SUPPORTING INFORMATION

for

Can Ammonium-Based Room Temperature Ionic Liquid Counteract the Urea – Induced Denaturation of a Small Peptide?

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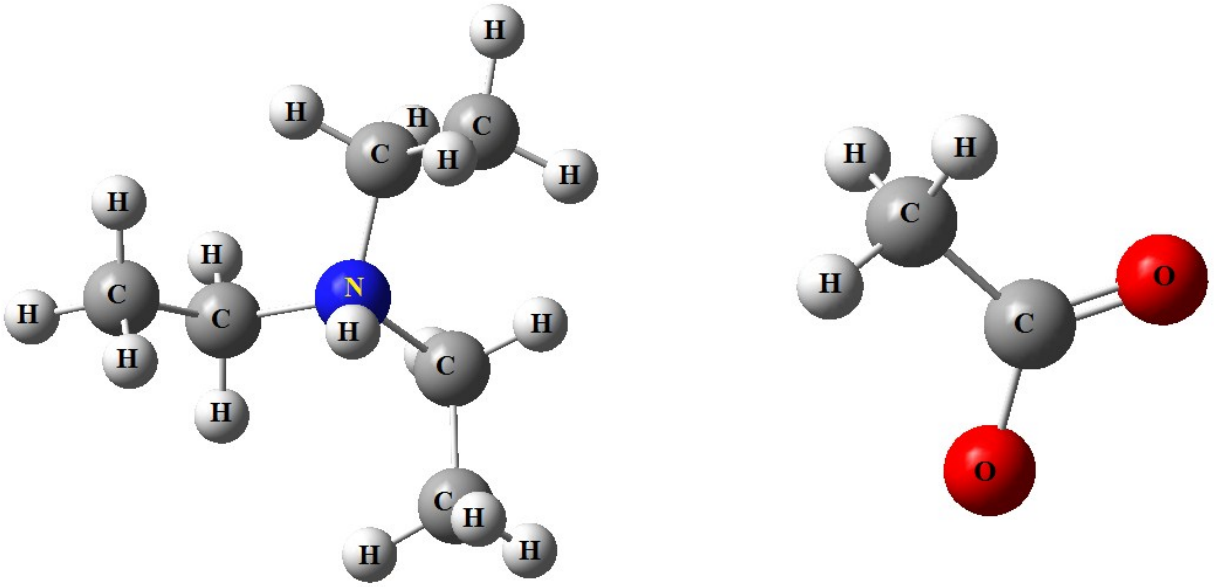

(a) **(b)**

FIG.S1. Geometry optimized structure of (a) triethylammonium cation (TEA) and (b) acetate anion (ACE) with suitable atomic labels.

Serial number	Ionic species	Atom name	Partial charge
1	TEA	N	-0.1658
2	TEA	C	-0.4425
3	TEA	C	-0.6560
4	TEA	H	0.2520
5	TEA	H	0.2760
6	TEA	H	0.2543
7	TEA	H	0.2670
8	TEA	H	0.2277
9	TEA	C	-0.1595
10	TEA	C	-0.8210
11	TEA	H	0.2303
12	TEA	H	0.2450
13	TEA	H	0.2622
14	TEA	H	0.2650
15	TEA	H	0.2112
16	TEA	C	-0.4373
17	TEA	C	-0.5282
18	TEA	H	0.2379
19	TEA	H	0.2731
20	TEA	H	0.2594
21	TEA	H	0.2481
22	TEA	H	0.2324
23	TEA	H	0.4684

Serial number	Ionic species	Atom name	Partial charge
1	ACE	C	-0.7072
2	ACE	H	0.1873
3	ACE	H	0.1893
4	ACE	H	0.2014
5	ACE	C	0.4021
6	ACE	O	-0.5632
7	ACE	O	-0.7098

Table S2. Partial charges on different atoms of TEA and ACE ions constituting the TEAA molecule.

Bond parameters			
Bond type	**Ionic species**	**Force constant (kJ mol^{-1} nm^{-2})**	**Equilibrium bond length (nm)**
N-H	TEA	363171	0.100
N-C	TEA	307105	0.147
C-H	TEA	284512	0.107
C-C	TEA	224262	0.154
C-O	ACE	548960	0.125
C-H	ACE	284512	0.109
C-C	ACE	265265	0.152
Angle parameters			
Angle type	**Ionic species**	**Force constant (kJ mol^{-1} rad^{-2}**	**Equilibrium angle (degree)**
N-C-H (alkyl hydrogen)	TEA	292.880	109.515
N-C-C	TEA	669.440	109.457
C-C-H	TEA	313.800	109.432
C-N-H (N-terminal hydrogen)	TEA	292.880	109.437
H-C-C	ACE	292.900	109.500
H-C-H	ACE	276.100	107.800
O-C-C	ACE	585.800	117.000
O-C-O	ACE	669.400	126.000
Dihedral parameters			
Dihedral type	**Ionic species**	**Phase (degree)**	**Multiplicity**
H-N-C-C	TEA	0	3
O-C-C-H	ACE	0	3

Table S3. Bonded interaction parameters for the molecule TEAA compatible with the OPLS-AA force field.

System	N_P	N_U	N_{IL} (TEA and ACE)	N_W	V ($nm^{3)}$	d (kg/m^3)	T (K)	P (bar)
PW	1	0	0	4269	132.822±0.001	998.482±0.007	310.004±0.002	1.113±0.001
PUW	1	640	0	2218	114.066±0.007	1165.66±0.038	309.97±0.021	1.134±0.001
PUILW	1	640	128	1139	111.983±0.008	1197.970±0.086	309.944±0.002	1.137±0.001
PILW	1	0	128	2861	117.899±0.008	1040.270±0.074	309.984±0.002	1.127±0.001

Table S4. A brief overview of each of the simulated systems. N_P, N_U, N_{IL} and N_W refer to the number of peptide, urea, each ions from the ionic liquid and water molecules respectively. Systems PW, PUW, PUILW and PILW denote the peptide in pure water, peptide in aqueous urea, peptide in mixed urea-TEAA and peptide in aqueous TEAA solution respectively. V, d, T, P represent the cubic box volume, density, temperature and pressure of each of the simulated systems respectively. Standard errors provided are calculated from two independent simulations for each system.

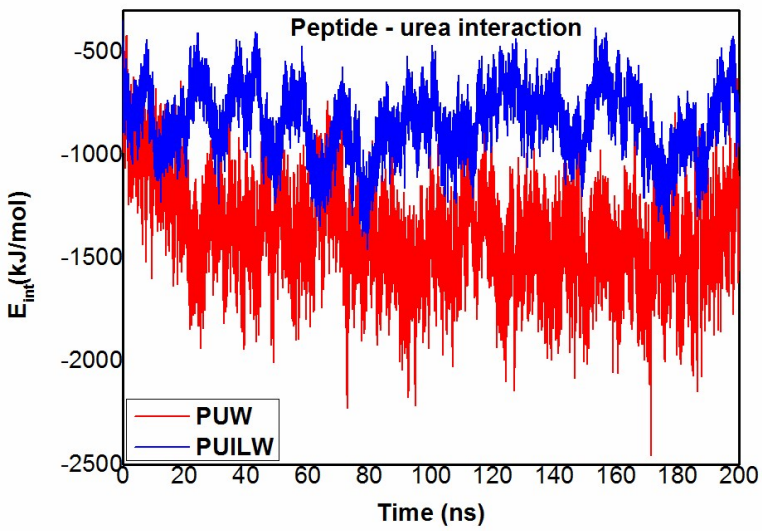

FIG.S5. Time evolution of the interaction energy between the peptide and urea in both the binary mixture (red line) as well as the ternary one (blue line).

Types of hydrogen bonds (HB)	PW	PUW	PUILW
HB_{PP}	9.630±0.274	2.887±0.851	9.026±0.348
HB_{PU}	-	26.087±0.353	16.025±0.589
HB_{PW}	49.197±0.650	39.347±0.987	24.706±0.737
HB_{PTEA}	-	-	0.820±0.217
HB_{PACE}	-	-	6.440±0.340

Table S6. Average number of hydrogen bonds (HB) between different species in three different systems under study. Peptide, urea, water, triethylammonium and acetate have been abbreviated as P, U, W, TEA and ACE respectively. Standard errors are calculated using block averaging over a single trajectory.

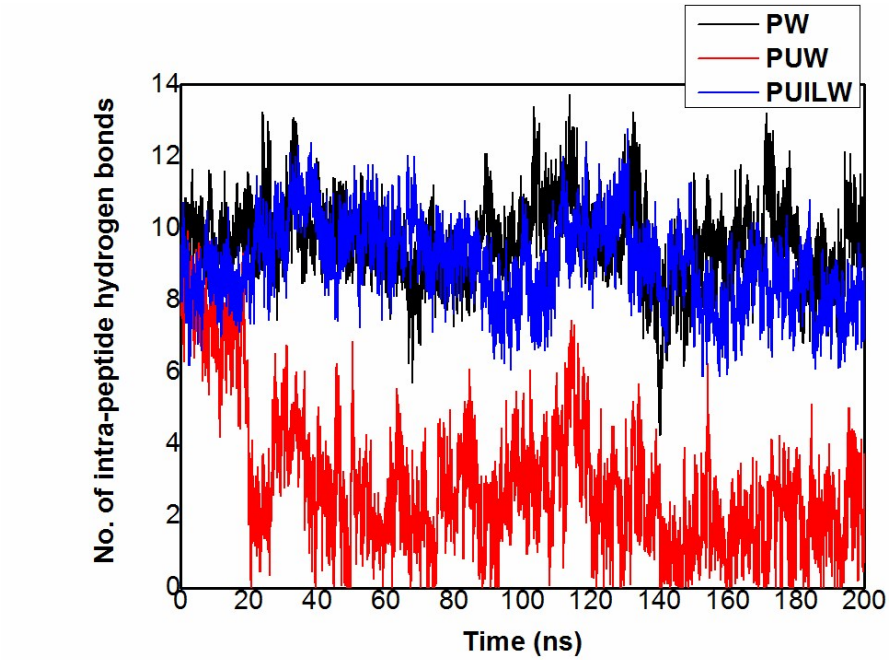

FIG.S7. Variation in the number of intra-peptide hydrogen bonds (HB_{PP}) with simulation time for three different systems under consideration.

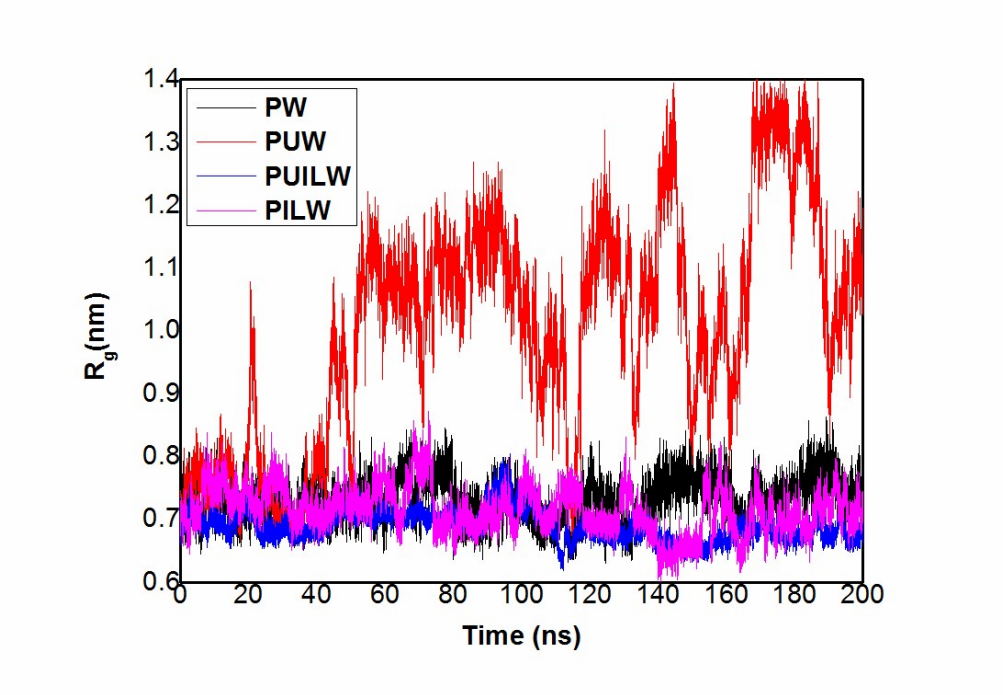

FIG.S8. Time evolution of radius of gyration (R_g) of the C_α carbon atoms of peptide residues 4-12 for four simulation systems containing pure water (PW), urea-water mixture (PUW), urea-ionic liquid-water (PUILW) and ionic liquid-water mixture (PILW) respectively.

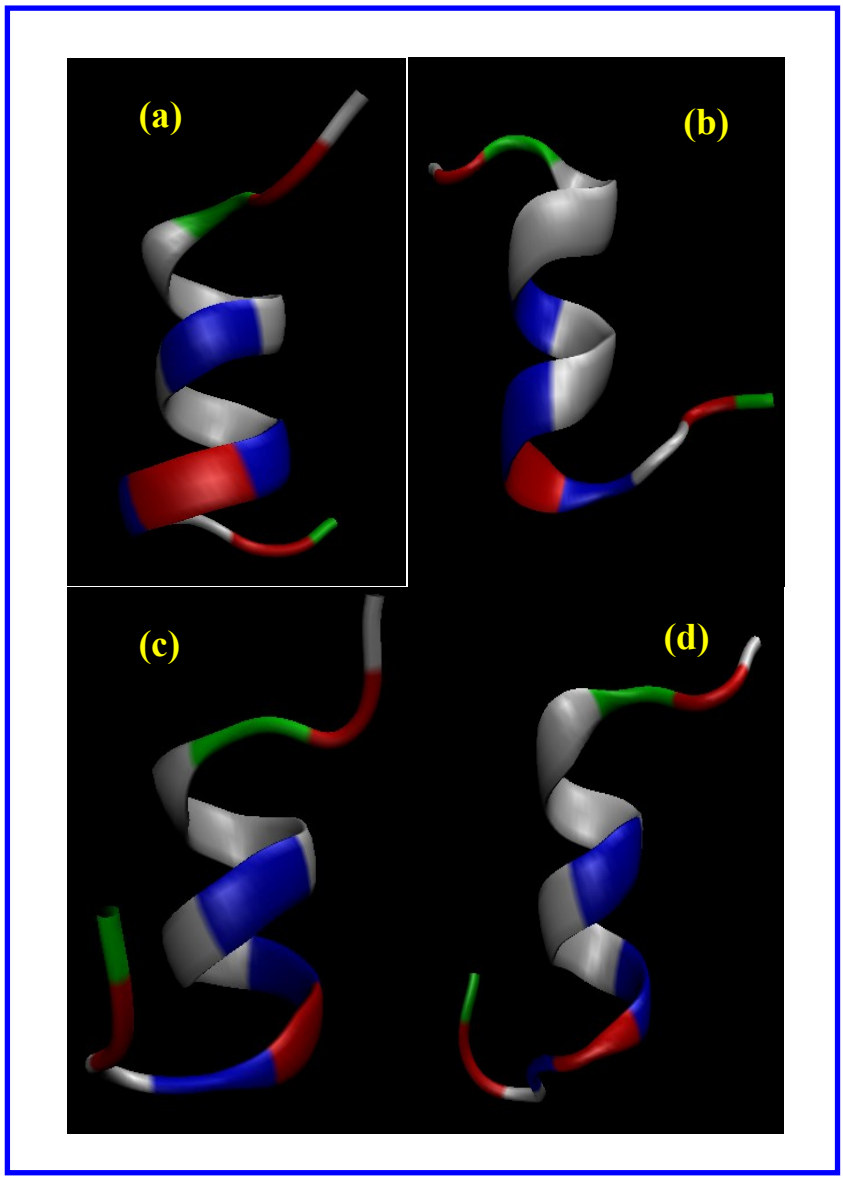

FIG. S9. Snapshots representing the conformation of the peptide during (a) 50 ns, (b) 100 ns, (c) 150 ns and (d) 200 ns of the simulation capturing the dynamics of the peptide in a 1.6M aqueous TEAA solution (system PILW).

System	Combination	Coordination number
PUILW	Urea-TEA	10.994±0.319
	Urea-ACE	3.2172±0.196

Table S10. Coordination number of two different ionic species composing TEAA within a distance of 5 Å from the urea molecules in the system denoted as PUILW. Standard errors are calculated using block averaging over a single trajectory.