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

Extension of the CAVS model to helical peptides in membrane environment.

Hujun Shen[1]*, Zhenhua Wu[2], Chan Lu[1]

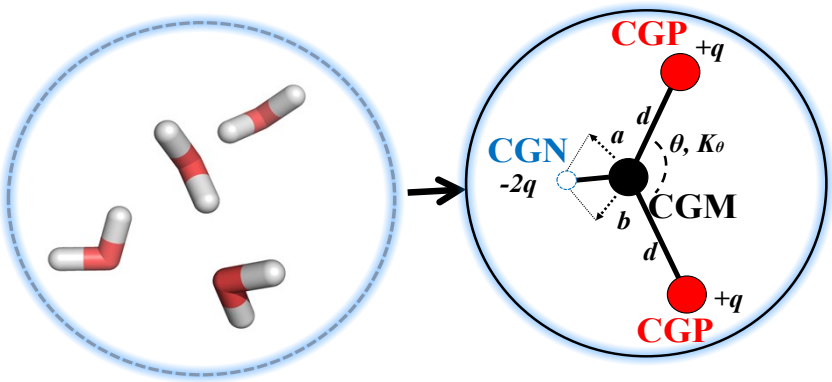
1. Guizhou Provincial Key Laboratory of Computational Nano-Material Science, Guizhou Education University, Guiyang, Guizhou 550018, P. R. China
2. Laboratory of Theoretical and Computational Chemistry, Institute of Theoretical Chemistry, Jilin University, Changchun 130023, P. R. China

*Corresponding author email: hujun.shen@hotmail.com

Supporting Information

Figure S1. (A) CAVS model of water: four water molecules are grouped into a collective unit that contains two positively charged (CGP) particles, one van der Waals (vdW) interaction center (CGM), and one virtual site (CGN) carrying a negative charge. (B) CAVS model of 1-octanol: Two consecutive CG units are connected by a harmonic bond formed between the neutral vdW centers (such as C3P-C3P and C3P-CEO), while a harmonic angle is formed by three consecutive CG beads (such as C3P-C3P-CEO). The neutral van der Waals (vdW) interaction sites (such as C3P) are represented by filled black circles, and the vdW interactions site carrying a positive charge (such as CEO) by filled blue circles.

(A)



(B)

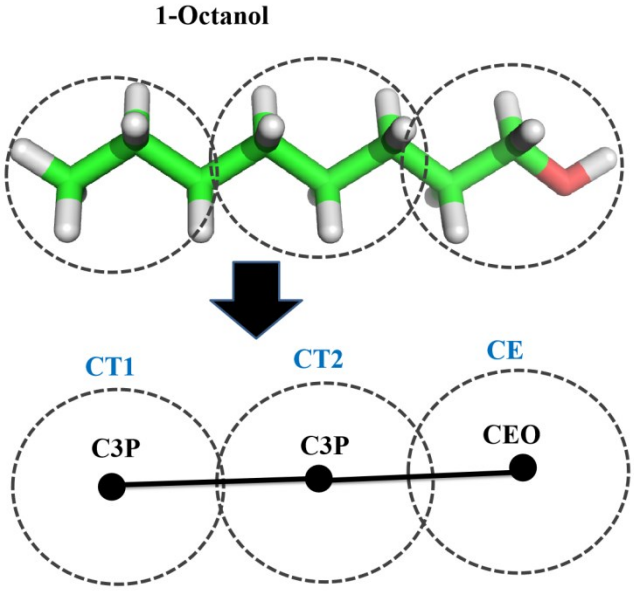
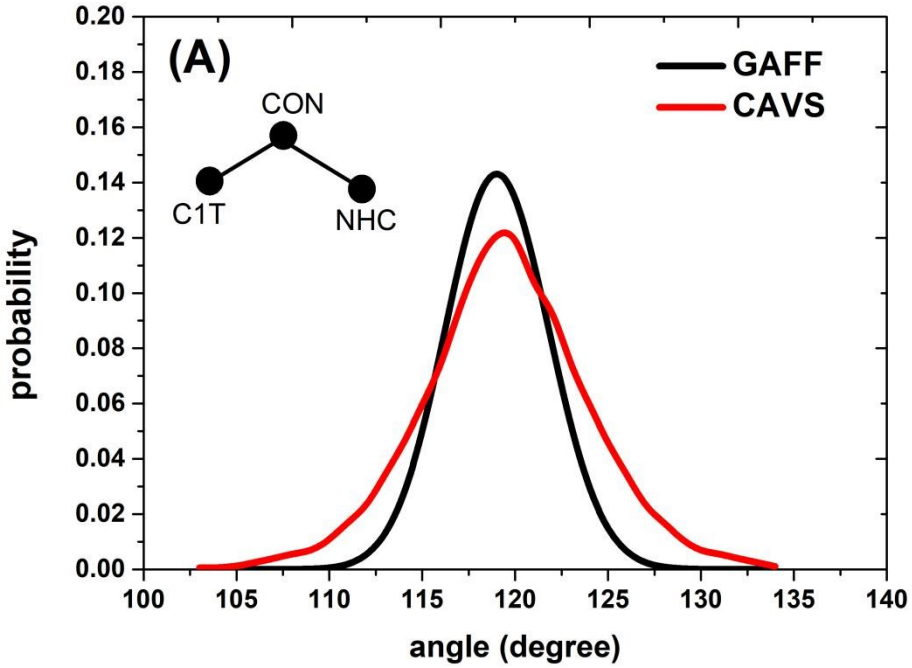


Figure S2. Comparison between CAVS and GAFF results for (A) the angle bending and (B) dihedral angle probability distributions of N-methyl-acetamide.



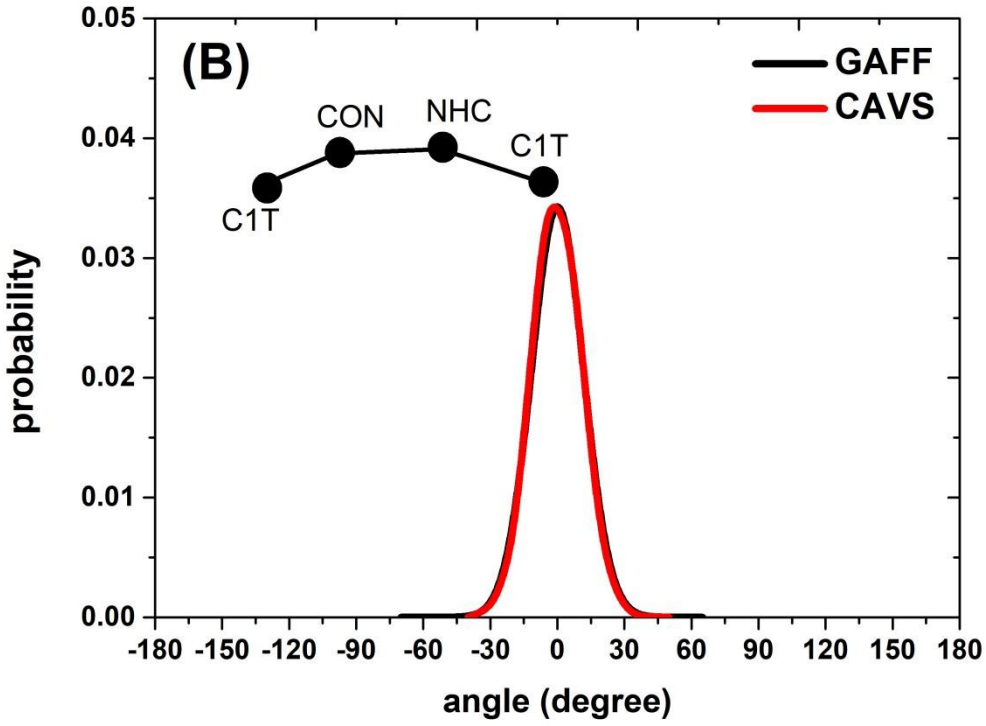


Figure S3. CG mapping for DMPC, the type names for interacting sites are indicated in black color and the names for CG units in blue color respectively. The neutral, non-interacting, positively charged, and negatively charged sites are respectively denoted by the black filled, black open, red filled, and blue filled circles.

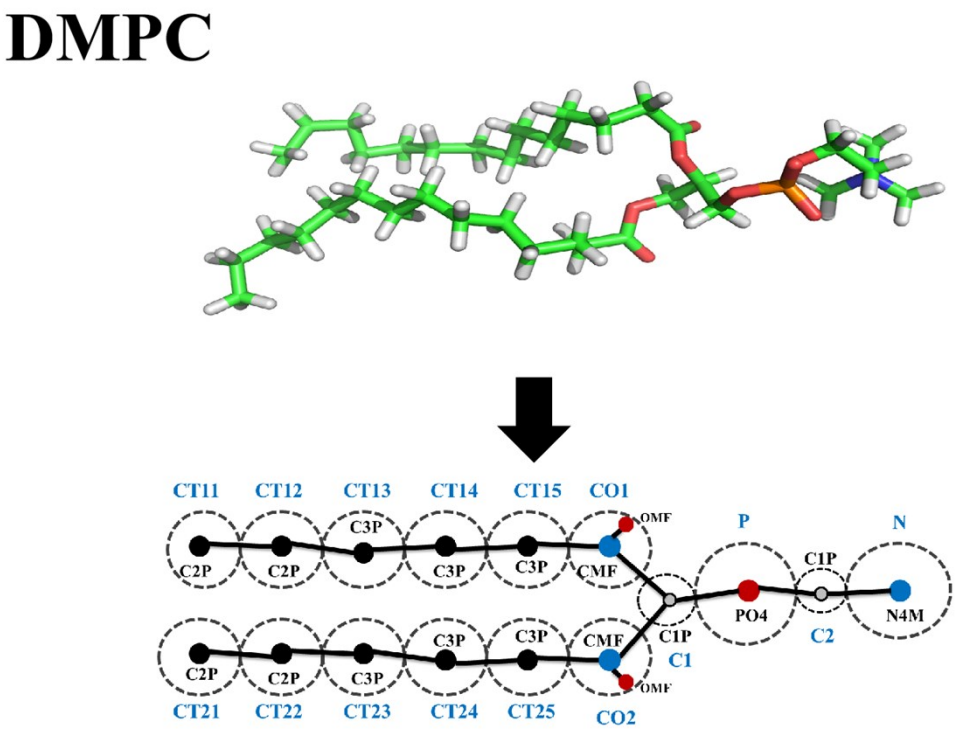
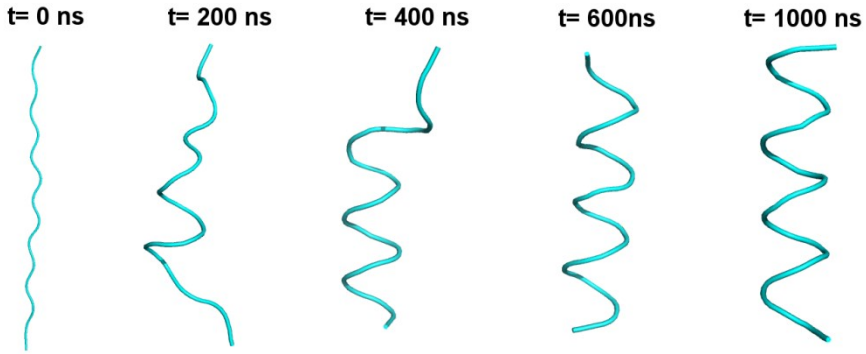
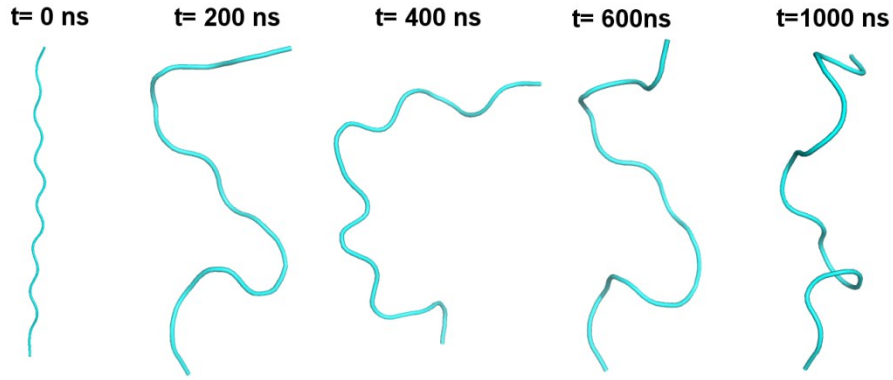


Figure S4. (A) Snapshots obtained from folding the extended structure of KALP15 to an alpha helix (one representative simulation from eight MD trajectories). (B) Snapshots obtained from folding the extended structure of KALP15 to a random coil (one representative simulation from two MD trajectories). (C) PMFs of the backbone (ϕ, ψ) distributions for KALP15 in water obtained from the CAVS simulations. In the PMF contour plot, the interval between the contour lines indicates a free energy difference of 0.5 kJ/mol.

(A)



(B)



(C)

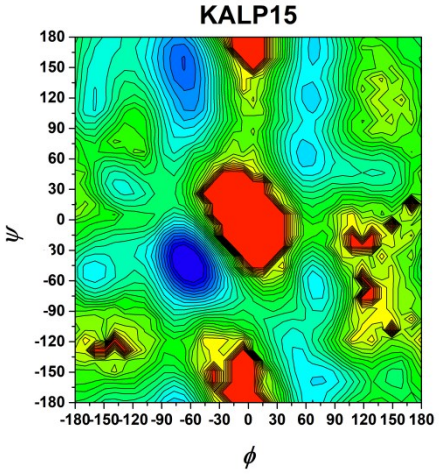


Figure S5. Electrostatic potential of DMPC bilayers without KALP15 (black) and with KALP15 (red), contributed from (A) water (the CAVS force field), (B) water (the CHARMM36 force field), (C) DMPC lipid (the CAVS force field), and (D) DMPC lipid (the CHARMM36 force field).

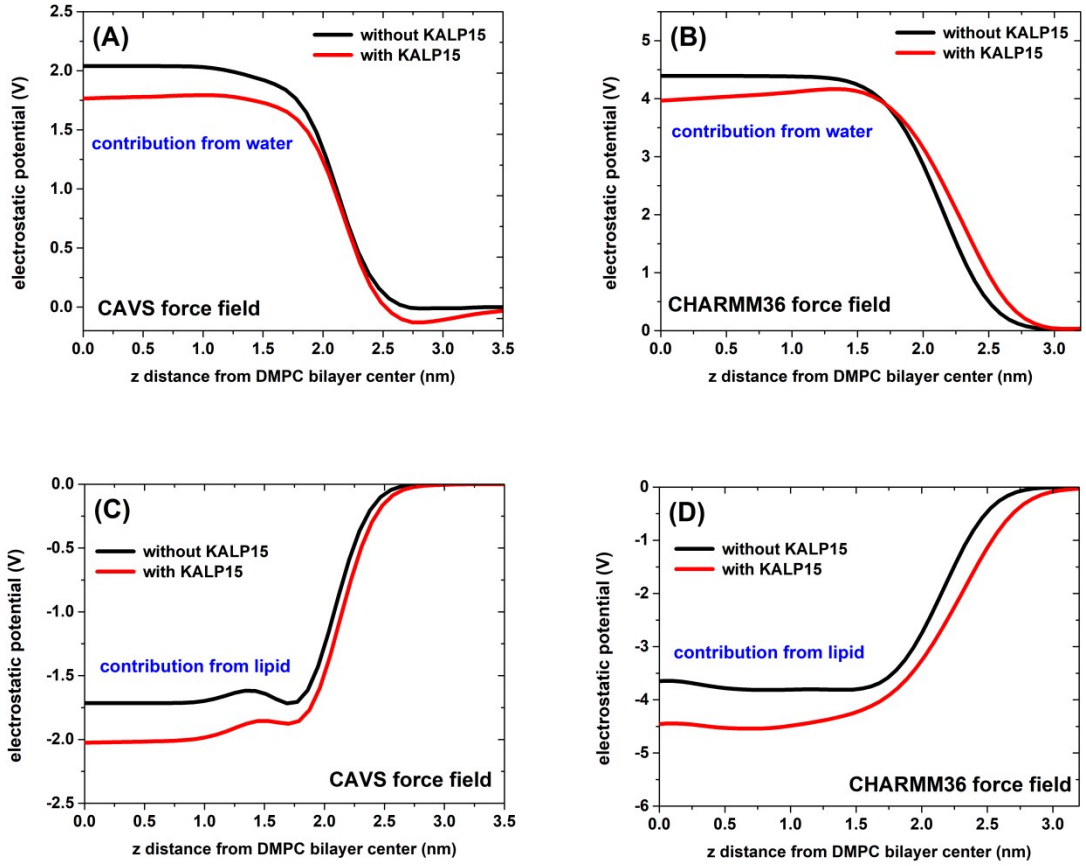


Figure S6. Definition of the bending angle θ_{bending} of KALP31 peptide. The helical axis of KALP31 is modeled as two segments.

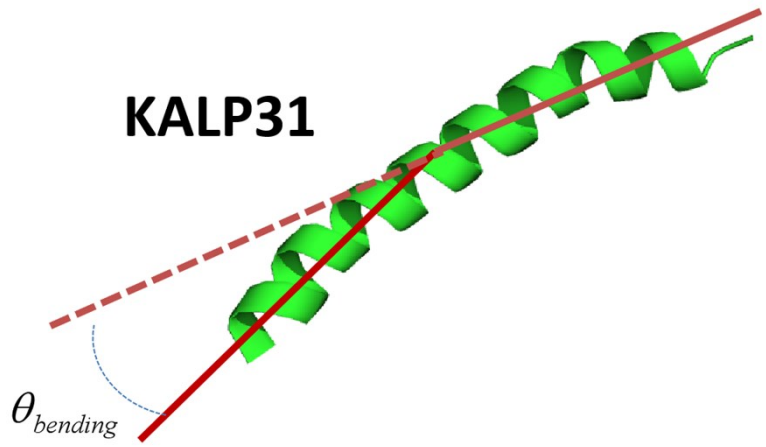


Table S1 Constrained distances between two consecutive CG beads.

CG bead (*i*)	CG bead (*j*)	Distance (nm)
C1T	CON	0.15
CON	OCN	0.12
CON	NHC	0.13
NHC	C1T	0.15

Table S2. The parameters in the angle bending potential for the CG NMA model

CG bead (*i*)	CG bead (*j*)	CG bead (*k*)	Equilibrium Angle (degree)	Force constant (kJ/mol)
C1T	CON	NHC	122	300
C1T	CON	OCN	117	300
OCN	CON	NHC	121	300
CON	NHC	C1T	120	300

Table S3. The parameters in the dihedral angle potential for the CG NMA model.

CG bead (*i*)	CG bead (*j*)	CG bead (*k*)	CG bead (*l*)	Equilibrium value (degree)	Force constant (kJ/mol)	multitude
C1T	CON	NHC	C1T	180	20	2

OCN	CON	NHC	C1T	180	20	2

Table S4 Pair-wise vdW parameters for various CG types.

CG Type (*i*)	CG Type (*j*)	Range parameter σ (nm)	Well depth ε (kJ/mol)
C1T	C1T	0.39	1.00
CON	CON	0.34	0.36
OCN	OCN	0.30	0.9
NHC	NHC	0.32	0.7
CGW	CGW	0.485	4.4
CGW	C1T	0.42	1.2
CGW	CON	0.42	1.2
CGW	OCN	0.40	5.0
CGW	NHC	0.42	5.0
CEO	CEO	0.46	5.5
CEO	C1T	0.42	1.2
CEO	CON	0.41	1.0
CEO	OCN	0.40	4.0
CEO	NHC	0.41	5.0
C3P	C3P	0.47	2.5
C3P	C1T	0.44	1.5
C3P	CON	0.42	1.0
C3P	OCN	0.41	1.0
C3P	NHC	0.43	1.5
C3P	NEC	0.46	2.3
C1T	CON	0.38	0.4
C1T	OCN	0.36	0.4
C1T	NHC	0.38	0.6
C1T	NEC	0.42	0.9
NEC	CON	0.42	0.9
NEC	OCN	0.40	3.0
NEC	NHC	0.42	3.0
C1T	PO4	0.42	1.0

CON	PO4	0.42	1.0
OCN	PO4	0.40	4.5
NHC	PO4	0.42	4.5
NEC	PO4	0.46	4.7
C1T	N4M	0.42	1.5
CON	N4M	0.42	1.5
OCN	N4M	0.40	3.5
NHC	N4M	0.42	3.5
NEC	N4M	0.46	4.7
C1T	CMF	0.42	1.2
CON	CMF	0.42	1.0
OCN	CMF	0.40	3.5
NHC	CMF	0.42	3.5
NEC	CMF	0.46	4.5

Table S5 Average tilt angle and the variance of bending angles, calculated from the CAVS CG simulations (last 400 ns) of KALP31 monomer and dimer.

	Monomer	**Dimer**	
		chain 1	**chain 2**
variance of bending angle (degree^2)	20.6	104.2	80.5
tilt angle (degree)	42.2	17.9	19.3