Supplementary Material

Vesicle protrusion induced by antimicrobial peptides suggests common carpet mechanism for short antimicrobial peptides

Peter Park[1,3], Danilo K. Matsubara[1], Domenico R. Barzotto[1], Filipe S. Lima[2], Hernan Chaimovich[1], Siewert J. Marrink[3,*], Iolanda M. Cuccovia[1,*]

[1] Departamento de Bioquímica, Instituto de Química, Universidade de São Paulo, São Paulo, Brazil;

[2] Departamento de Química Fundamental, Centro de Ciências Exatas e da Natureza, Universidade Federal de Pernambuco, Recife, Brazil.

[3] Groningen Biomolecular Sciences and Biotechnology Institute (GBB), University of Groningen, 9747 AG Groningen, the Netherlands

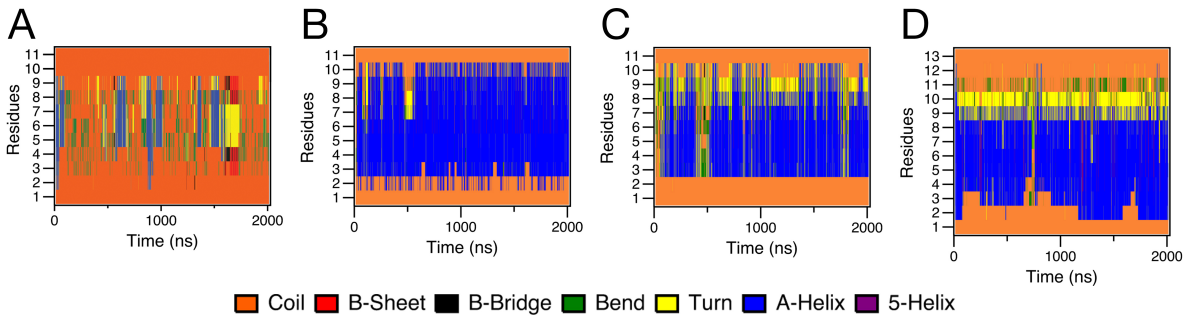
		BP100	Decoralin	NK-1	Temporin
Sequence		KKLFKKILKYL	SLLSLIRKLIT	RPKPQQFFGLM	FVQWFSKFLGRIL
Aminoacids		11	11	11	13
Overall charge		+6	+3	+3	+3
<H> Hydrophobicity		0.427	0.780	0.501	0.906
Aminoacids composition	Polar	5 (45.45%)	5 (27.78%)	5 (27.78%)	5 (27.78%)
	Non-Polar	6 (54.54%)	6 (33.33%)	6 (33.33%)	8 (44.44%)
	Charged	5 (45.45%)	3 (27.27%)	2 (18.18%)	3 (27.27%)
	Aromatic	2 (18.18%)	0 (0%)	2 (18.18%)	4 (30.76%)

Table S1: Structural properties of the antimicrobial peptides studied. The hydrophobicity <H> was calculated using the Fauchere-Pliska scale[1].

	Eq 1	Eq 2	Eq 3	Eq 4	Eq 5	Production
Water pore size (Å)	20	15	10	5	2	0
Time step (fs)	2	5	10	15	20	20
Time (ns)	100	25	25	25	25	10000
Barostat	Berendsen					Parrinello-Rahman
			1 bar isotropic τ_p= 5.0 ps^{-1} β= 4.5e^{-5}			1 bar isotropic τ_p= 12.0 ps^{-1} β= 4.5e^{-5}
Thermostat	V-rescale (τ_t=1.0, T=303.15 K)					

Table S2: Vesicle-only system equilibration and production information. β is compressibility, τ_p is the pressure coupling constant, and τ_t is the temperature coupling constant

Secondary Structure in Water



BP100	Decoralin	Neurokinin-1	Temporin
Helicity (%)			
9	65	49	49
Random Coil (%)			
67	29	36	36

Figure S1: Secondary structure analysis (DSSP) of peptides in water from atomistic simulations. BP100 (A), Decoralin (B), NK-1 (C), and Temporin-L (D). The table below shows the respective percentage of helicity obtained from the DSSP analysis.

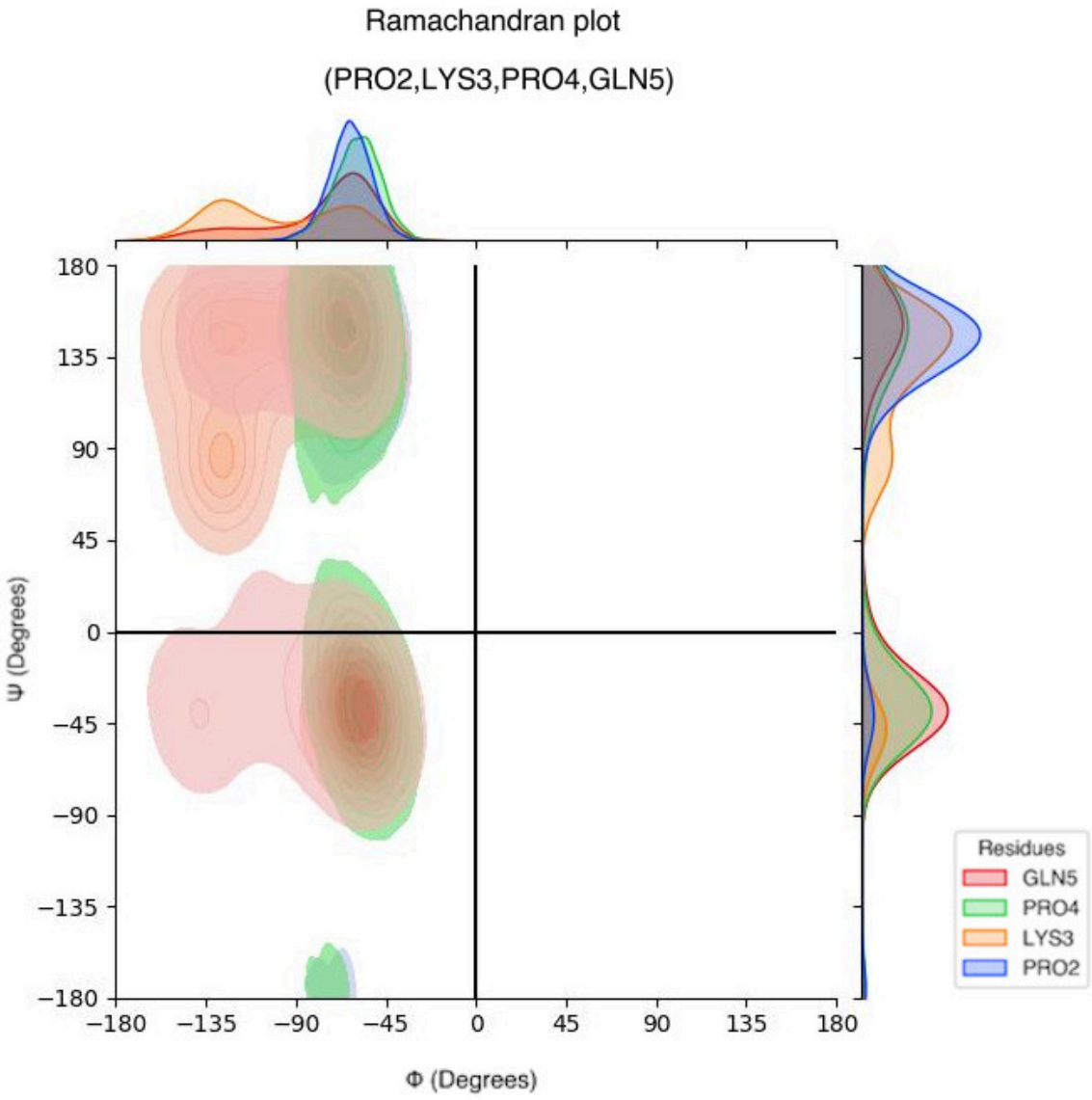


Figure S2: Ramachandran plot and respective histograms for NK-1 N-terminus region from the atomistic simulation in POPC/POPG membrane. The plot reveals the region has higher flexibity, as in a random coil conformation, which means residues can occupy randomly different regions of the graph at different times[2], with some restrictions due to the more rigid nature of proline, given that it can only bend at a range of roughly -90 to -45 degrees along the ϕ axis[3]. For example, GLN5 occupies regions typically associated with beta sheets, PPII helices and alpha helices[4].

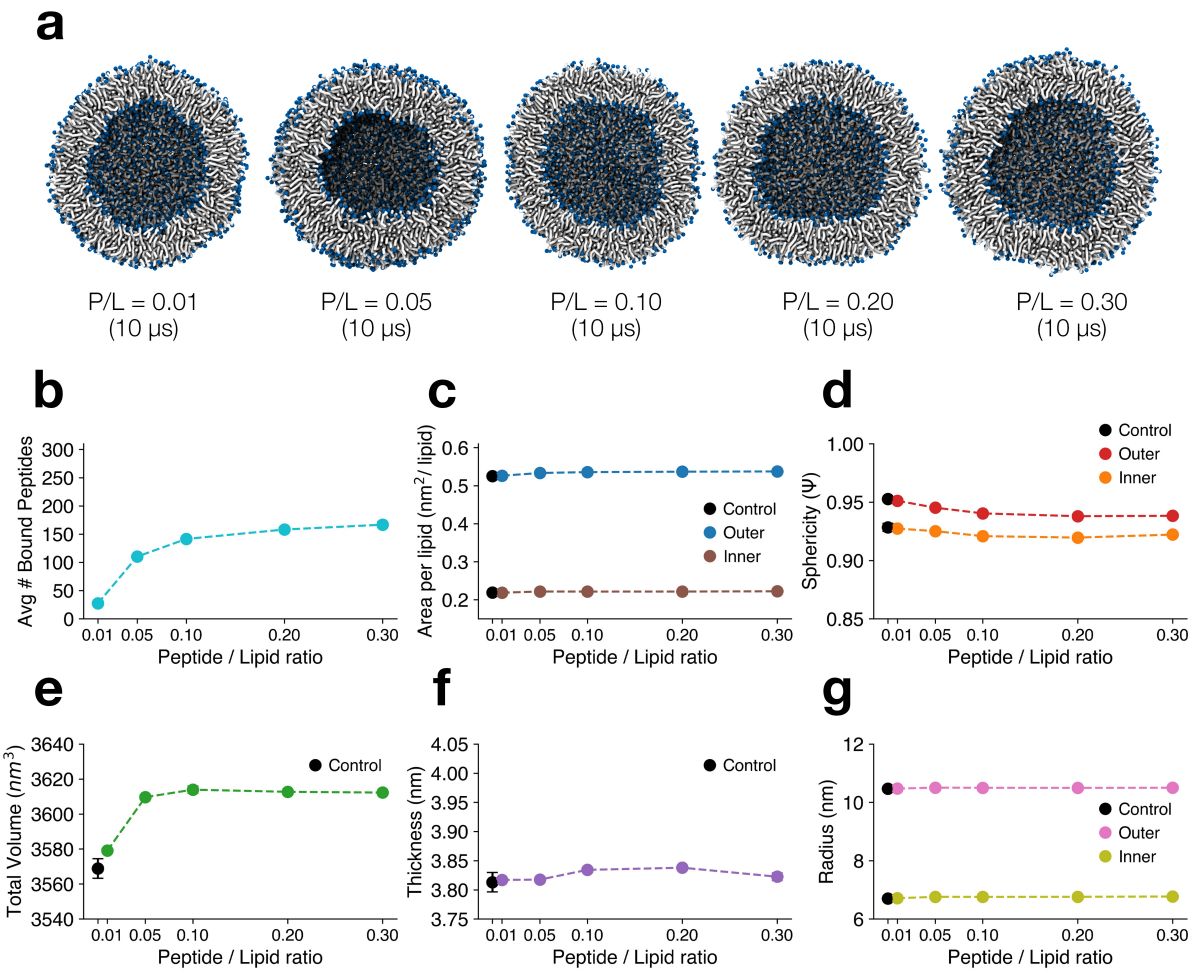


Figure S3: Simulations of BP100 in POPC vesicles. (a) Cut-away cross-sectional last frame snapshots of POPC vesicle/BP100 system at low (P/L = 0.01 and 0.05), medium (P/L = 0.10), and high (P/L = 0.20 and 0.30) concentrations. Peptides, water and ions are not shown for clarity. Obtained averaged peptide binding outcomes in vesicles according to the respective P/L are presented (b-g). Data points with no error bars had an error below 5%. Data points and error bars were obtained averaging the last 5μ of each simulation.

System	APL_{outer} (nm^2/lipid)	APL_{inner} (nm^2/lipid)	V_{total} (nm^3)	D_{HH} (nm)	R (nm)	φ
Control	0.525	0.219	3568	3.81	10.4	0.952
P/L = 0.01	+0.19%	-0.17%	+0.29%	-0.17%	+0.07%	-0.15%
P/L = 0.05	+1.54%	+1.24%	+1.14%	+1.24%	+0.37%	-0.78%
P/L = 0.10	+1.99%	+1.16%	+1.26%	+1.16%	+0.32%	-1.29%
P/L = 0.20	+2.20%	+1.18%	+1.23%	+1.18%	+0.30%	-1.54%
P/L = 0.30	+2.32%	+1.52%	+1.22%	+1.52%	+0.34%	-1.50%

Table S3: Summary of vesicle structural properties from BP100 in POPC vesicle simulations. Variation in percentage of POPC vesicle structural properties compared to control.

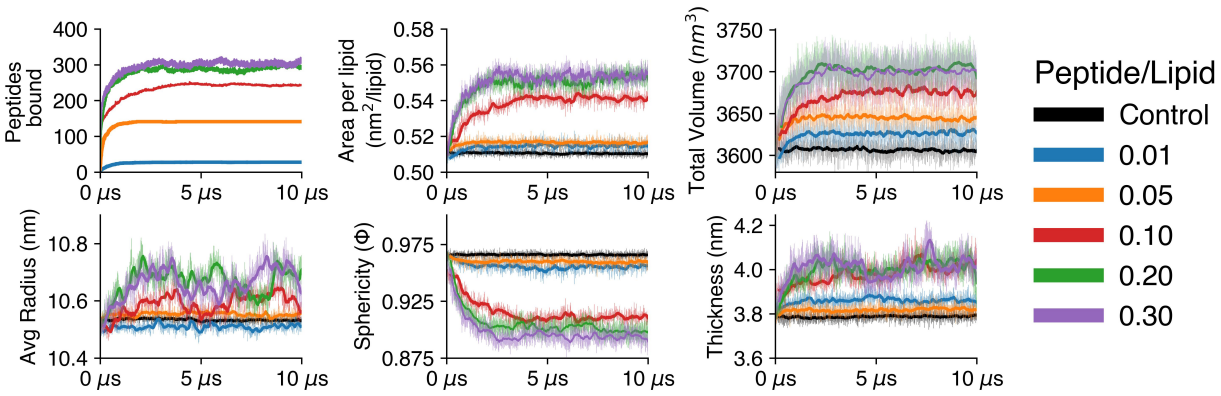


Figure S4: Temporal analysis of vesicle structural properties from BP100 in POPC:POPG (50:50) vesicle simulations.

System	D_{HH} (nm)
Control	3.924
P/L = 0.01	-0.71%
P/L = 0.05	-3.47%
P/L = 0.10	-6.15%
P/L = 0.20	-6.34%
P/L = 0.30	-6.50%

Table S4: Membrane thickness from BP100 in POPC:POPG (50:50) planar membrane simulations. Variation in percentage of POPC:POPG membrane thickness compared to control. Estimated errors by block averaging were below 5%.

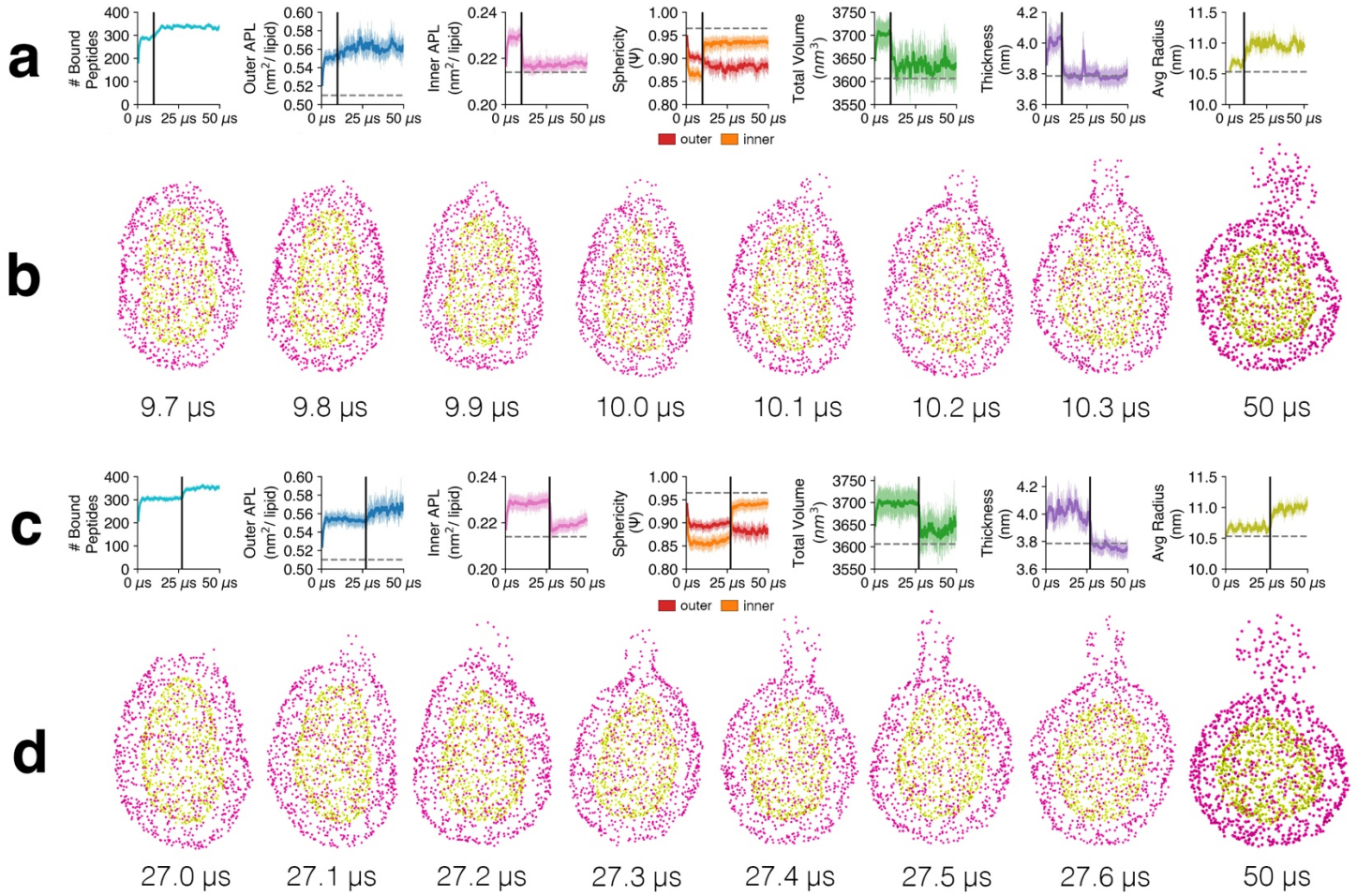


Figure S5: Antimicrobial peptide BP100 induces vesicle budding at high concentrations. (A) and (C) show computed properties for POPC:POPG vesicles throughout BP100/vesicle simulation at P/L = 0.20 and P/L = 0.30, respectively. We show the number of bound peptides, outer and inner area per lipid, outer leaflet sphericity, total vesicle volume, membrane thickness and average radius. Black vertical lines indicate the approximate time when budding started. (B) and (D) show snapshots of the vesicles of both simulations during membrane protrusion. Only phosphorus atoms are shown and are colored in magenta (outer) and yellow (inner).

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References

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