

# Supplementary Information for

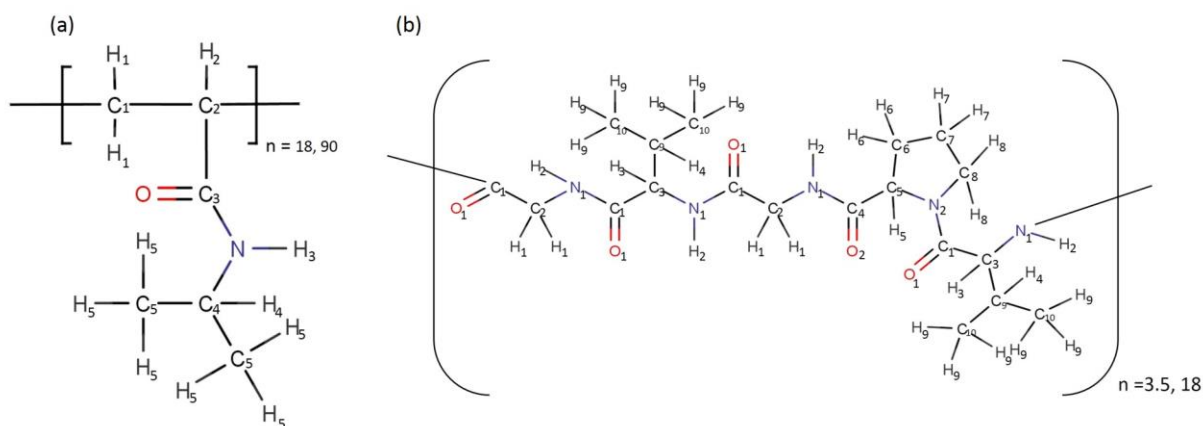
## A comparison between the Lower Critical Solution Temperature behavior of polymers and biomacromolecules

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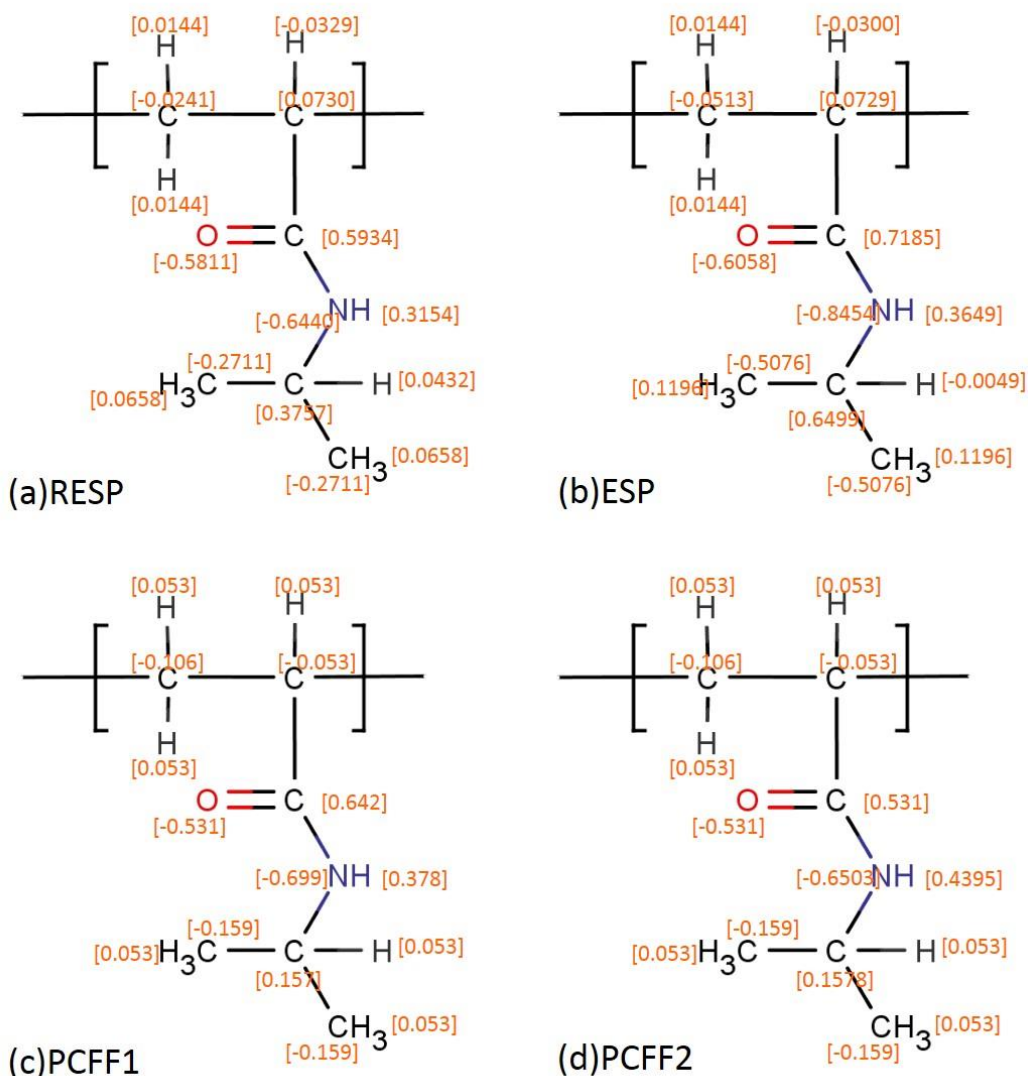
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**Figure S1.** Chemical structure of (a) PNIPAM monomer and (b) (VPGVG) ELPs.

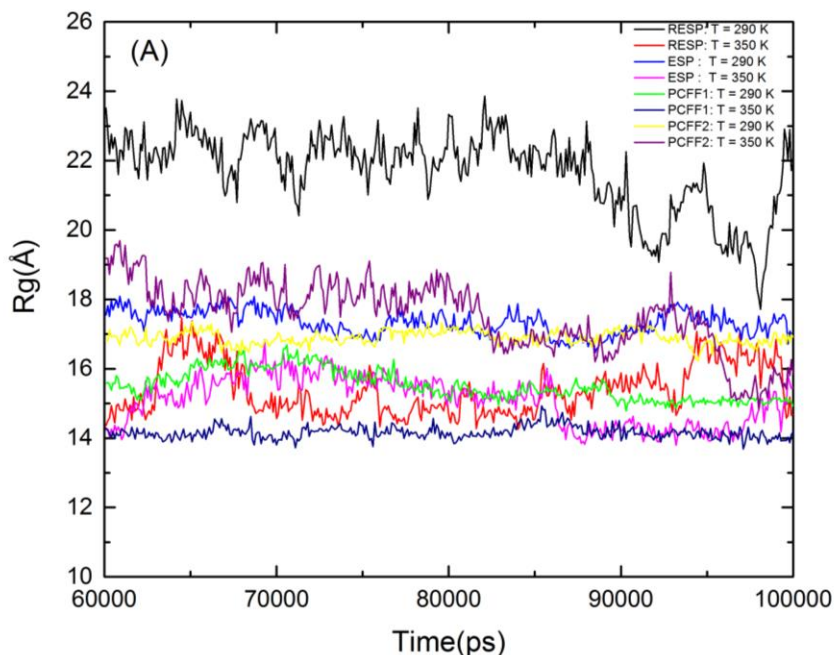
### Calculations of Partial Charges on PNIPAM:

Hydrogen bonding is known to play an important role in assisting the LCST transition in thermo-sensitive polymers.<sup>1-4</sup> To explore the role of hydrogen bonding between polymer and water and polymer and polymer in determining the LCST transition, we simulated the PNIPAM system with four different partial charges, in presence of TIP3P water model. Thus by keeping rest of the force-field parameters the same we could alter the extent and strength of hydrogen bonding between polar groups of PNIPAM. To calculate the partial charges we have implemented following methods: These partial charges were obtained from (I) The Restrained Electrostatic Potential (RESP) method, (II) Electrostatic Potential (ESP) method, (III) polymer consistent force-field (PCFF) parameters from reference<sup>5</sup> and (IV) Original PCFF force-field.<sup>6</sup> Figure S2 shows the different partial charges calculated from these methods.

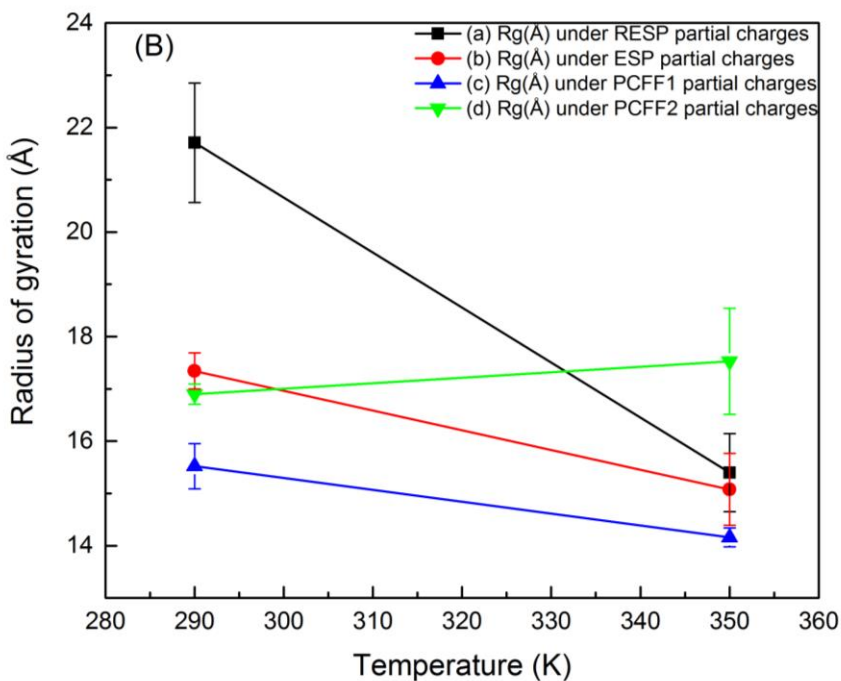


**Figure S2.** Partial charges calculated using different methods or different force field.

Previous experimental and computations studies show a clear difference in the  $R_g$  of PNIPAM chains as they undergo LCST transition.<sup>5, 7-9</sup> Hence, to choose the optimum set of partial charges we have calculated the radius of gyration ( $R_g$ ) of 90-mer of PNIPAM. The  $R_g$  can be used to analyze the structural evaluation of polymer chains.



**Figure S3(A).**  $R_g$  for 90-mer of PNIPAM for last 40 ns. The difference in the average  $R_g$  values calculated at 290 K and 350 K for systems (a), (b), (c), and (d) are 6.3 Å, 2.3 Å, 1.4 Å, and 0.6 Å as shown in Figure S3 (B), respectively. Therefore based on the difference in the  $R_g$  values calculated below and above the LCST of PNIPAM, namely at 290 K and 350 K, we chose a simulation trajectory where partial charges on PNIPAM were calculated by using method (I) Restrained Electrostatic Potential (RESP) method.



**Figure S3(B).** Radius of gyration are applied to 90mer PNIPAM based on different RESP and ESP partial charges for Temperature  $T=290$  K and  $T=350$  K. (a) RESP, (b) ESP, (c) PCFF1, (d) PCFF2 in Figure S3(B).

**Table S1:** Partial charges for PNIPAM and (VPGVG)<sub>n</sub> ELPs obtained from AMBER force-field

Partial charges of PNIPAM												
Atom	C1	C2	H1	H2	C3	O	N	H3	C4	H4	C5	H5
Partial Charges	-0.0241	0.0730	0.0144	-0.0329	0.5934	-0.5811	-0.6440	0.3154	0.3757	0.0432	-0.2711	0.0658
Partial charges of VPGVG												
Atom	C1	C2	O1	N1	H1	H2	C3	H3	C4	O2	N2	C5
Partial Charges	0.5973	-0.0252	-0.5679	-0.4157	0.0698	0.2719	-0.0875	0.0969	0.5896	-0.5748	-0.2548	-0.0266
Atom	C6	C7	C8	C9	C10	H4	H5	H6	H7	H8	H9	
Partial Charges	-0.0070	0.0189	0.0192	0.2985	-0.3192	-0.0297	0.0641	0.0253	0.0213	0.0391	0.0791	

**Polymer Relaxation Time:**

To confirm the convergence of the polymer chains we analyzed the orientational relaxation of backbone carbon-carbon bonds.<sup>10</sup> To calculate orientational relaxation a unit vector  $\hat{\mathbf{b}}_i$  was assigned along each C-C bond in the backbone of PNIPAM (CH<sub>2</sub>-CH bond) and ELPs (C<sub>α</sub>-C<sub>α</sub> bond) as well as a second unit vector  $\hat{\mathbf{d}}_i$  that is normal to each pair of adjacent skeletal bonds, originating at their common C atom. The vectors  $\hat{\mathbf{b}}_i$  and  $\hat{\mathbf{d}}_i$  were calculated by using following equation:

$$\hat{\mathbf{b}}_i = \frac{\mathbf{r}_{i+1} - \mathbf{r}_i}{|\mathbf{r}_{i+1} - \mathbf{r}_i|} \quad \text{Eq. S1}$$

$$\hat{\mathbf{d}}_i = \frac{\hat{\mathbf{b}}_{i+1} \times \hat{\mathbf{b}}_i}{|\hat{\mathbf{b}}_{i+1} \times \hat{\mathbf{b}}_i|} \quad \text{Eq. S2}$$

Where  $\hat{\mathbf{d}}_i$  = out-of-plane vector.<sup>11</sup>

The time evolution of these two types of vectors was followed by constructing time autocorrelation functions in terms of the first ( $\mathbf{P}_1$ ) and second order ( $\mathbf{P}_2$ ) Legendre polynomials of the first kind. The  $\mathbf{P}_1$  and  $\mathbf{P}_2$  can be represented as:

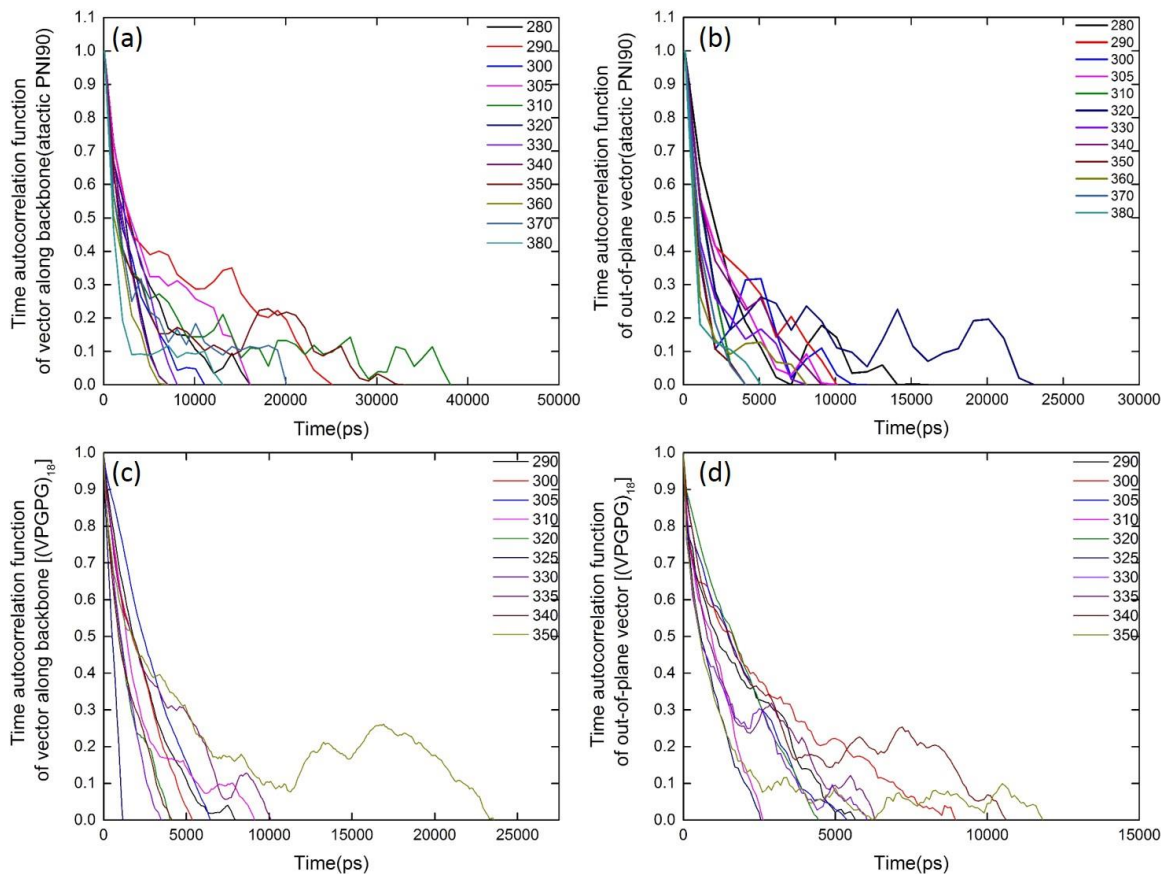
$$\mathbf{P}_1(t; \hat{\mathbf{u}}_i) = \cos \beta \quad \text{Eq. S3}$$

$$\mathbf{P}_2(t; \hat{\mathbf{u}}_i) = \frac{1}{2} [3 \cos^2 \beta - 1] \quad \text{Eq. S4}$$

$$\cos \beta = \hat{\mathbf{u}}_i(t) \cdot \hat{\mathbf{u}}_i(0) \quad \text{Eq. S5}$$

Essentially, parameters  $\mathbf{P}_1$  and  $\mathbf{P}_2$  shown in equation S3 and S4, respectively, provide an idea of the rate at which bonds lose memory of their orientation through thermal motion. Figure S4 (a) and (c) shows the  $\mathbf{P}_2$  that is calculated by averaging over all backbone bonds in a given bin. The local reorientational tendencies of the out-of-plane vectors are represented in terms of the autocorrelation

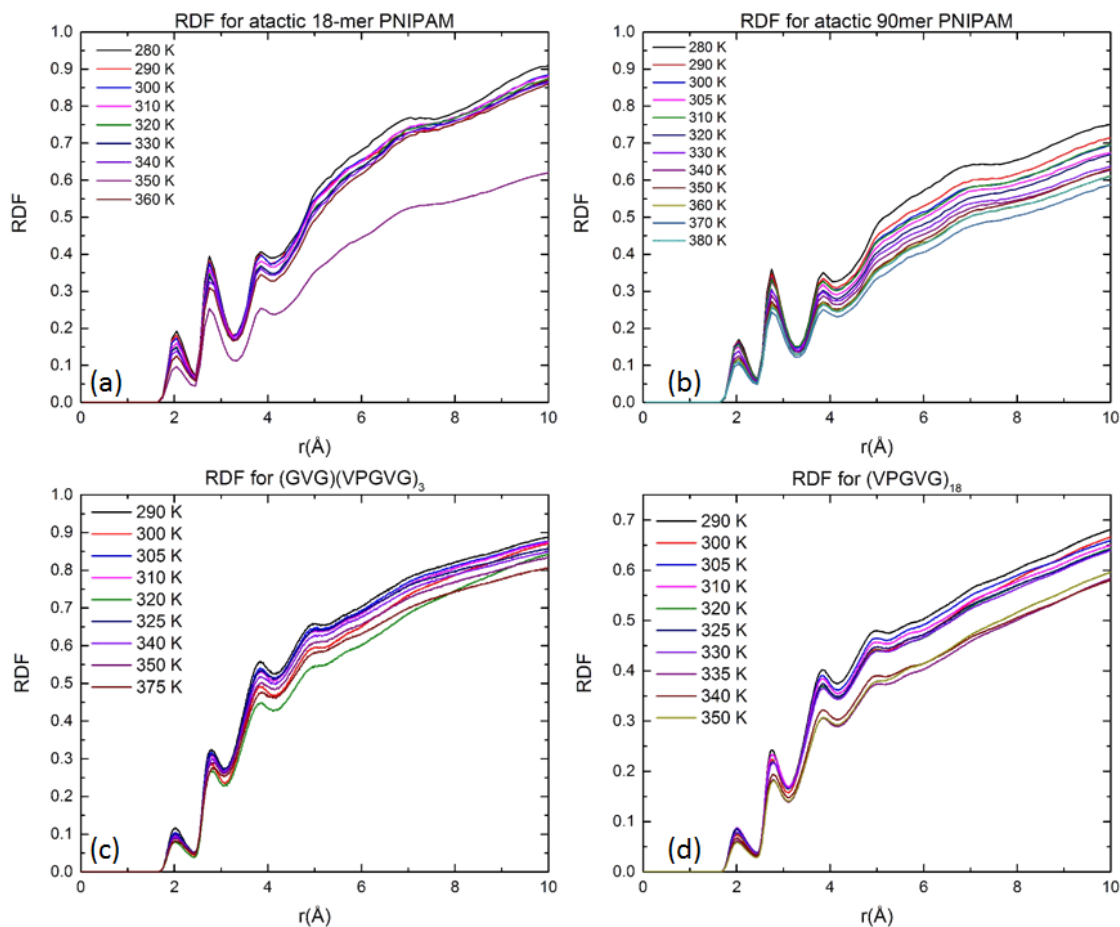
function  $P_1$  in Figure S4 (b) and S4 (d) for PNIPAM and (VPGVG)<sub>n</sub> ELPs, respectively. Based on this we can estimate the relaxation time of  $P_1$  for PNIPAM backbone vectors from the time autocorrelation profiles which is less than 40 ns. Similarly for (VPGVG)<sub>n</sub> ELPs the relaxation time of 30 ns can be estimated from Figure S4 (c) and (d).



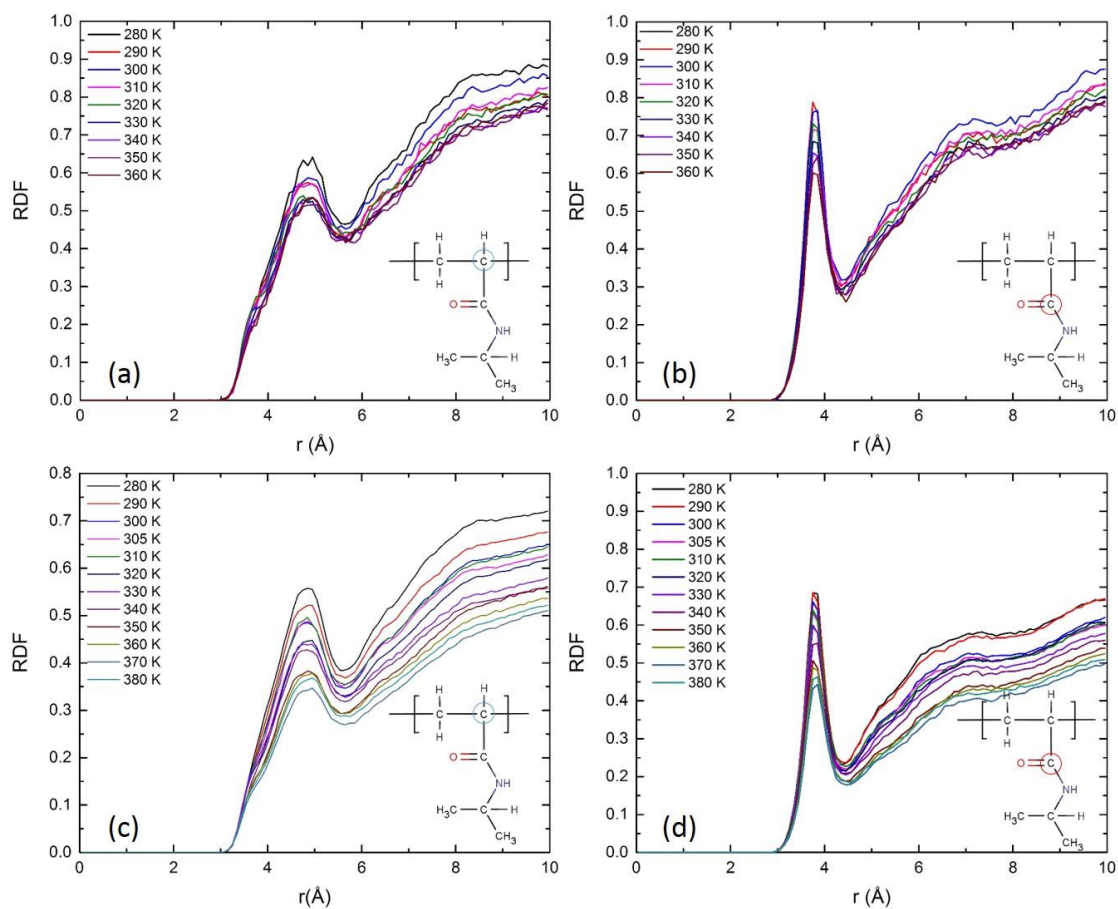
**Figure S4.** Time autocorrelation function of polymer backbone C1- C2 bond vectors: (a) and (c) unit vector along backbone C1- C2 bond; (b) and (d) unit vector out of plane.

### Radial Distribution Function (RDF):

Figure S5, S6, S7, and S8 show the RDF of PNIPAM and (VPGVG)<sub>n</sub> ELPs with water molecules at all simulated temperature.

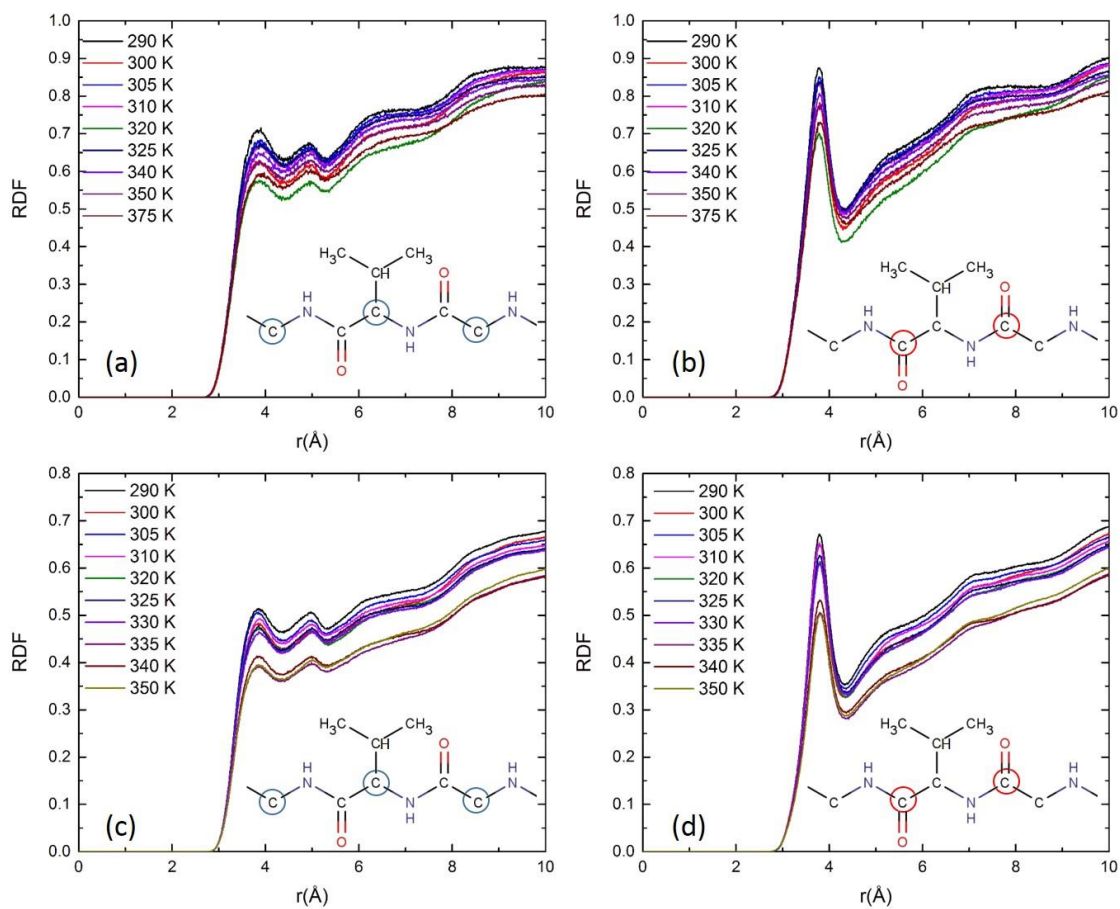


**Figure S5.** Radial Distribution Function between hydrophilic group of ELP or PNIPAM to oxygen of water. (a)RDF for 18-mer PNIPAM; (b) RDF for 90-mer PNIPAM; (c) RDF for 18-mer ELP (GVG(VPGVG)<sub>3</sub>); (d) RDF for 90-mer ELP ((VPGVG)<sub>18</sub>).



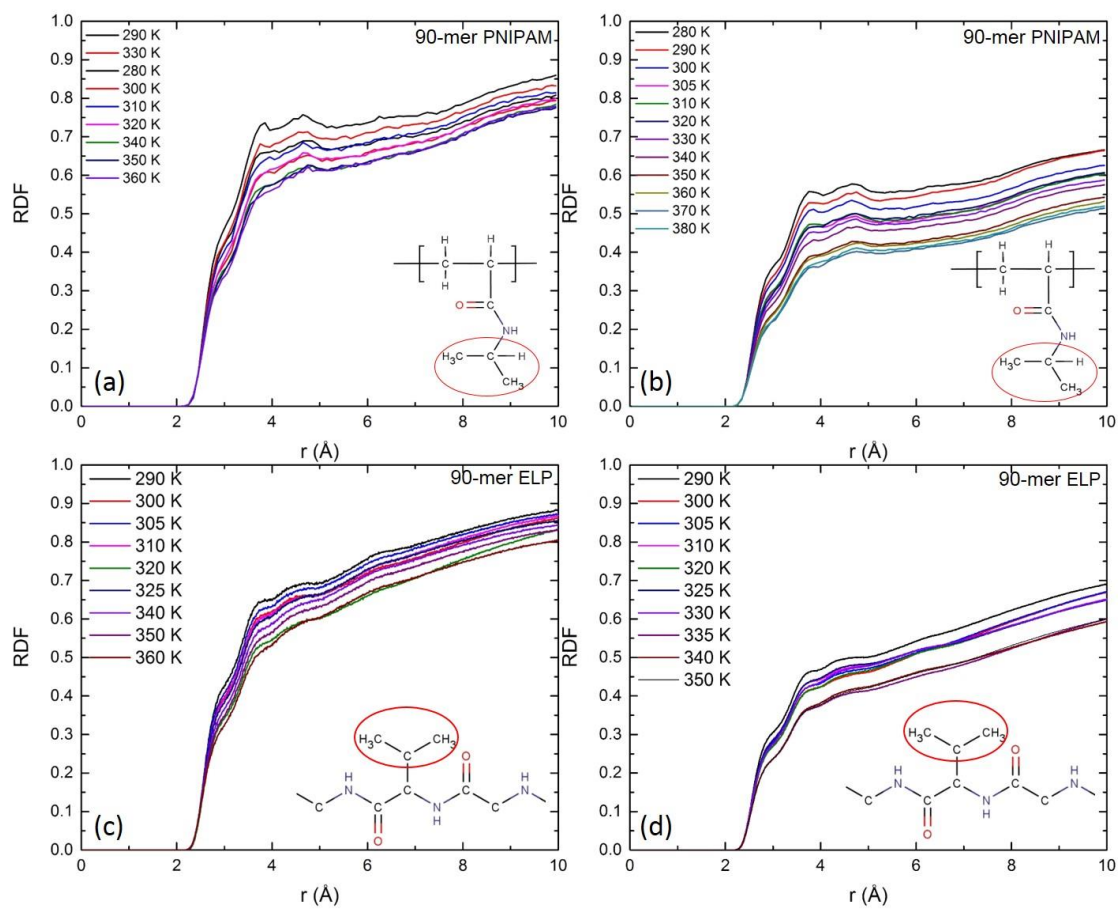
**Figure S6.** Radial Distribution Function between carbon atoms on backbone/sidechain of PNIPAM to oxygen of water. (a) RDF between highlighted carbon atoms of insert figure to oxygen of water for 18-mer PNIPAM; (b) RDF for 18-mer PNIPAM; (c) RDF between highlighted carbon atoms of insert figure to oxygen of water for 90-mer PNIPAM; (d) RDF for 90-mer PNIPAM.





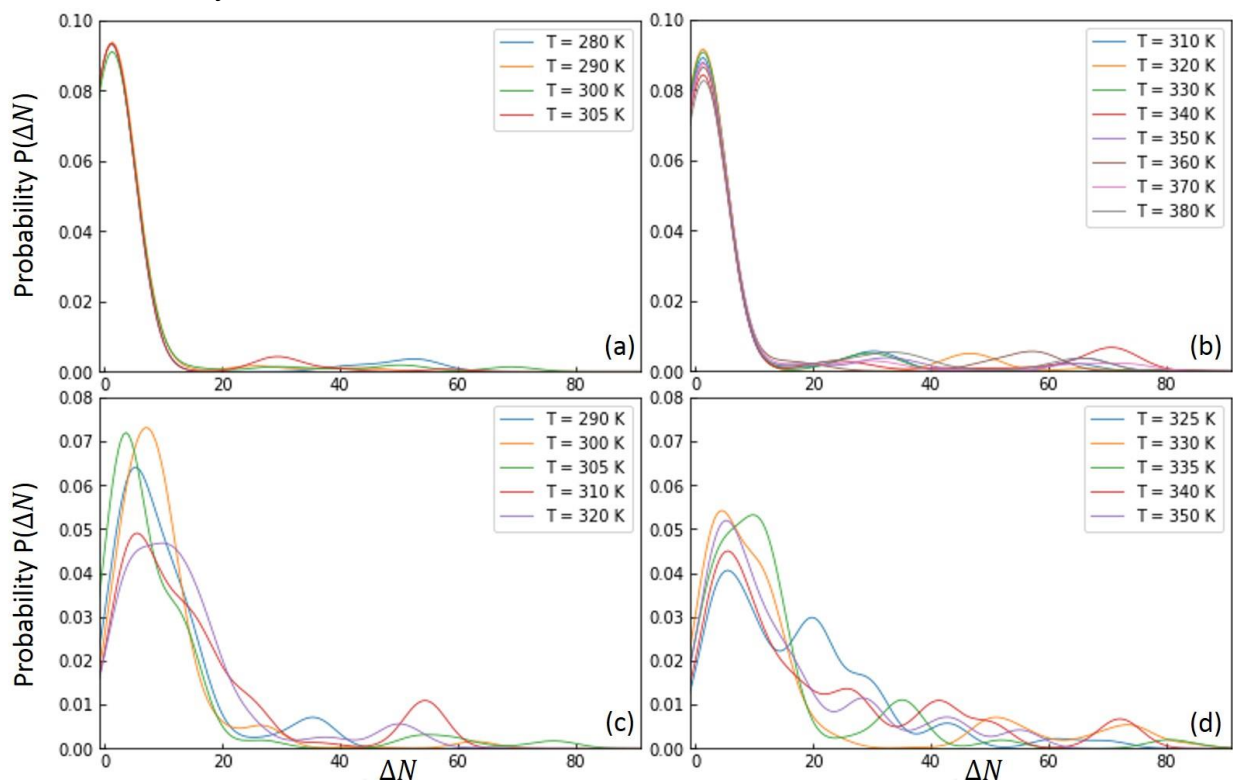
**Figure S7.** Radial Distribution Function between carbon atoms on backbone of ELP to oxygen of water. (a) RDF between highlighted carbon atoms of insert figure to oxygen of water for 18-mer ELP (GVG(VPGVG)<sub>3</sub>); (b) RDF for 18-mer ELP (GVG(VPGVG)<sub>3</sub>); (c) RDF between highlighted carbon atoms of insert figure to oxygen of water for 90-mer ELP ((VPGVG)<sub>18</sub>); (d) RDF for 90-mer ELP ((VPGVG)<sub>18</sub>).





**Figure S8.** Radial Distribution Function between isopropyl group of ELP or PNIPAM to oxygen of water. (a) RDF for 18-mer PNIPAM; (b) RDF for 90-mer PNIPAM; (c) RDF for 18-mer ELP (GVG(VPGVG)<sub>3</sub>); (d) RDF for 90-mer ELP ((VPGVG)<sub>18</sub>).

## A. Probability Distribution



**Figure S9.** Hydrogen bonding time probability distribution as function of residue-distance ( $\Delta N$ ) for 90-mer PNIPAM and 90-mer ELPs respectively. (a) Curves for 90-mer PNIPAM between  $T = 290\text{ K} \sim 305\text{ K}$ , (b) Curves for 90-mer ELPs between  $T = 310\text{ K} \sim 380\text{ K}$ , (c) Curves for 90-mer PNIPAM between  $T = 290\text{ K} \sim 320\text{ K}$ , (d) Curves for 90-mer ELPs between  $T = 325\text{ K} \sim 350\text{ K}$ .

## Radius of gyration

**Table S2:** Radius of Gyration ( $R_g$ ) ( $\text{\AA}$ ) for PNIPAM and ELPs

Temperature (K)	280	290	300	305	310	320	325	330	335	340	350	360	370	375	380
18-mer ELP		8.4±1.1	7.8±1.4	8.4±1.1	8.6±1.7	7.2±1.0	8.8±1.7			9.1±1.6	8.7±1.6			8.7±1.6	
90-mer ELP		14.1±0.7	14.7±1.4	13.3±0.5	12.9±0.6	12.8±0.6	13.1±0.5	13.3±1.0	12.1±0.5	11.9±0.6	12.3±0.4				
18-mer PNIPAM	11.3±0.4	10.5±0.7	9.3±0.7		9.6±1.1	11.2±1.3		10.6±1.0		10.0±1.0	9.7±0.6	9.5±1.0			
90-mer PNIPAM	16.4±0.5	16.7±1.0	15.2±0.3	14.5±0.3	14.8±0.6	14.9±0.3		14.3±0.3		14.4±0.2	13.8±0.2	14.0±0.4	13.6±0.4		14.0±0.3

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