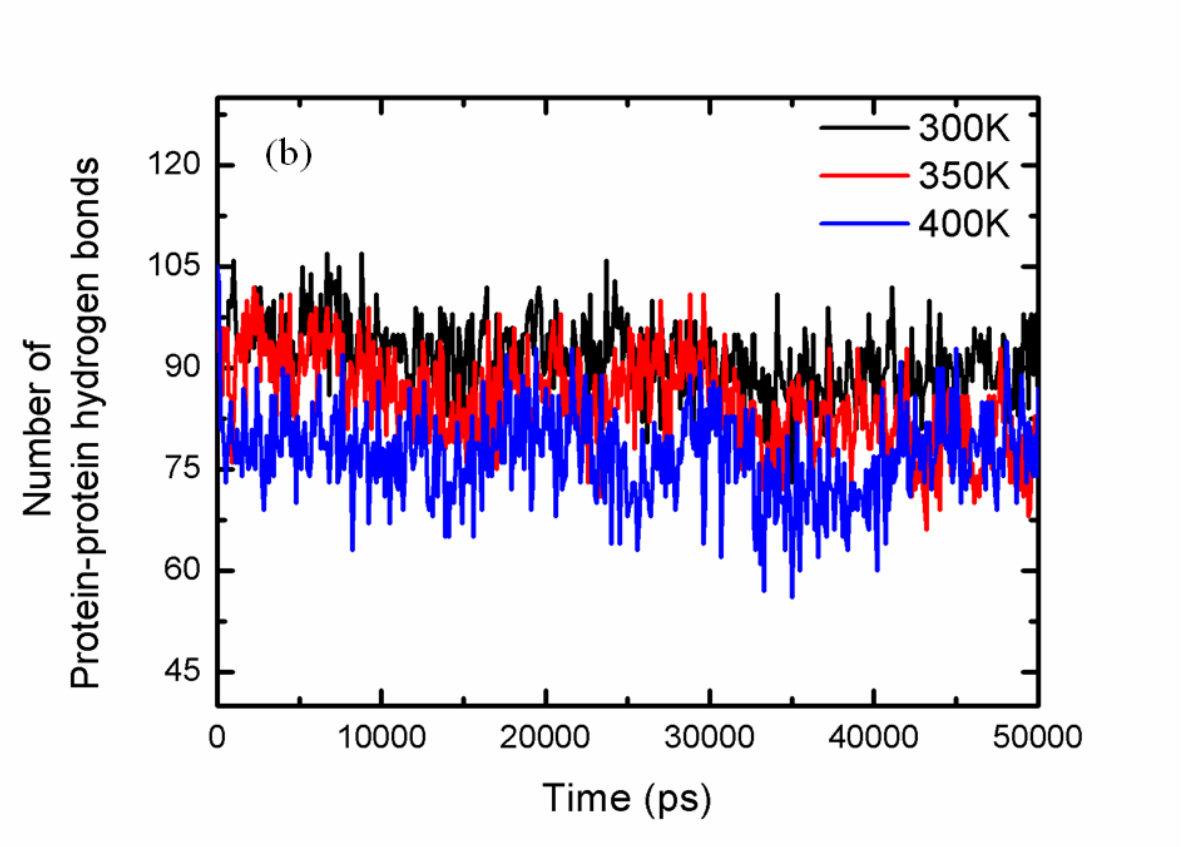
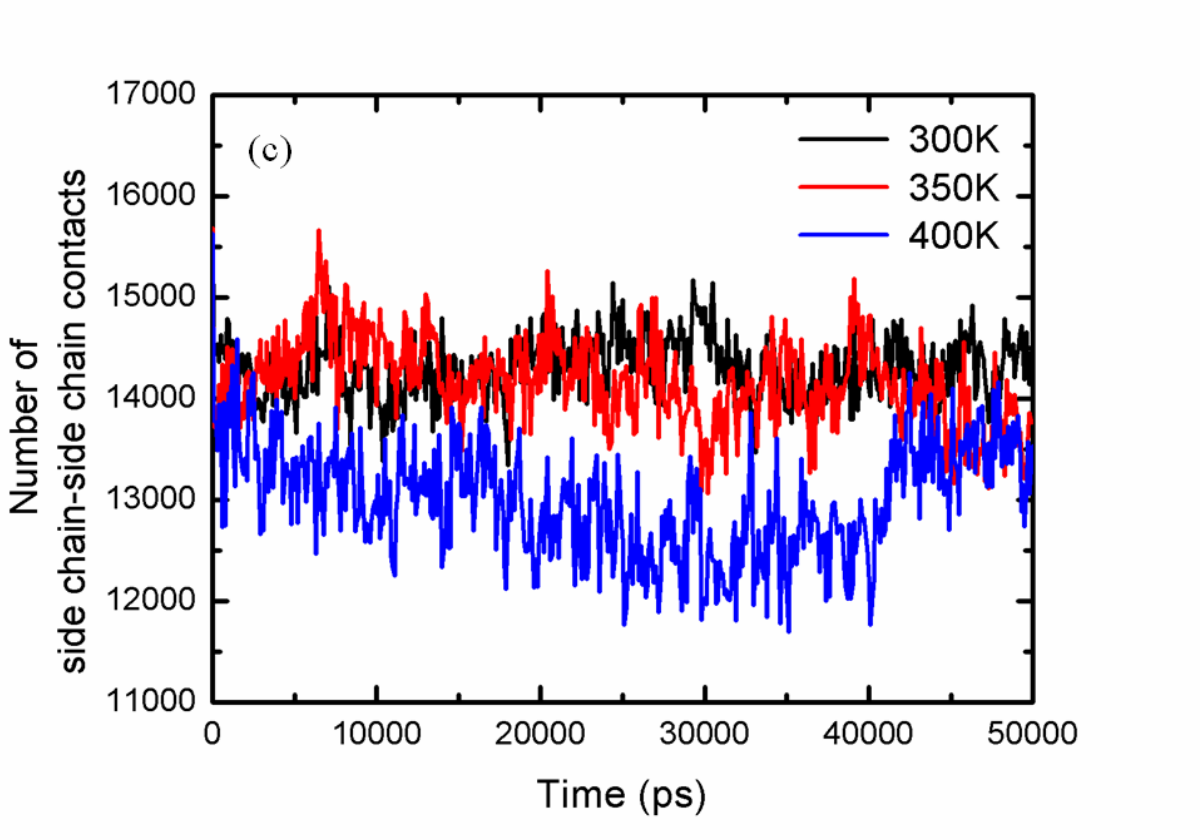
Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.



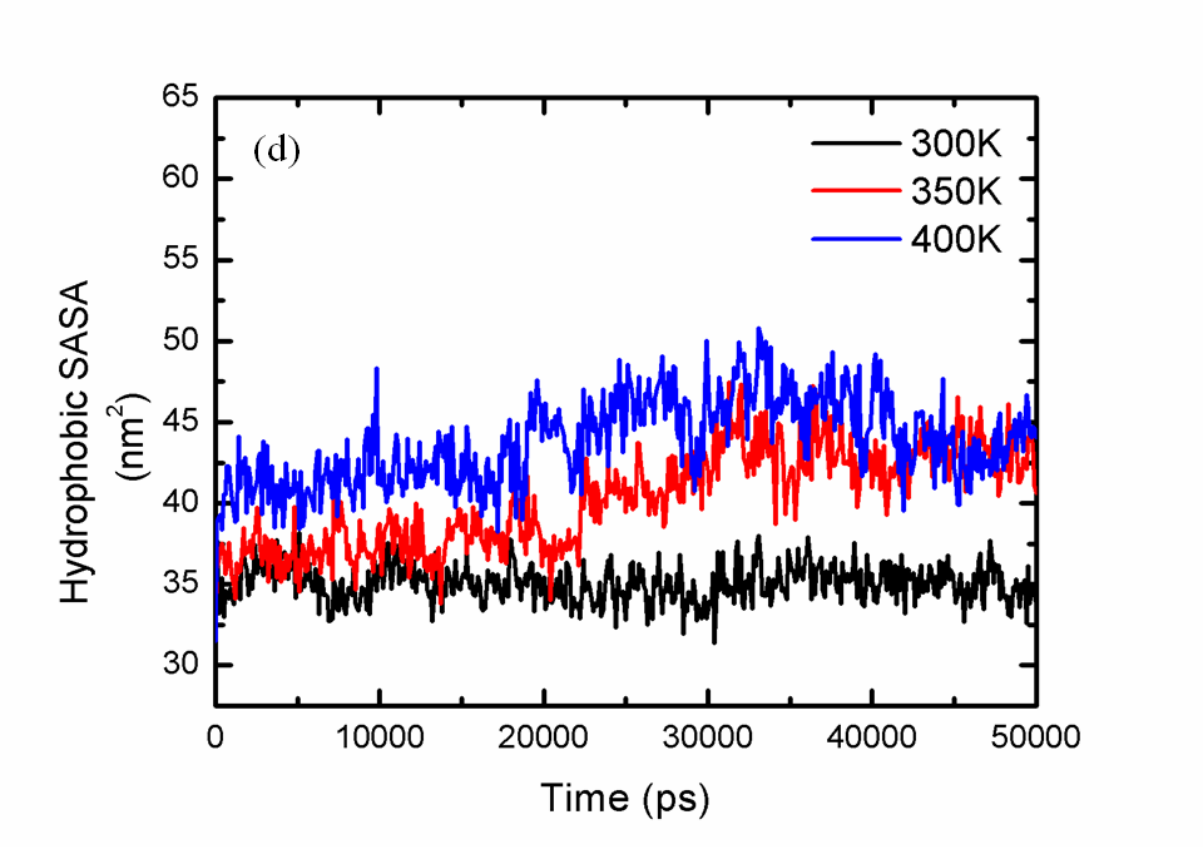
SI Fig.S1(a): Time variation of RMSD of C-alpha atoms from the first time frame as the reference structure at 300 K (black), 350 K (red) and 400 K (blue).



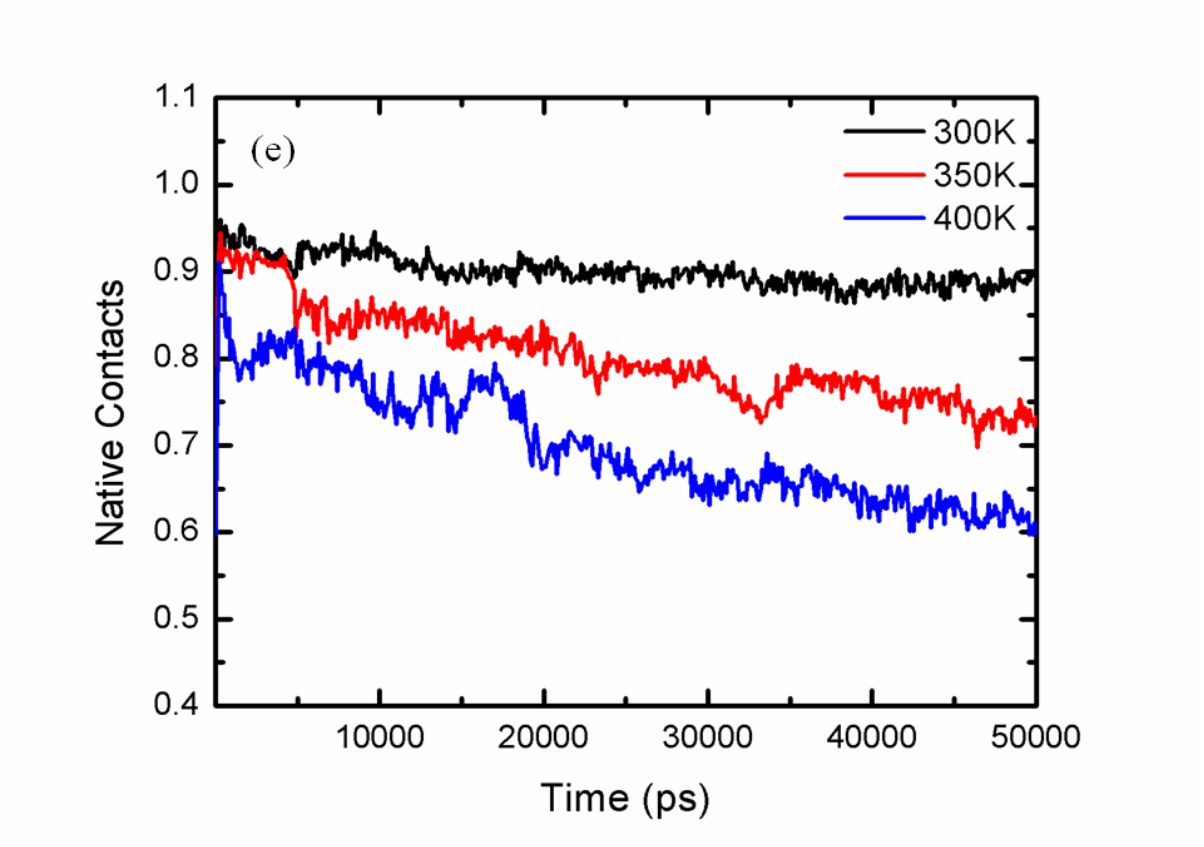
SI Fig.S1(b): Time variation of number of intra-protein hydrogen bonds at 300 K (black), 350 K (red) and 400 K (blue).



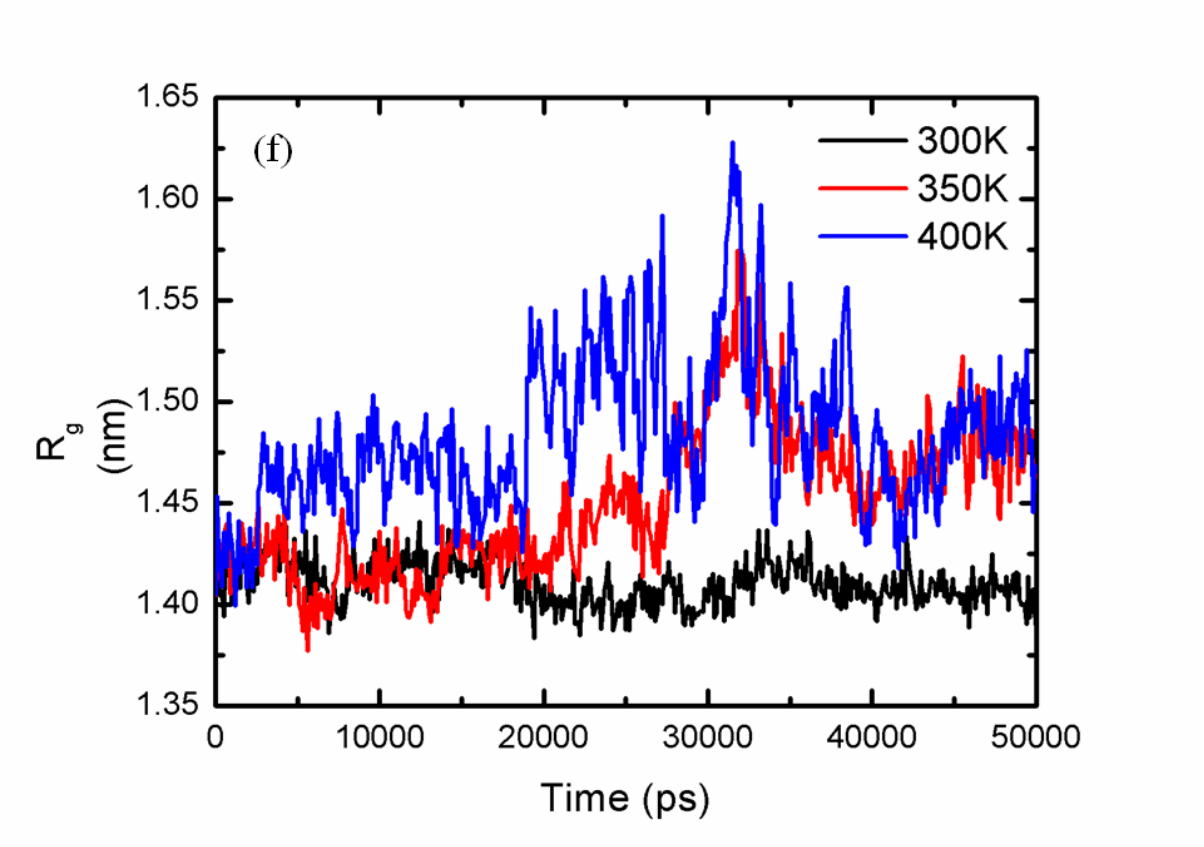
SI Fig.S1©: Time variation of number of side chain- side chain contacts at 300 K (black), 350 K (red) and 400 K (blue).



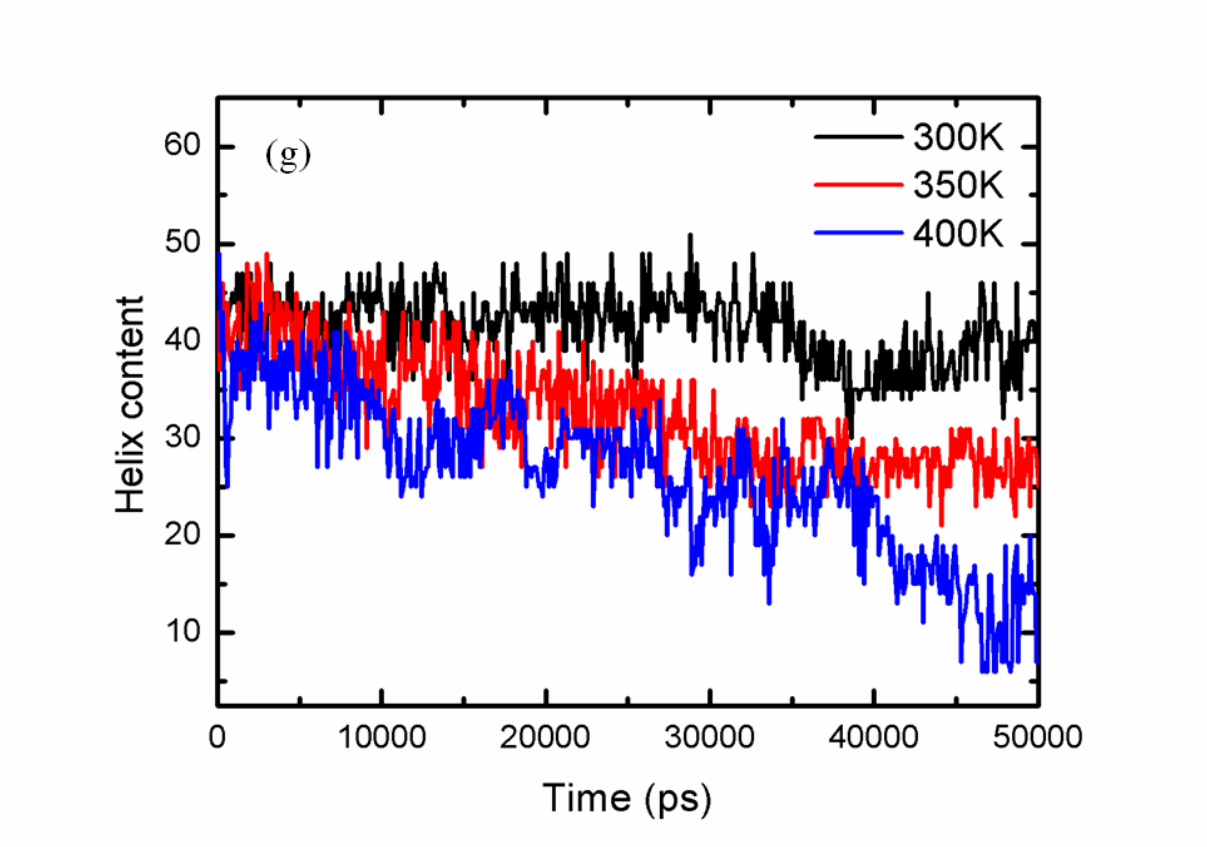
SI Fig.S1(d): Time variation of hydrophobic solvent accessible surface area at 300K (black), 350K (red) and 400K (blue).



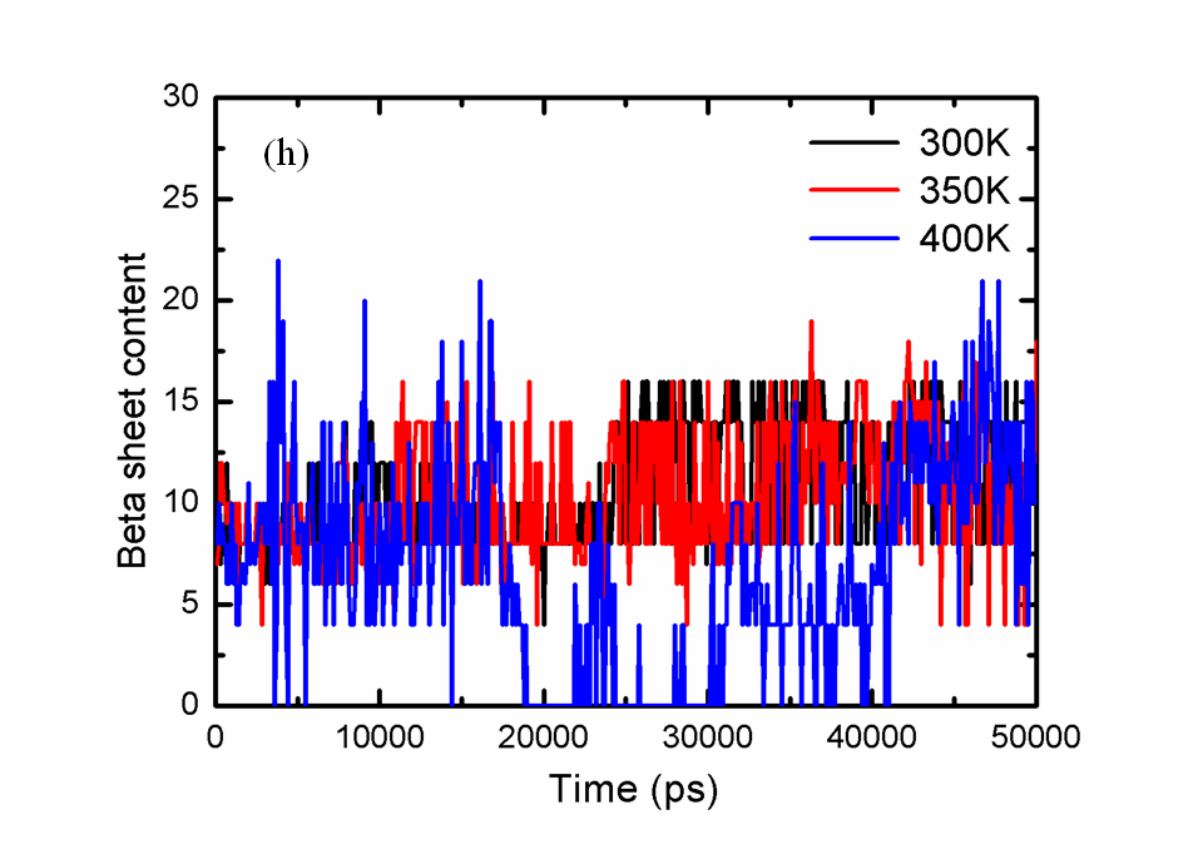
SI Fig.S1(e): Time variation of fraction of native contacts retained at 300 K (black), 350 K (red) and 400 K (blue). Value of 1 signifies that the frame under consideration has all the contacts present in reference native structure.



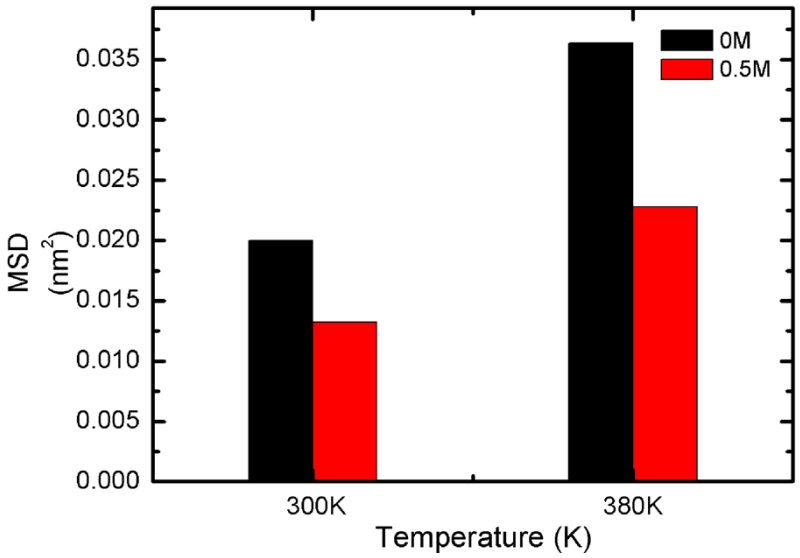
SI Fig.S1(f): Time variation of radius of gyration of protein at 300 K (black), 350 K (red) and 400 K (blue).



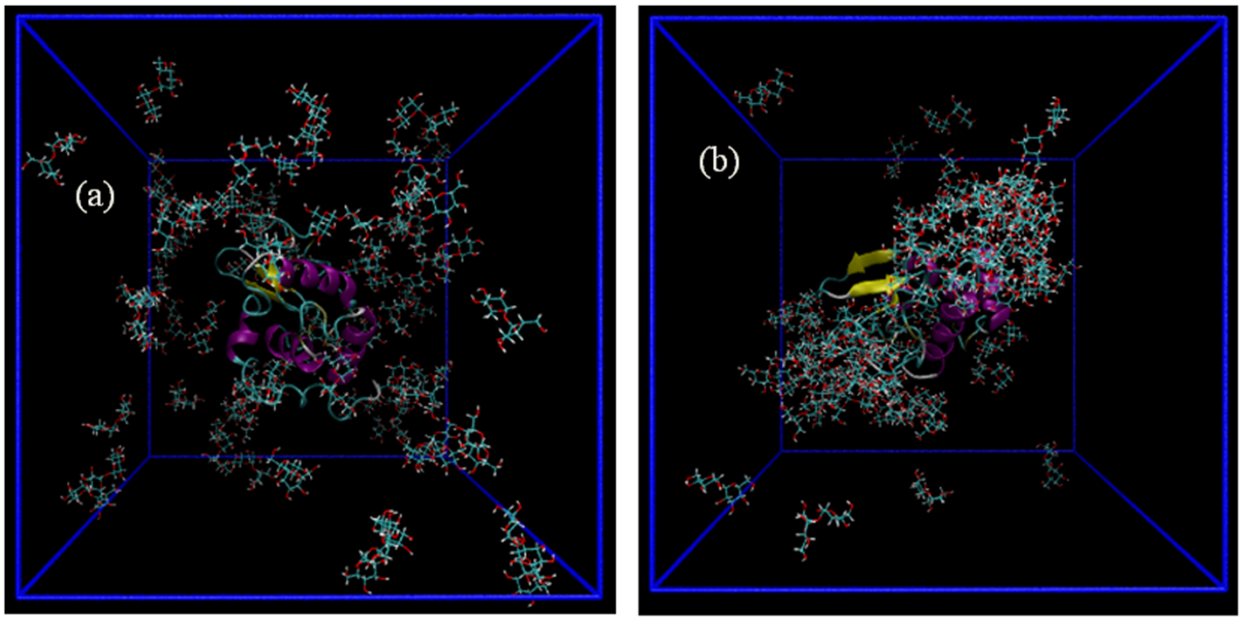
SI Fig.S1(g): Time variation of alpha helical content (using DSSP algorithm) at 300 K (black), 350 K (red) and 400 K (blue).



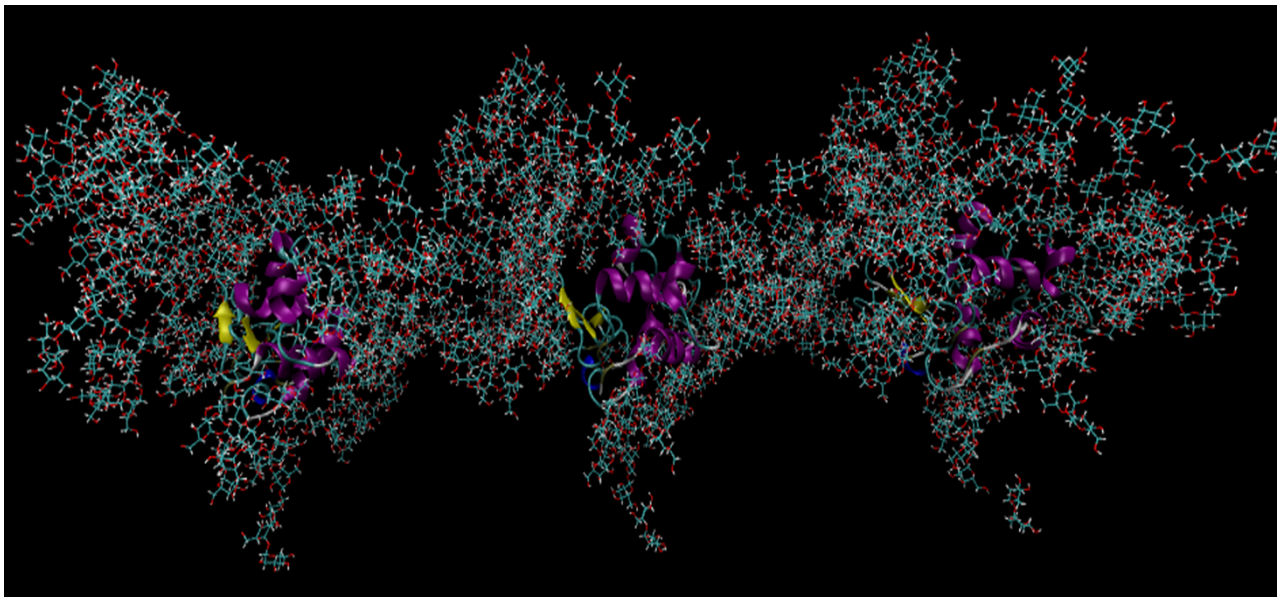
SI Fig.S1(h): Time variation of beta sheet content (using DSSP algorithm) at 300 K (black), 350 K (red) and 400 K (blue).



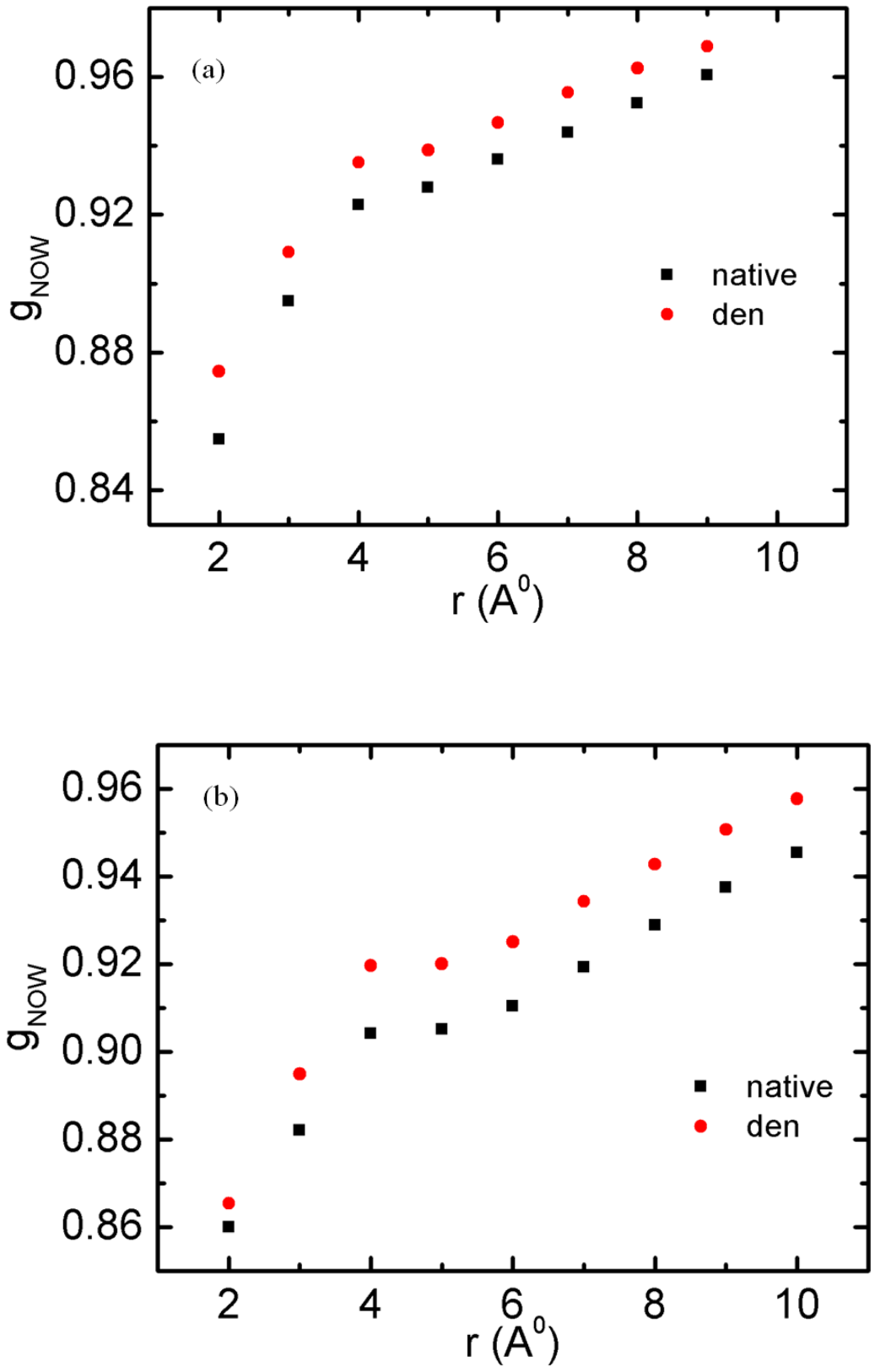
SI Fig S2: Mean square displacement of lysozyme hydrogen atoms at 300 K and 380 K in absence and presence of 0.5 M Trehalose



SI Fig. S2: Snapshots of system containing protein in 0.3 M trehalose solution at (a) 1 ns (b) 50 ns at 300 K. Protein is shown in secondary structure representation and trehalose molecules are depicted in line representation.



SI Fig. S3: Trehalose protein percolating cluster that transcends the borders of periodic simulation cell at 0.5 M trehalose concentration. Trehalose molecules are shown in lines representation and protein molecules in secondary structure representation.



SI Fig. S4: Plot of g_{NOW} versus distance for native and denatured state (den) of protein at 300K in the presence of (a) 0.05 M (b) 0.1 M trehalose.