Supporting Information:

Nanocapsule Designs for Antimicrobial Resistance

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	Capzip	AM-β-annulus
Shape	Truncated icosahedron	Dodecahedron
Nr molecules	120	60
Net charge	$+720\,e$	$+180\,e$
SASA	2094 nm^2	1100 nm^2
Q_{SASA} (positive amino acids)	0.55	0.30
Q_{SASA} (negative amino acids)	0.10	0.06
Q_{SASA} (polar amino acids)	0.10	0.16
Q_{SASA} (hydrophobic amino acids)	0.25	0.48

Table 1: **Characteristics of the capzip and AM-β-annulus capsules.**

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β-annulus          Sequence                        REU
WT                 ITHVGGVGGSIMAPVAVSRQLVGS    -2272.71
AM (not soluble)   ITHVGGVGGSIMAPVAVSRRWTWE    -2062.63
AM                 INHVGGVKGSIMAPVSVSRRWTWE    -2543.30
                   *.***** *******:***. . .
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Figure 1: **Alignment of β-annulus sequences**: Wild Type, with grafted antimicrobial sequence (AM, not soluble) and with antimicrobial sequence and three mutated residue to improve AM-β-annulus capsule solubility. On the right, the Rosetta Energy Units of the dodecahedron generated with the three sequences.

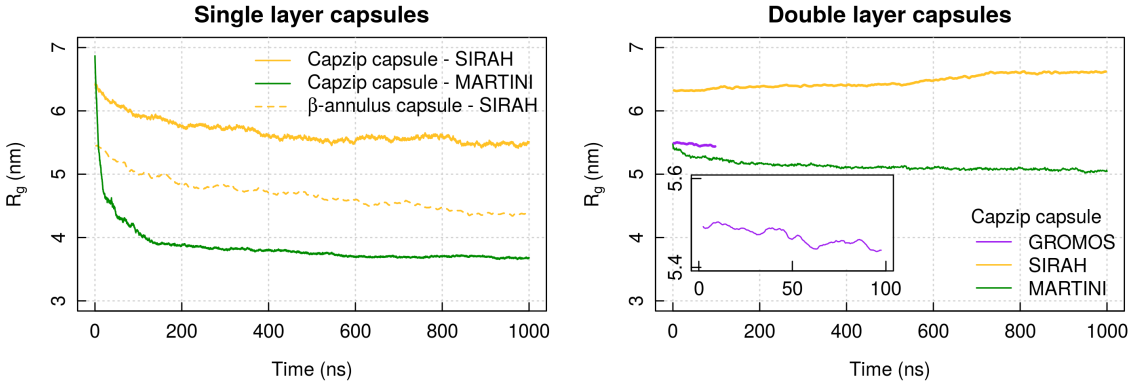

Figure 2: **Simulations of single layer capzip and AM-β-annulus capsules (left) and double layer capzip capsule (right) at atomistic and coarse-grained level**: radius of gyration R_g computed on the protein backbone of the capsule. Inset: zoom on the atomistic GROMOS atomistic R_g.

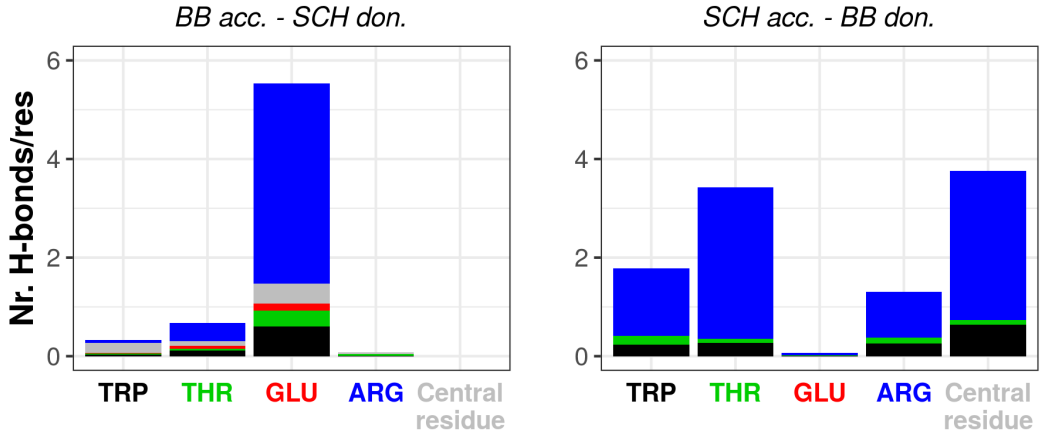

Figure 3: **Atomistic simulation of capzip capsule (replica 1): average number of hydrogen bonds per residue** occurring between amino acids backbone and side chains in the last 50 ns of simulation (Central residue refers to the moiety linking the antimicrobial arms - see Figure 1 in the main text). For each bar, the residue on the x-axis is the acceptor, and the bar is split by the identity of the donors.

GROMOS simulations		
Nr. lipids	E (mV/nm)	ApL (nm^2)
740	–	0.569(4)
740	-20	0.568(3)
Polar MARTINI simulations		
2880	–	0.611(1)
2880	-20	0.614(1)
2880	-40	0.619(2)

Table 2: **Membrane alone simulations.** Area per Lipid (ApL) of DLPC/DLPG 3:1 membrane simulated with atomistic and coarse-grained resolution, at 150 mM NaCl salt concentration, with and without electric field (E). For comparison, experimental values for a DLPC bilayer (without salt) are: 0.608-0.632 nm^2 for ApL[2], and 3 μm^2 for D.[1] Experimental values for DLPC/DLPG 3:1 not assessed at the time of the publication.

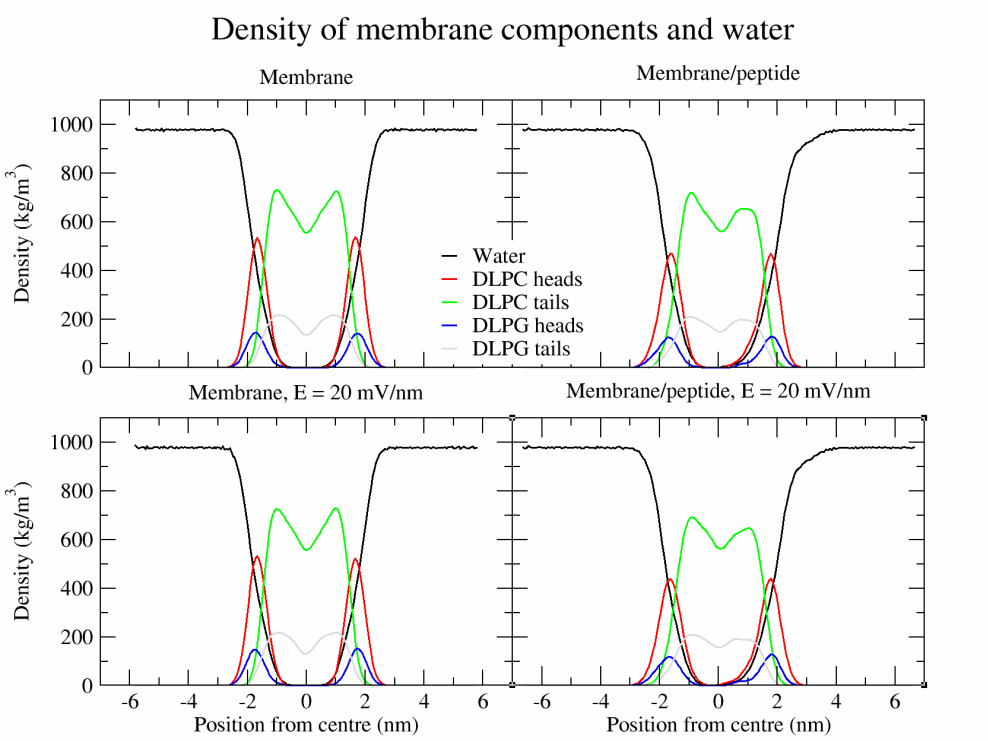

Figure 4: **Membrane alone simulations.** Lateral density profile of lipid components in atomistic simulations of DLPC/DLPG 3:1 membrane, with and without electric field, with and without capzip peptide.

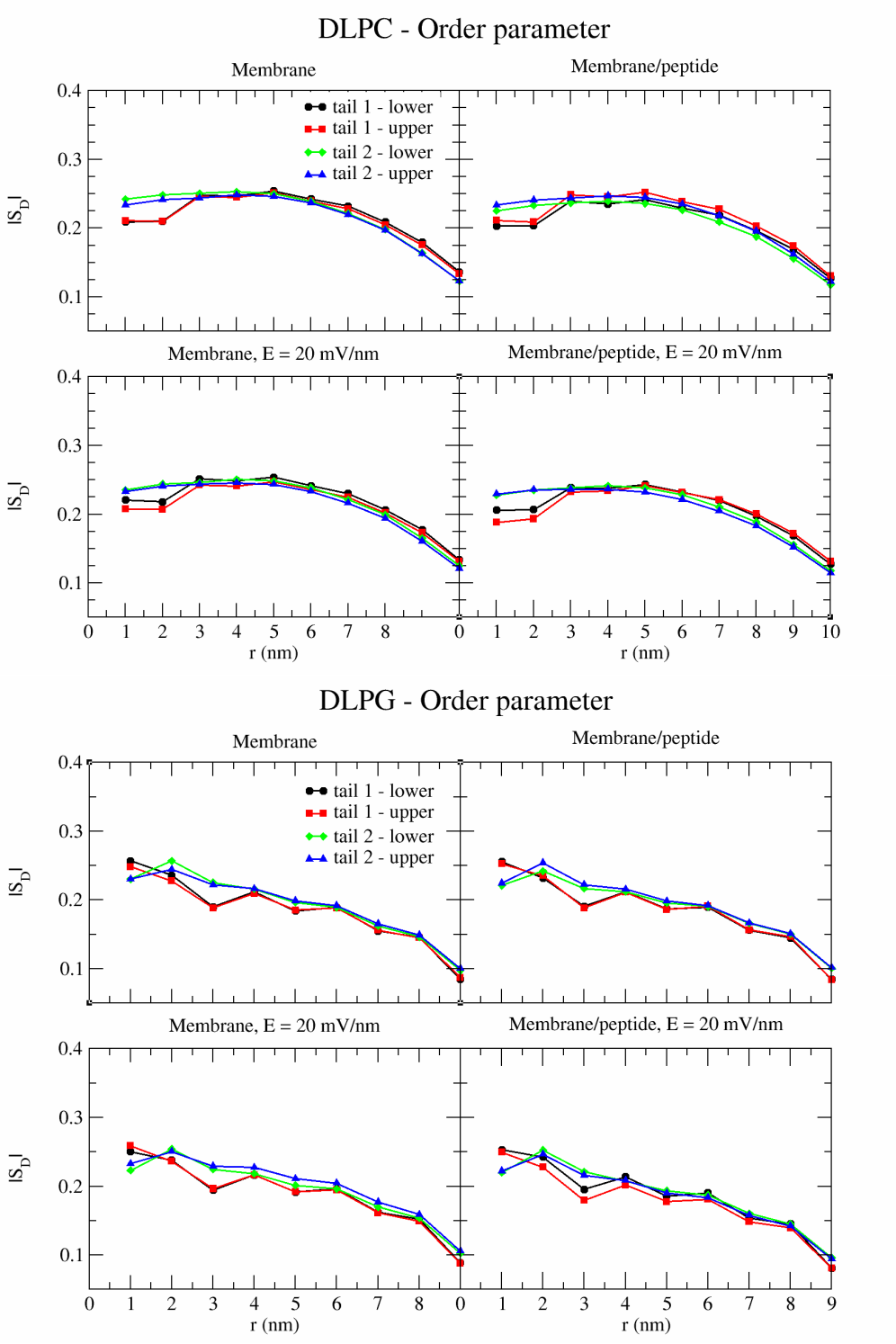

Figure 5: **Membrane alone simulations.** Tail order parameter for both DLPC and DLPG in atomistic simulations of a DLPC/DLPG 3:1 membrane, with and without electric field, with and without capzip peptide.

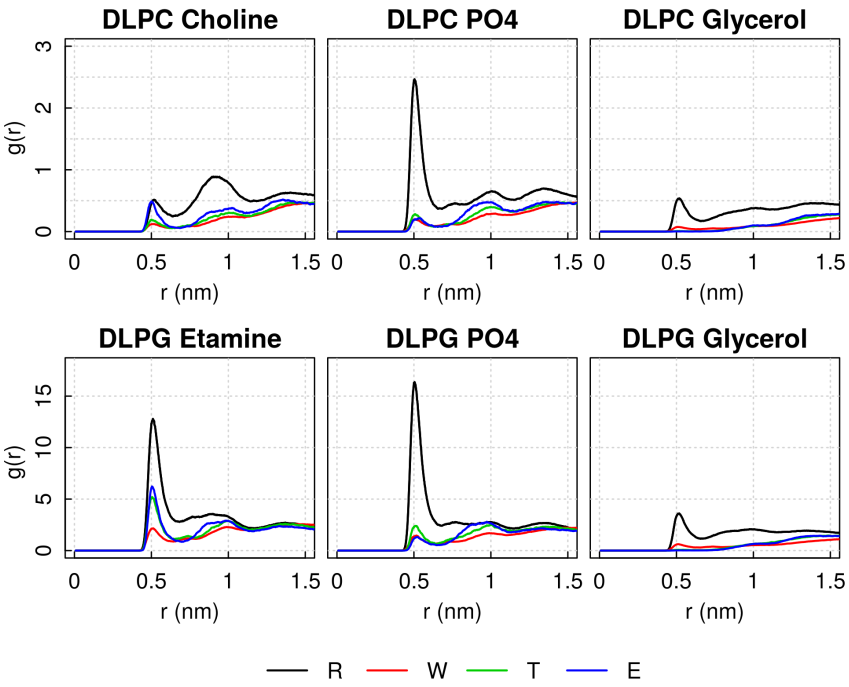

Figure 6: **MARTINI simulation of capzip capsule on a bacterial model membrane**: Radial Distribution Function of capzip amino acids around typical moieties of lipids heads, averaged over the time simulated after the capsule binding.

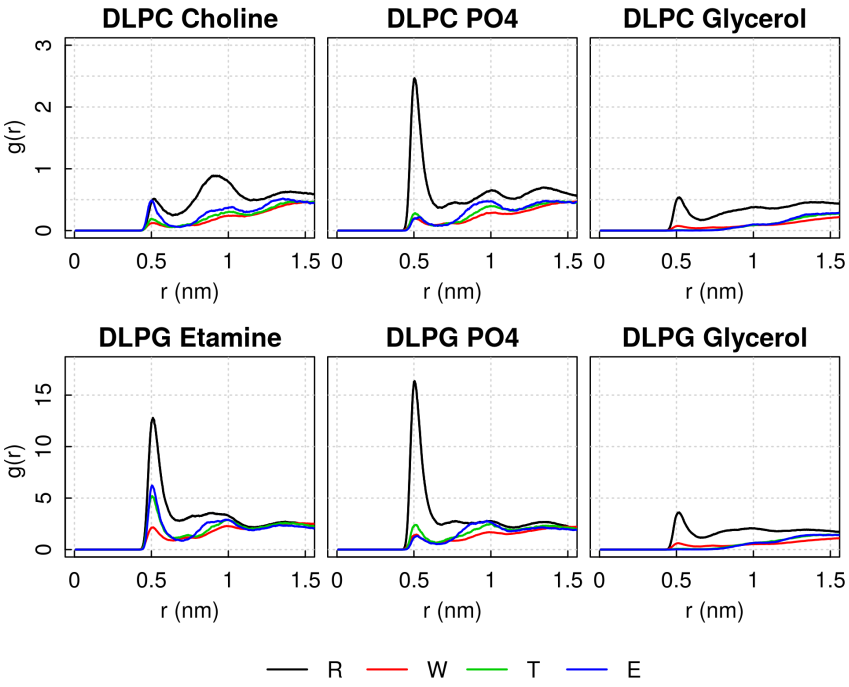

Figure 7: As in Figure 6, for SIRAH simulation.

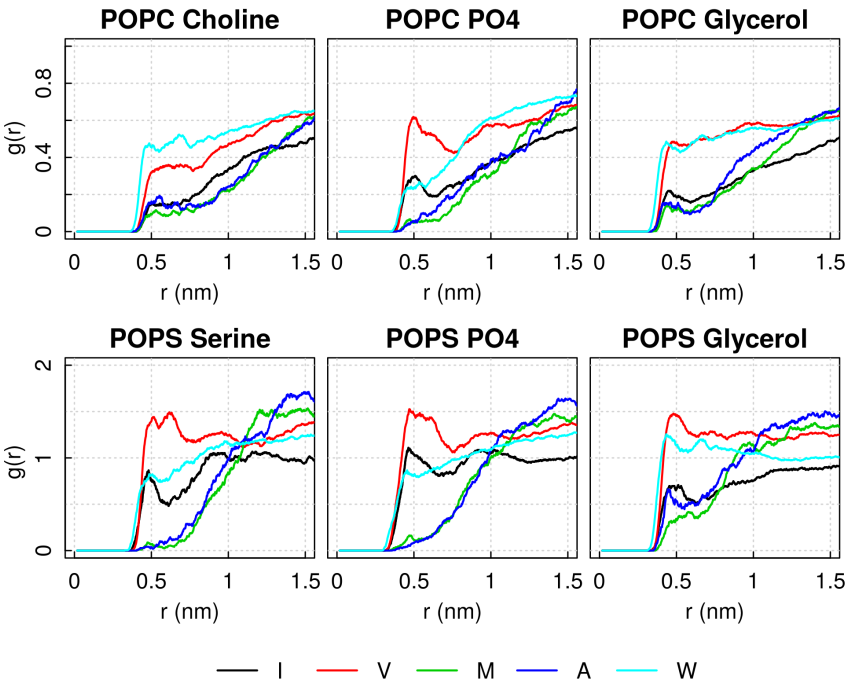

Figure 8: **SIRAH simulation of AM-β-annulus capsule on a bacterial model membrane**: Radial Distribution Function of AM-β-annulus *hydrophobic* amino acids around l typical moieties of lipids heads, averaged over the time simulated after the capsule binding.

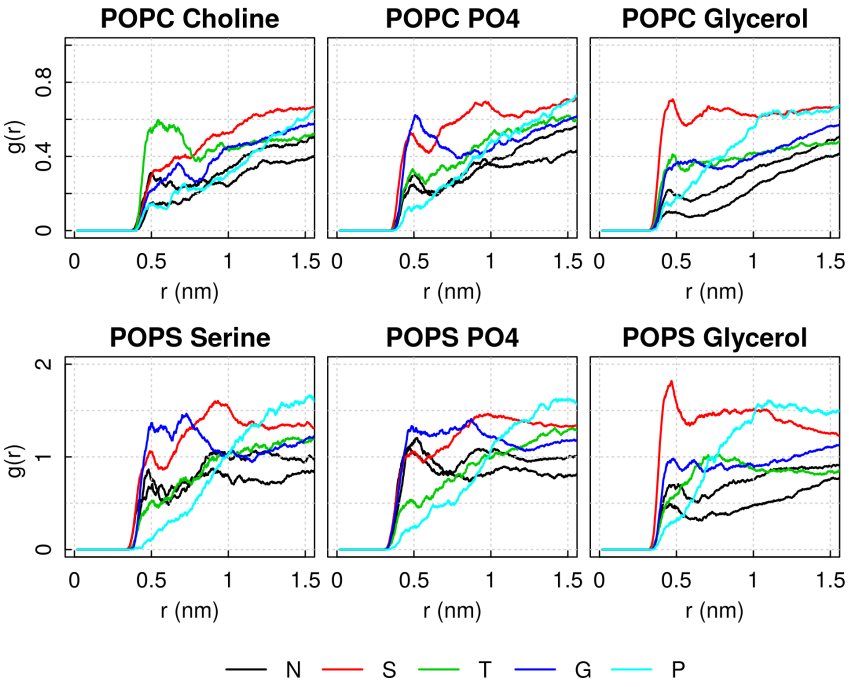

Figure 9: As in Figure 8, for *polar* and *special* amino acids.

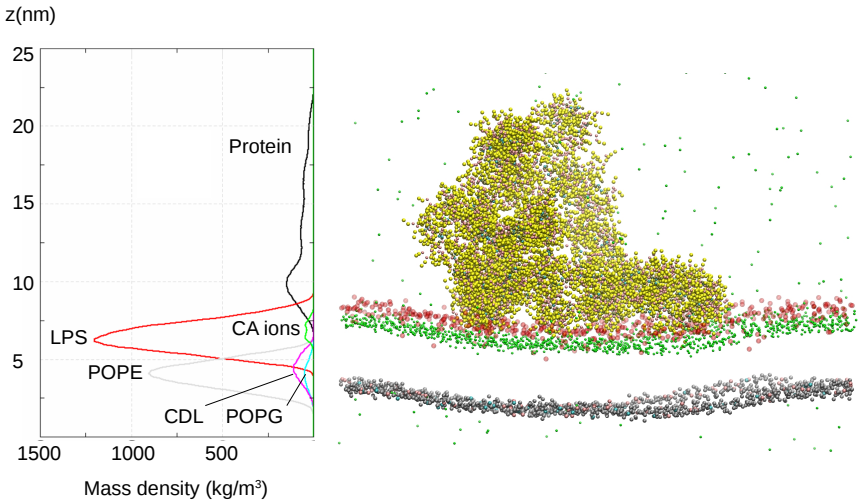

Figure 10: **MARTINI simulation of capzip capsule on a LPS (top) and POPE/POPG/CDL 85:5:10 (bottom leaflet) membrane.** Left: mass density profile along z averaged over after the stabilisation of capzip capsule on the membrane (at 600 ns). Right: snapshot of the final configuration (1 μs). Peptides shown in van der Waals representation; phosphate beads of POPE, POPG and CDL shown in grey, cyan and pink beads respectively. The top layer of LPS molecules (beads S10) shown as red transparent beads, CA ions as green small beads.