Supplementary Information

Membrane disintegration by the antimicrobial peptide (P)GKY20: lipid segregation and domain formation

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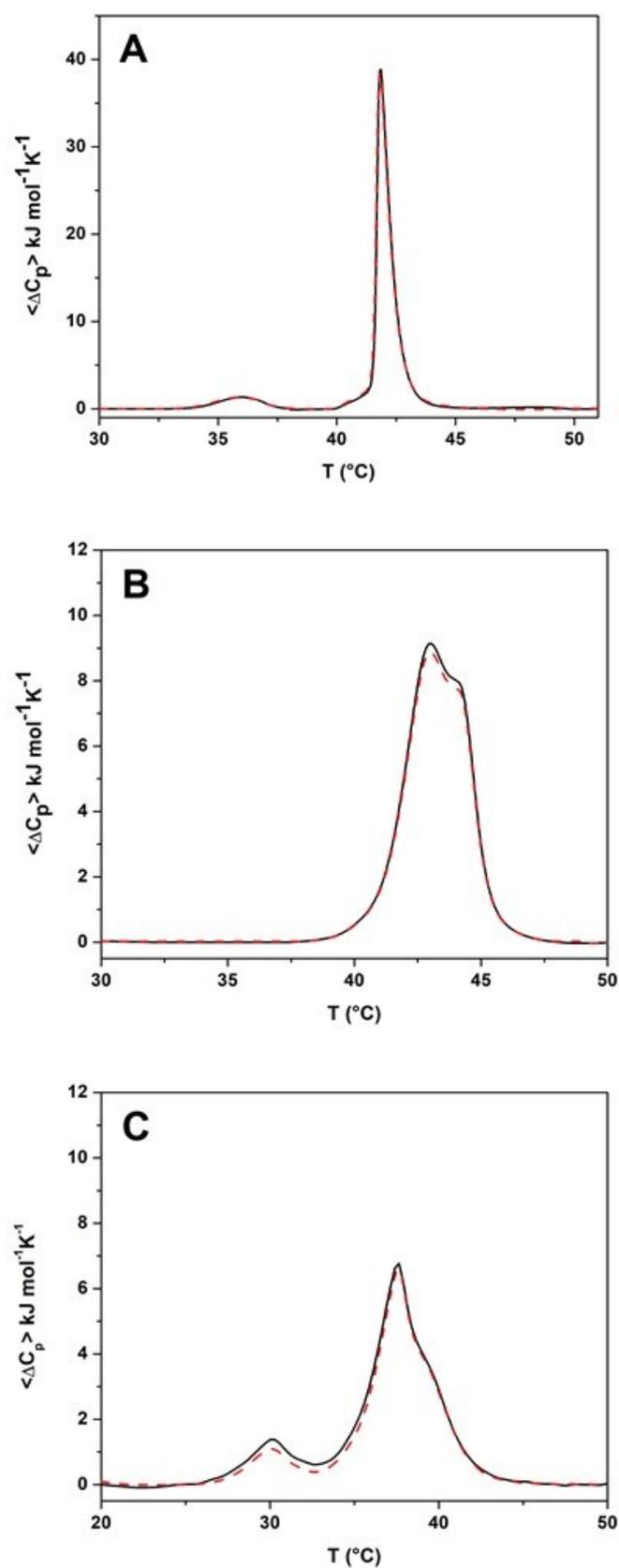
Fig. S1 Superimposition of the second (black line) and third (red dashed line) heating DSC scans of (A) DPPC, (B) DPPC/DPPG and (C) DPPC/POPG multilamellar vesicles in the presence of (P)GKY20 peptide at L/P = 10.
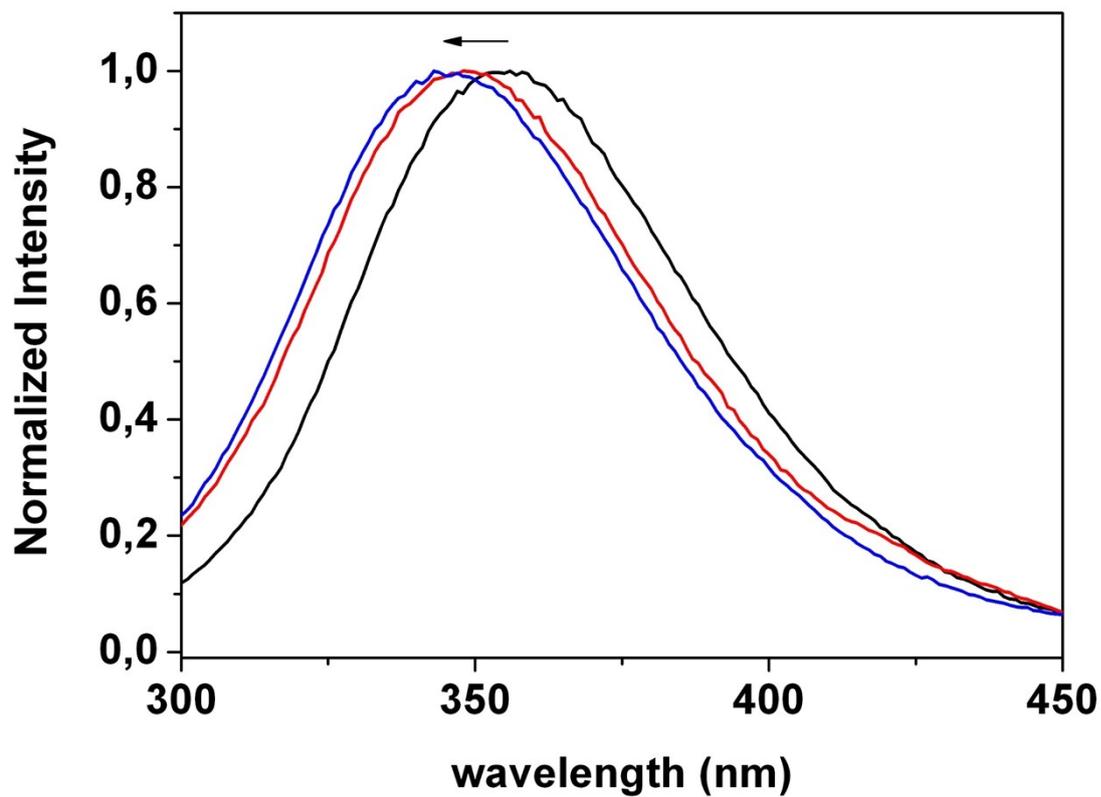
Fig. S2 Normalized fluorescence emission spectra of (P)GKY20 peptide in phosphate buffer (black line) and in the presence of POPC (red line) and POPC/POPG (blue line) unilamellar vesicles at a lipid-to-peptide ratio of 200. The spectra were recorded in a 1-cm path length quartz cuvette at the temperature of 25 °C.
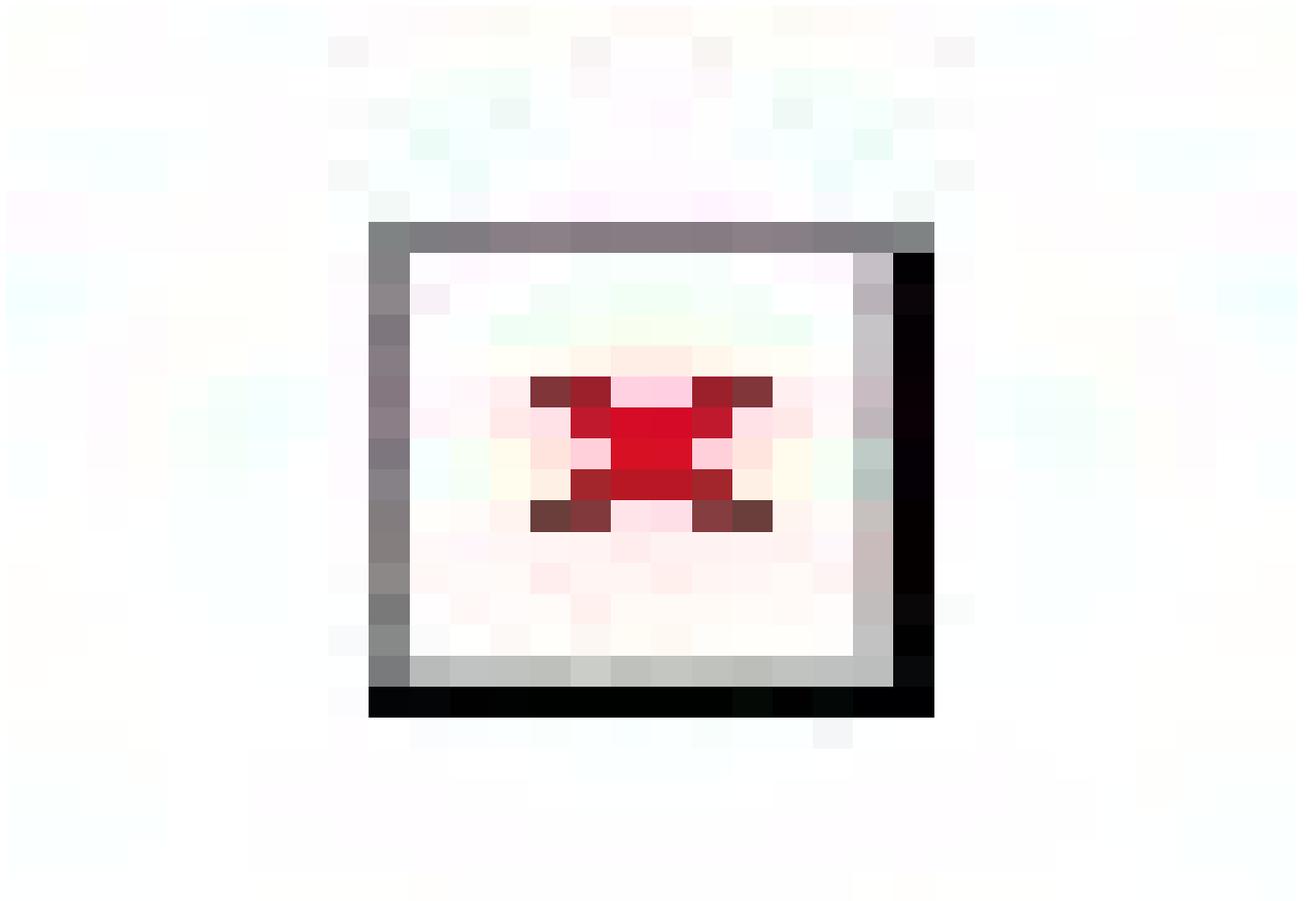
Fig. S3 Generalized Polarization (GP) function for Laurdan embedded in POPC (black line) and POPC/POPG (red line) as a function of peptide concentration. All the experiments were carried out in 10 mM phosphate buffer, pH 7.4 at the temperature of 25 °C.
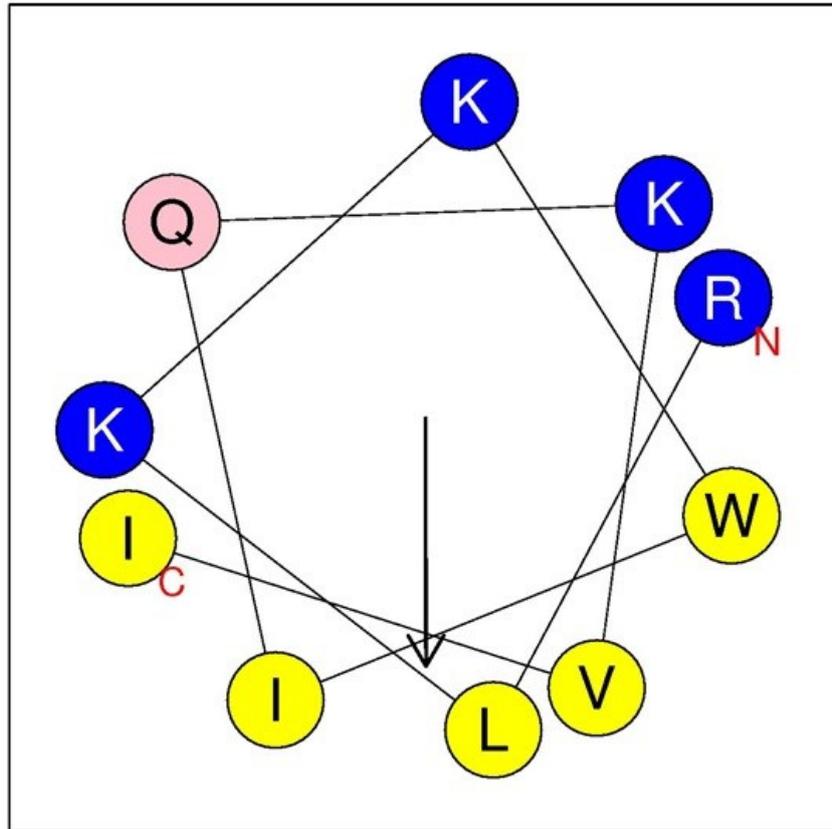
Fig. S4 The helical wheel projection of the RLKKWIQKVI segment of (P)GKY20. The arrow represents the hydrophobic moment vector (0.778). Yellow circles represent hydrophobic residues, blue circles positively charged residues and pink circles polar residues with no charge. The projection was made by means of Heliquest software (http://heliquest.ipmc.cnrs.fr/cgi-bin/ComputParams.py)