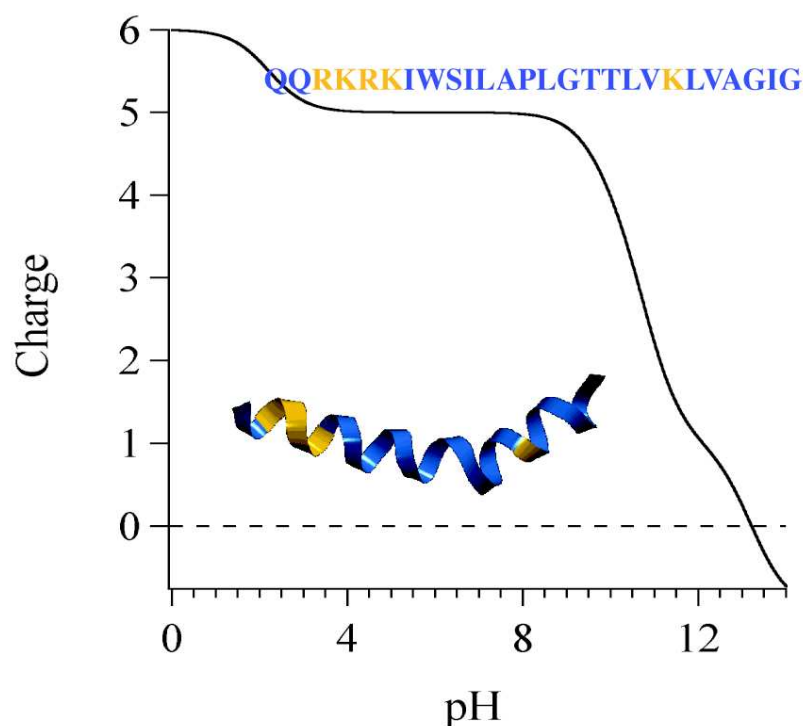


## Supporting Information

### Melittin adsorption and lipid monolayer disruption at liquid–liquid interfaces

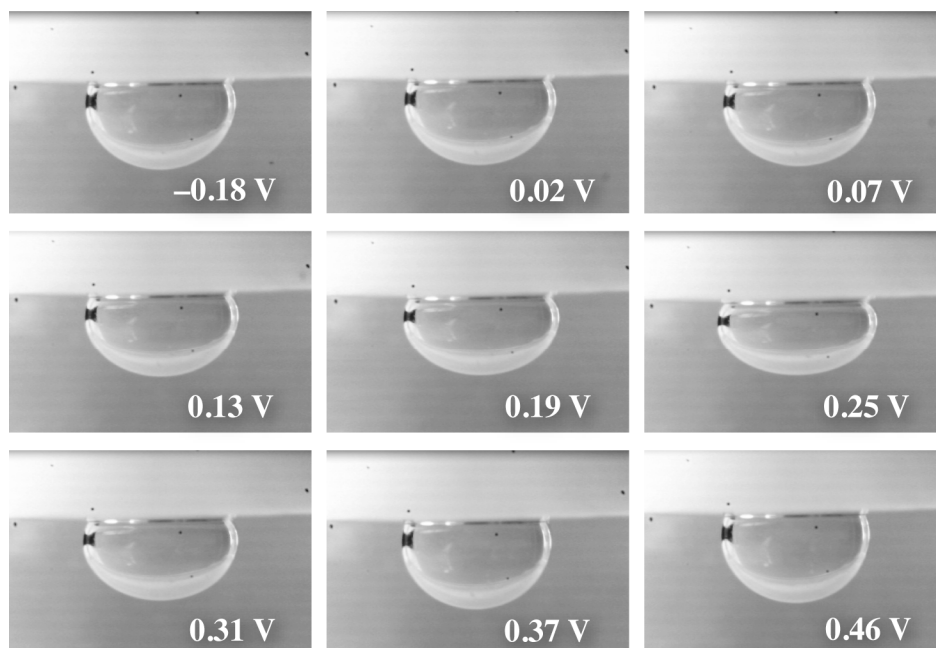
The calculation of the charge vs. pH curve for the peptide was carried out, in a very first approximation, by summing up the charge contributions from the various groups according to the Henderson-Hasselbalch equation<sup>1</sup>. The peptide structure presented in this figure was drawn using the software VMD<sup>2</sup> and the PDB file of the X-ray structure with a resolution of 2 Å.<sup>3</sup>



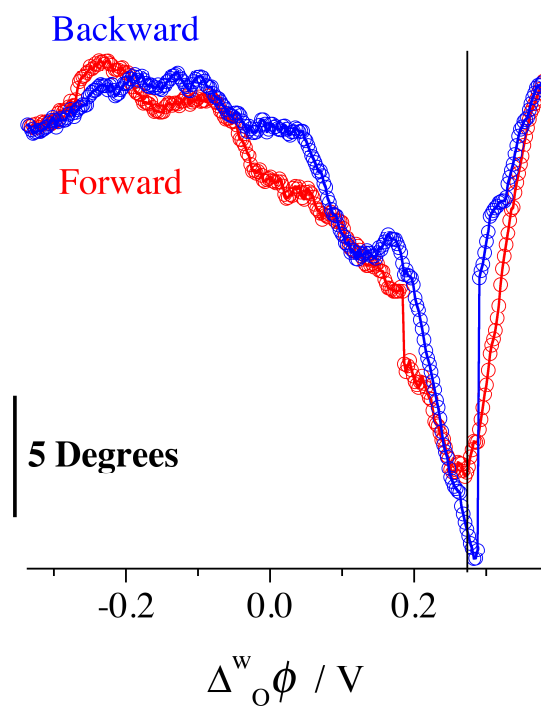
**Fig. S1.** Calculated charge versus pH curve for melittin (H<sub>2</sub>N–QQRKRKIWSILAPLGTTLV KLVAGIG) where arginine (R) and lysine (K) residues have been appear in yellow in the graphical representation of the peptide obtained with VMD.

Melittin has a maximum net charge of +6, four of which are consecutive and located in the basic N-terminal region (R-K-R-K), and the remaining positively charged, K-

20, close to the C-terminal region (G-26). This asymmetric distribution of polar and non-polar residues makes of melittin an amphipathic peptide that adopts an  $\alpha$ -helical conformation. The peptide helix has also been confirmed to bend because of the presence of a proline (P-13) in its sequence.<sup>3</sup>



**Fig. S2.** Video snapshots at different galvanic potentials of an aqueous droplet containing melittin ( $x = 20 \mu\text{M}$ ) and DCE in absence of DPPC.



**Fig. S3.** Four phase junction boundary angle dependence on the galvanic potential across the interface formed between DCE in absence of DPPC and an aqueous solution containing melittin ( $x = 20 \mu\text{M}$ ) obtained for the forward (red) and backward (blue) scan at  $10 \text{ mV}\cdot\text{s}^{-1}$ .

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- (2) Humphrey, W.; Dalke, A.; Schulten, K. *J. Molec. Graph.* **1996**, *14*, 33-38.
- (3) Terwilliger, T. C.; Elisenberg, D. *J. Biol. Chem.* **1982**, *257*, (11), 6010-6015.