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Supplemental Information

In Vitro and MD Simulation Study to Explore Physicochemical Parameters for Antibacterial Peptide to Become Potent Anticancer Peptide

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Supporting Information

In vitro & molecular dynamic simulation study to explore physicochemical parameters for antibacterial peptide to become potent anticancer peptide

Rui Ma[1], Sin Wa Wong[1], Lilin Ge[2], Chris Shaw[3], Shirley W. I. Siu[4], Hang Fai Kwok[1,*]

[1]Cancer Centre, Faculty of Health Sciences, University of Macau, Avenida de Universidade, Taipa, Macau SAR

[2]State Key Laboratory Cultivation Base for TCM Quality and Efficacy, Nanjing University of Chinese Medicine, Qixia District, Nanjing, China

[3]Natural Drug Discovery Group, School of Pharmacy, Medical Biology Centre, Queen's University, Belfast BT9 7BL, Northern Ireland, UK

[4]Department of Computer and Information Science, Faculty of Science and Technology, University of Macau, Avenida de Universidade, Taipa, Macau SAR

Corresponding author

[*]Correspondence: hfkwok@um.edu.mo

Room 4006, Faculty of Health Sciences (E12), University of Macau, Avenida de Universidade, Taipa, Macau SAR

Table S1. The physicochemical properties of AcrAP1 and its six mutants

Name	Primary structure	MW	z	Hydrophobicity	Hyd.Moment	FreqPolar	FreqNoPolar
AP1-Z1	FLFSLIPHAISGLISAFK	1960.37	1	0.90167	0.43720	0.333	0.667
AP1-Z3a	FLFSLIKHAIKGLISAFK	2032.53	3	0.75389	0.51323	0.389	0.611
AP1-Z3b	FLFSLIKHAISKLISAFK	2062.55	3	0.75167	0.48449	0.389	0.611
AP1-Z5a	FLFKLIPKAIKGLIKAFK	2074.69	5	0.68111	0.63973	0.333	0.667
AP1-Z5b	FLFKLIKHAIKGLIKAFK	2114.72	5	0.64833	0.61675	0.389	0.611
AP1-Z7	FLFKLIKKAIKKLIKAFK	2176.87	7	0.53111	0.68802	0.389	0.611
AP1-Z9	FLFKLIKKKIKKLIKKFK	2291.06	9	0.38667	0.63527	0.500	0.500

Table S2. Summary of the system and bilayer properties averaged from the last 200-ns trajectory

Lipid composition	Box dimensions (nm)	Bilayer thickness (nm)	Headgroup orientation[a] DOPC, DOPS	Peptide adsorption observed	Time to peptide association with membrane (ns)[#]
DOPC	5.9 x 5.9 x 7.2	38.7	21.7, -	-	n/a
DOPC-S1	6.0 x 6.0 x 12.4	37.9	23.5, -	yes	371
DOPC-S2	5.9 x 5.9 x 12.7	38.5	22.1, -	no	-
DOPC-S3	5.9 x 5.9 x 12.8	38.7	21.9, -	no	-
DOPC/DOPS	5.8 x 5.8 x 7.4	39.2	22.2, 20.0	-	n/a
DOPC/DOPS-S1	5.9 x 5.9 x 13.0	39.0	22.9, 21.1	yes	73
DOPC/DOPS-S2	5.9 x 5.9 x 12.7	38.5	22.8, 21.6	yes	53
DOPC/DOPS-S3	5.9 x 5.9 x 12.8	38.4	22.9, 22.9	yes	78

[#]Time to the formation of uninterrupted hydrogen bonds between the peptide and the membrane (see Supplementary Figure S2)

Table S3. Summary of the membrane and peptide-membrane simulations.

Membrane mimic	Lipid composition	Peptide conformation	Water	Ions (Na^+, Cl^-)	Time (ns)
Normal mammalian cell	102 DOPC	--	3954	9, 9	200
	102 DOPC	S1	10300	27, 33	1000
	102 DOPC	S2	10300	27, 33	1000
	102 DOPC	S3	10300	27, 33	1000
Cancer cell	76 DOPC, 26 DOPS	--	4084	35, 9	200
	76 DOPC, 26 DOPS	S1	10400	53, 33	1000
	76 DOPC, 26 DOPS	S2	10400	53, 33	1000
	76 DOPC, 26 DOPS	S3	10400	53, 33	1000

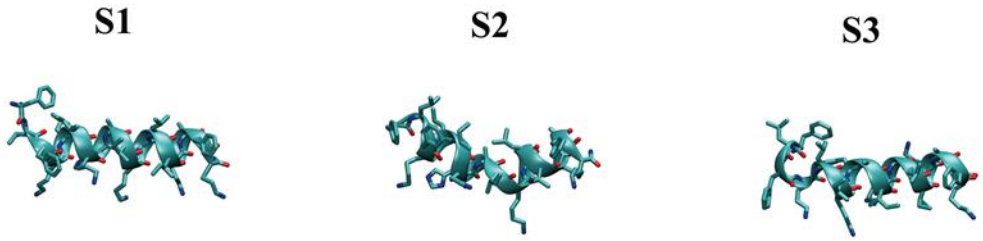

Figure S1. Three representative configurations of the AP1-Z5b peptide obtained by clustering analysis of the peptide simulation in solvent (200 ns). N-terminal of the peptide was displayed in the left end; hydrogen atoms were not shown for clarity.

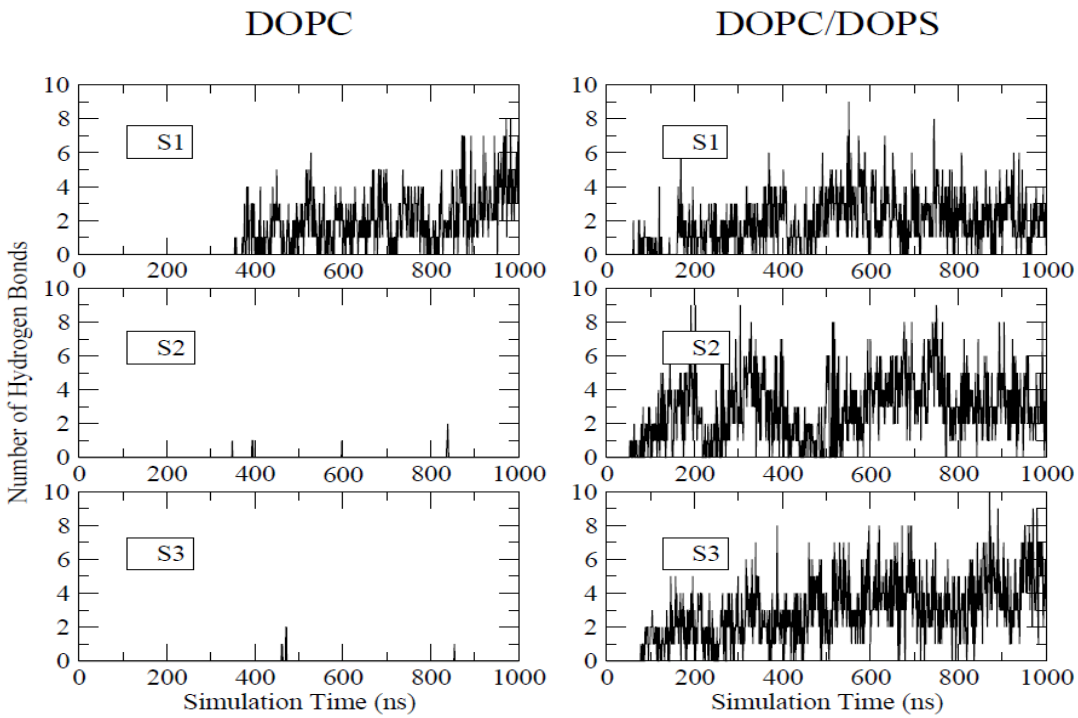

Figure S2. Hydrogen bond analysis of peptide-membrane simulations.

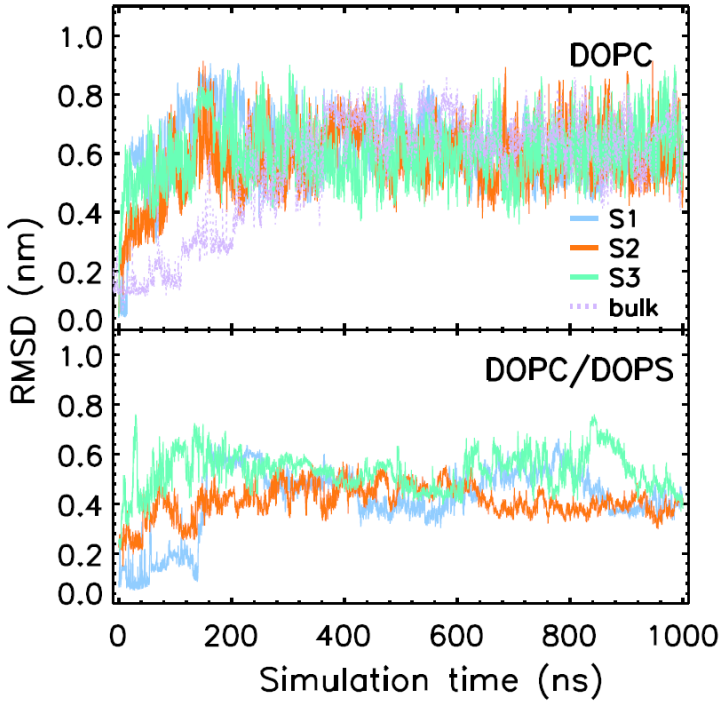

Figure S3. Root mean squared deviation (RMSD) of the AP1-Z5b backbone as a function of simulation time.

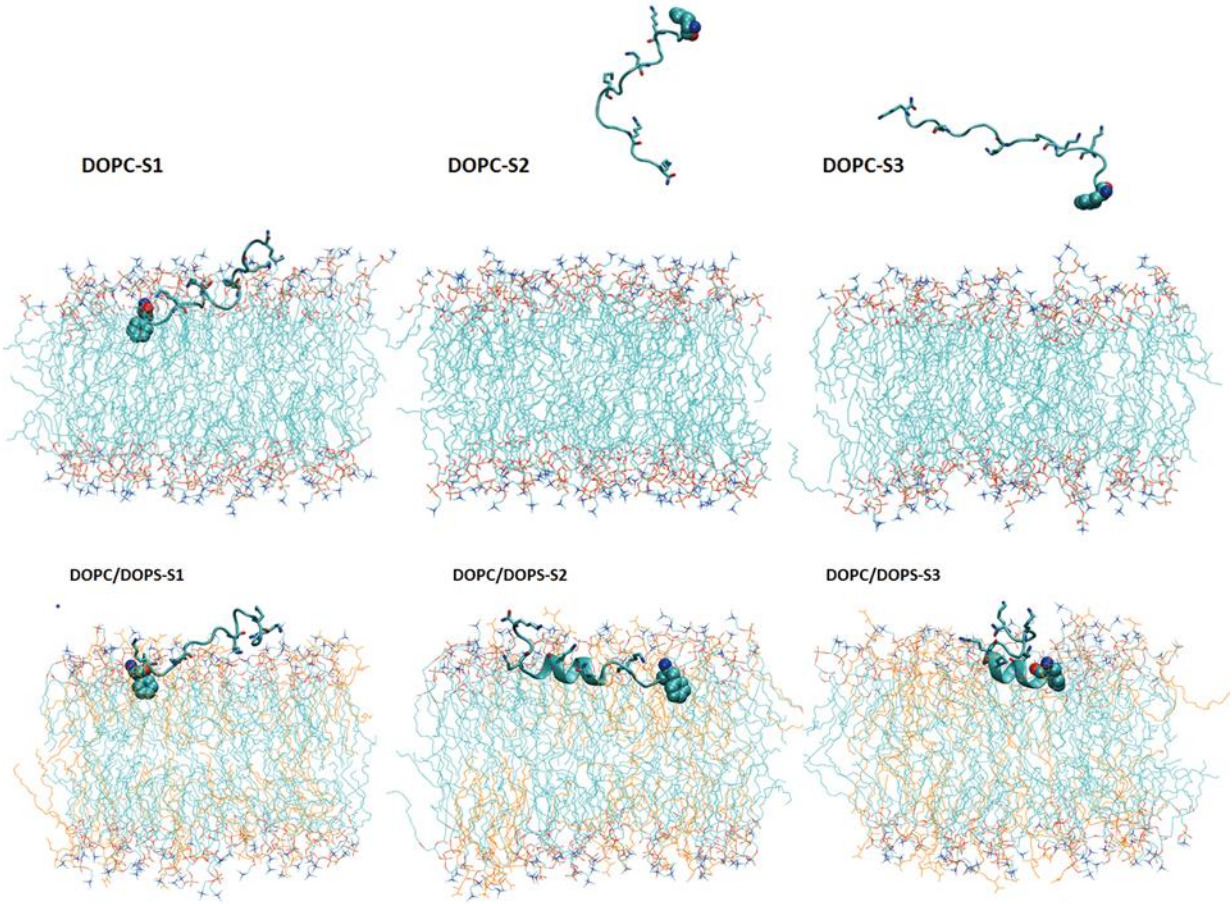

Figure S4. Final snapshots of all peptide-membrane simulations. The peptide was displayed with cartoon style, charge residues were shown as sticks, and the first residue of the peptide was shown as spheres. Water and ions were not displayed for clarity. DOPC lipids were in cyan color (tails) and DOPS lipids in orange color.