

Supplementary Information
for
Self-Assembly of Dipeptide Sodium Salts Derived
from Alanine: A Molecular Dynamics Study

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Table S1. Summary of the Simulated Systems

System	N-dipeptide	N-solvent	T (K)	Time (ns)
I	110, (L, L)	6672	298	200
II	110, (D, D)	6672	298	200
III	110, (L, D)	6672	298	200
IV	110, (D, L)	6672	298	200

Table S2. Force Filed Parameters

Van der Waals Interaction		
Angle type	σ (nm)	ϵ (kJ/mol)
C	0.33611	0.40587
CH	0.37998	0.31394
CH ₂	0.39199	0.48959
CH ₃	0.38750	0.73227
H(N)	0.23734	0.11838
N	0.29760	0.87677
O	0.26259	1.72504
Bond Interaction		
Bong type	Ideal bond length b_0 (nm)	Force constant K_b ($10^6 \text{kJmol}^{-1} \text{nm}^{-4}$)
CH ₃ -CH ₂	0.1520	5.43e ⁶
CH ₂ -CH ₂	0.1520	5.43e ⁶
CH ₁ -CH ₃	0.1530	7.15e ⁶
CH ₁ -C	0.1530	7.15e ⁶
CH ₁ -N	0.1470	8.71e ⁶

C-N	0.1380	1.10e ⁷
N-H	0.1000	1.87e ⁷
C=O	0.1250	1.34e ⁷
C=O (COO ⁻)	0.1265	1.31e ⁷

Angle Interaction

Angle type	Ideal bond angle θ_0 (degree)	Force constant K_θ (kJ/mol)
CH ₂ -CH ₂ -CH ₂	111.0	530
CH ₂ -C=O	121.0	685
CH ₂ -C-N	115.0	610
O=C-N	121.4	690
C-N-H	120.0	390
C-N-CH ₁	122.0	700
H-N-CH ₁	115.0	460
N-CH ₁ -C	111.0	530
N-CH ₁ -CH ₃	111.0	530
C-CH ₁ -CH ₃	109.5	285
CH ₁ -C=O	121.0	685
CH ₁ -C-N	115.0	610
CH ₁ -C=O (COO ⁻)	117.0	635
O=C-O	126.0	770

Torsion Interaction

Torsion	Ideal dihedral angle ζ_0 (degree)	Force constant K_ζ (kJmol ⁻¹ degree ⁻²)	m
-CH _n -	0.00	5.92	3
C-C-C-N	0.00	1.00	6
C-C-N-C	180.00	33.50	2
C-N-C-C	180.00	1.00	6
N-C-C-N	0.00	1.00	6

N-C-C=O		180.00	1.00	6	
Torsion Interaction					
Atom	Charge (e)	Atom	Charge (e)	Atom	Charge (e)
C1	0.003	C11	0.002	C18	0.262
C2	-0.003	C12	0.006	O2	-0.433
C3	0.000	C13	-0.006	C21	0.000
C4	0.002	C14	-0.049	N2	-0.229
C5	0.000	C15	0.026	H2	0.250
C6	-0.002	C16	0.302	C19	0.036
C7	-0.002	O1	-0.377	C20	0.339
C8	-0.002	N1	-0.354	O3	-0.566
C9	-0.002	H1	0.229	O4	-0.566
C10	-0.002	C17	0.108	C22	0.000

* The parameters were derived from GROMOS 45a3 united-atom force field.

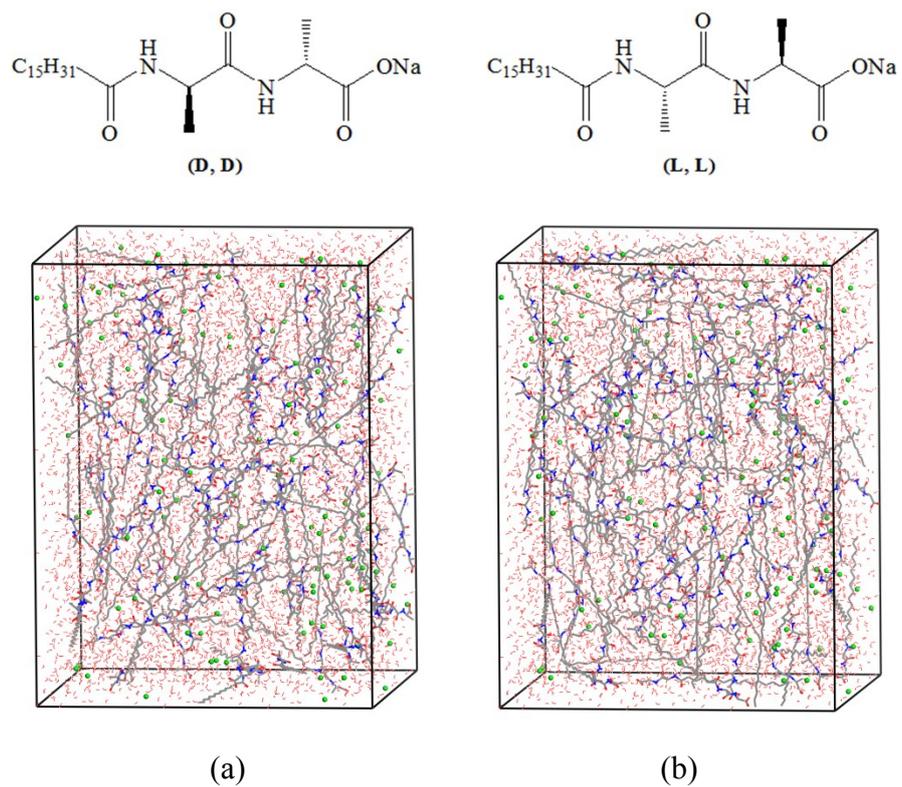
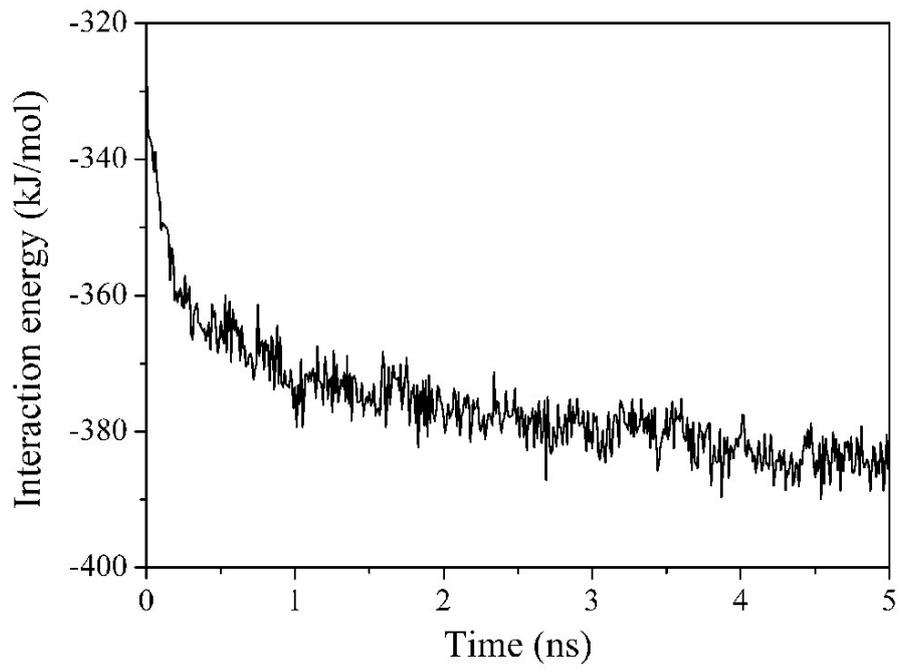
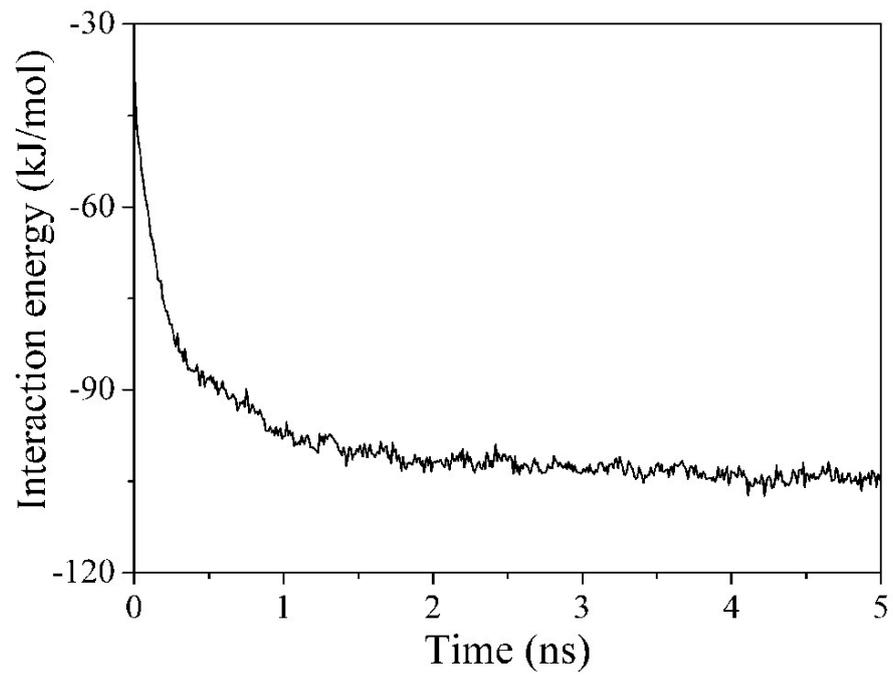


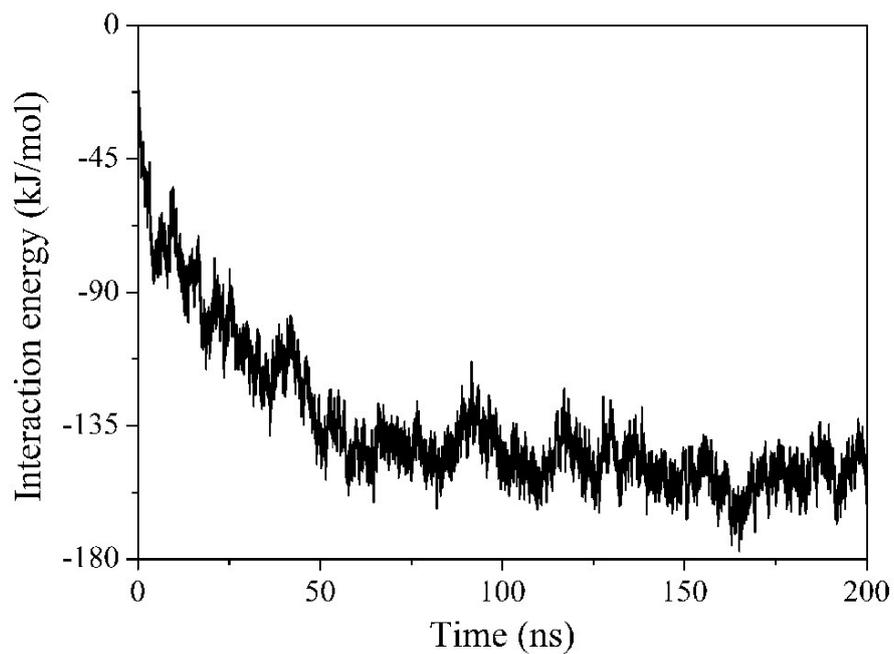
Fig. S1. Molecular structures of the dipeptides and the original structures of system I (a) and system II (b). Dipeptides are shown in lines. Water molecules and Na^+ are represented by red and green dots, respectively.



a



b



c

Fig. S2. Time evolution of (a) additive energy of peptides, water molecules and sodium ions. (b) van der Waals interaction energy between peptide molecules, (c) Coulomb interaction energy between peptides and sodium ions. As an example of peptide molecule (**D, D**).

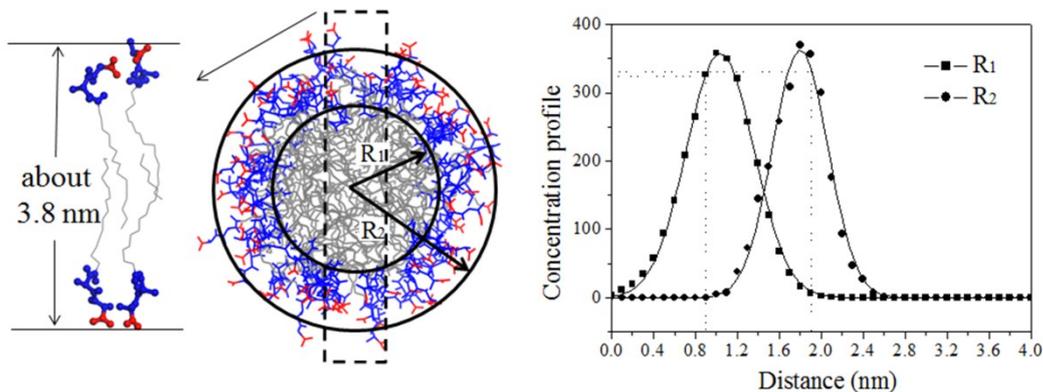


Fig. S3. System I: the analysis of radius of fibril (with an error of 0.1 nm). The carboxyl groups are shown in red, and other hydrophilic groups and alkyl chains of dipeptide molecules are shown in blue and grey, respectively.

The carbon atom of carbonyl group near the alkyl chain was defined as the end of hydrophilic dipeptide molecule, thus the radius of hydrophobic core, R_1 , is calculated in Fig. S3a. According to ninety percent of the peak height¹, it is about 0.9 nm. This means that the hydrophilic shell around the fibril is about 1.0 nm from R_1 to R_2 . It indicates that more water molecules or ions can be located in the 1.0 nm hydrophilic shell around the nanostructure. These water molecules or ions have important effect on the stabilization of nanostructure in the solution through strong H-bonding or electrostatic interaction.

We note that in Li's experiment,²⁻³ the radius of self-assembly is about several decades nanometers. It is far more than our simulated radius of fibril. We think that the self-assembly structure in Li's experiment is aggregated by many fibril like our simulated system. On the other hand, maybe our simulated fibril is the basic unit of dipeptide self-assembly in Li's experiment. The simulated nanostructure also can give some information at the molecular level as the experimental supplement.

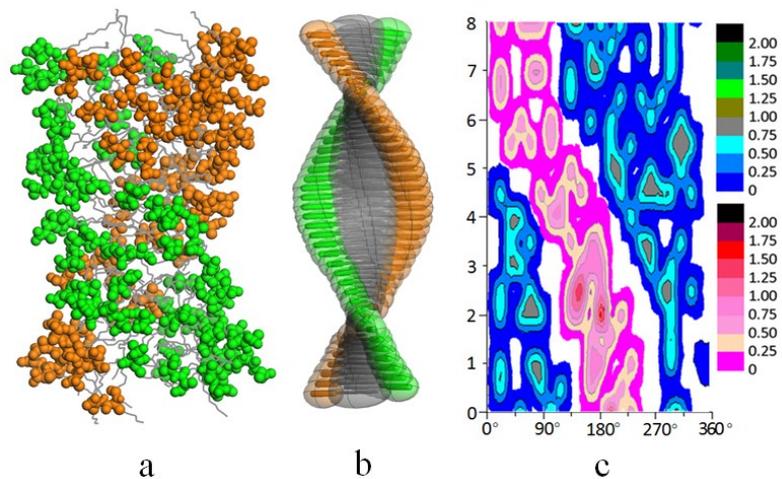


Fig. S4. System II: views of hydrophilic groups of dipeptide molecules (L, L) (a) at 200 ns, suggested model (b) and real density distribution (c) of hydrophilic groups on the fibril. The color bar of (c) is used to identify the low or high number density.

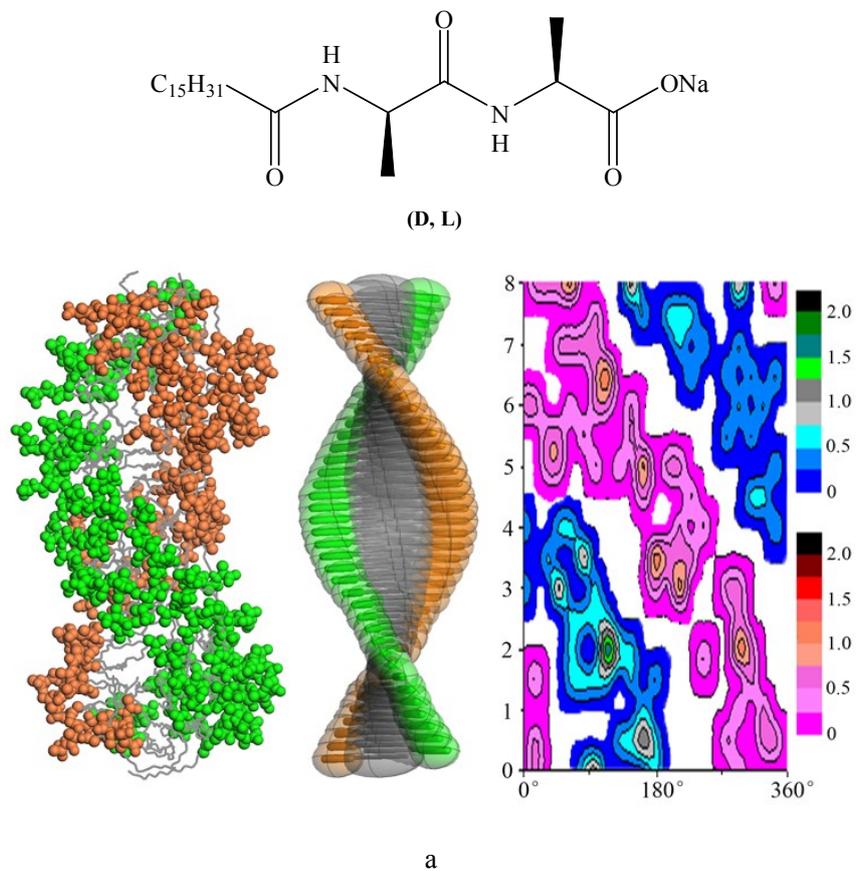


Fig. S5. System III: views of hydrophilic groups of dipeptide molecules (**D, L**) (a) at 200 ns, suggested model (b) and real density distribution (c) of hydrophilic groups on the fibril. The color bar of (c) is used to identify the low or high number density.

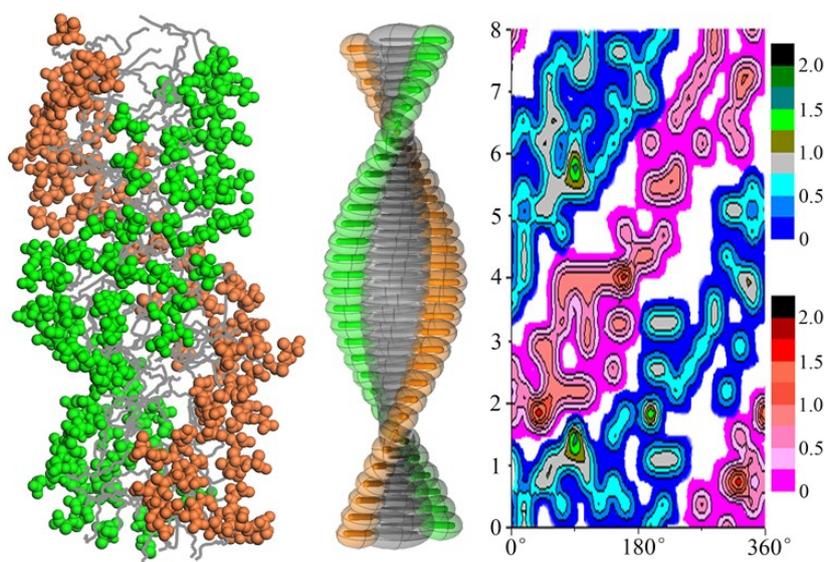
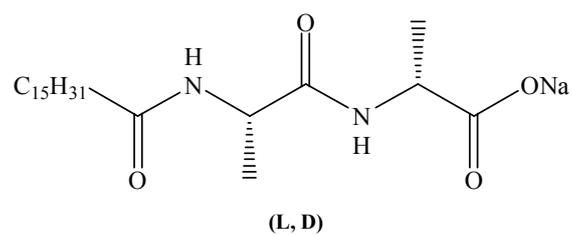


Fig. S6. System IV: views of hydrophilic groups of dipeptide molecules (**D, L**) (a) at 200 ns, suggested model (b) and real density distribution (c) of hydrophilic groups on the fibril. The color bar of (c) is used to identify the low or high number density.

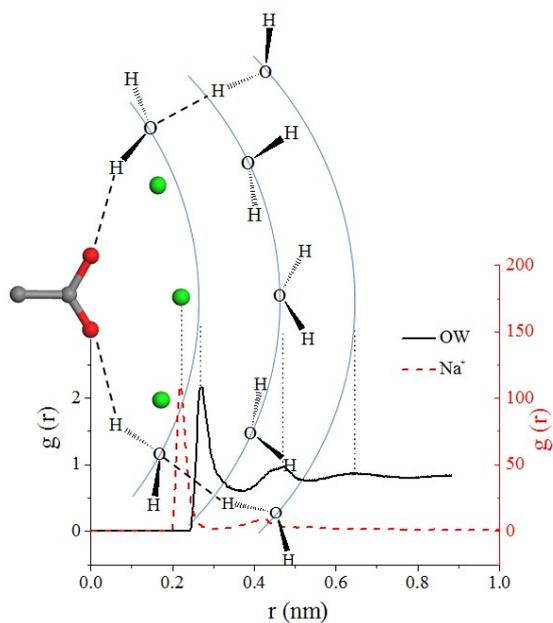
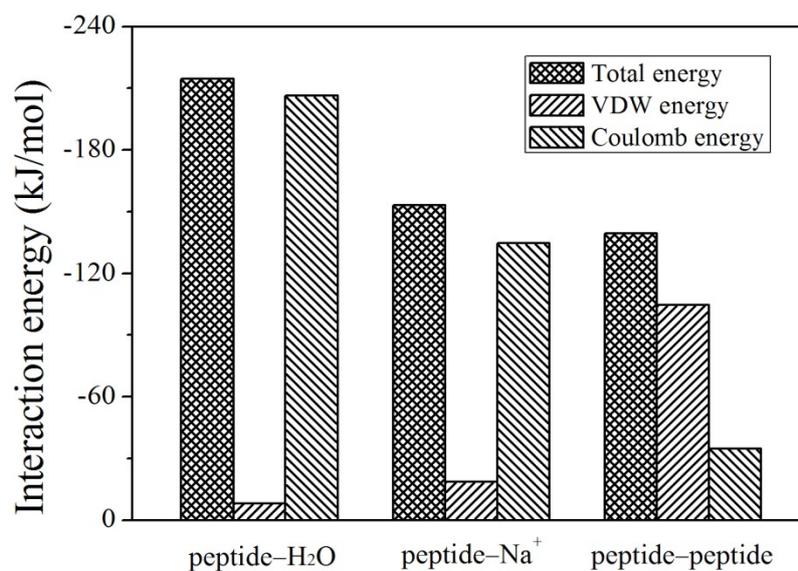
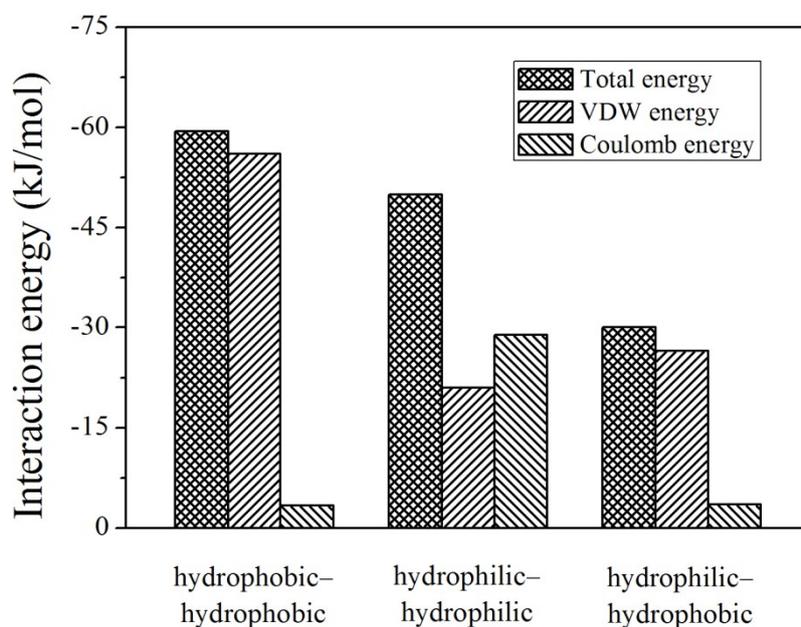


Fig. S7. System I: the structure of water molecules and ions around the carboxyl group of dipeptide. Radial distribution functions of water oxygen (OW) and Na⁺ around the carboxyl group. Carbon atoms, carbonyl oxygen and sodium ion are represented by gray, red and green balls.

By comparing RDF of sodium ions and water oxygen around the carboxyl group, we found that the sodium ions are mainly concentrated in the first hydration shell of carboxyl group. And because of strong electrostatic and hydrogen bond interaction, three regions, one in front of two carboxyl oxygen atoms and two along the direction of each carbon-oxygen bond of carboxyl group, are occupied around the carboxyl group.



a



b

Fig. S8. System II: the interaction energy per dipeptide molecule including total energy and VDW and Coulomb terms for system II of dipeptide molecule (L, L). a, the energy of peptide and water molecules or sodium ions; b, the individual energy between the hydrophilic and hydrophobic parts of dipeptide. All data are averaged using the last 20 ns MD simulations.

References

- (1) F. F. Gao, H. Yan,; Q. W. Wang, S. L. Yuan, *Phys. Chem. Chem. Phys.*, 2014, **16**, 17231-17237.
- (2) Y. Li, B. Z. Li, Y. T. Fu, S. W. Lin, Y. G. Yang, *Langmuir*, 2013, **29**, 9721-9726.
- (3) Y. T. Fu, B. Z. Li, Z. B. Huang, Y. Li, Y. G. Yang, *Langmuir*, 2013, **29**, 6013-6017.