Supporting Information:

Spectroscopic and computational study of melittin, cecropin A, and the hybrid peptide CM15

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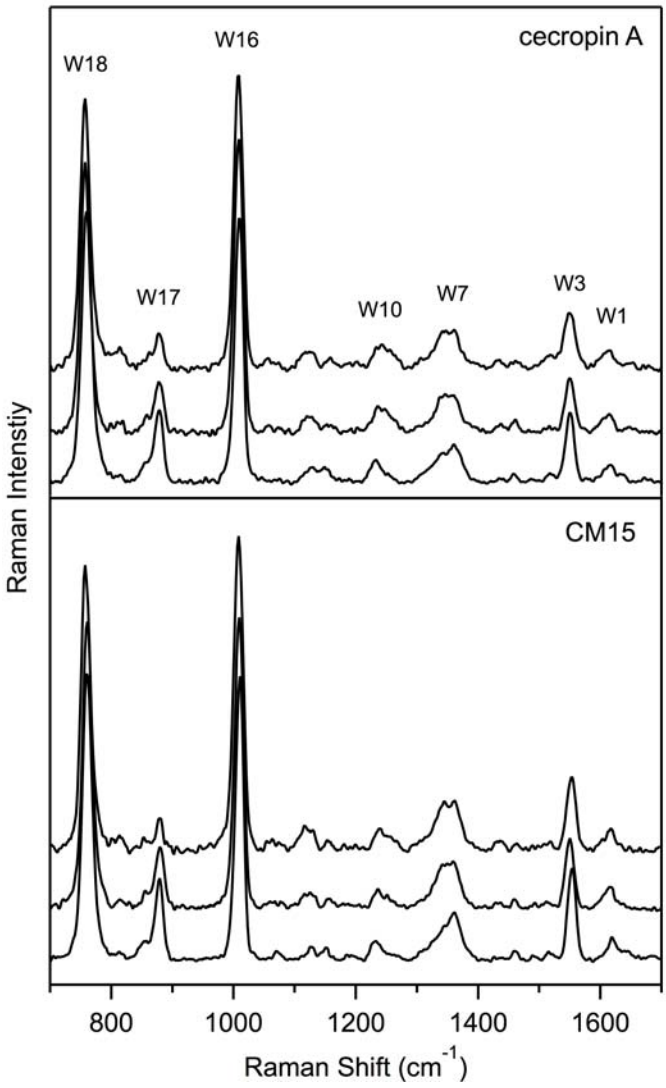

Figure S1: Expanded 230 nm UVRR spectra of cecropin A and CM15. Top spectra are of peptide in phosphate buffer, middle spectra are of peptide in zwitterionic vesicles, and bottom spectra are peptide in anionic vesicles.

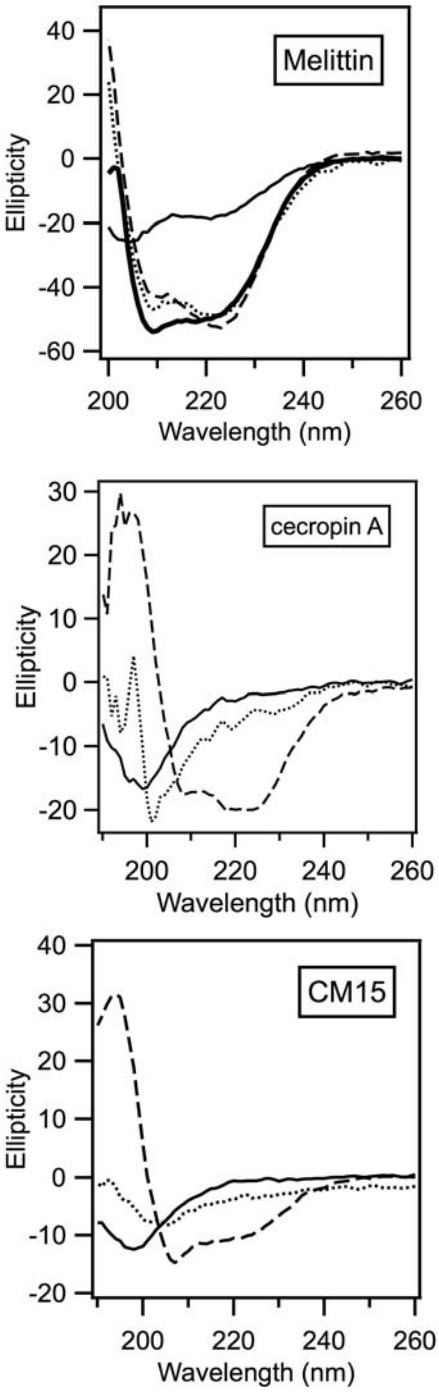

Figure S2: CD spectra of peptides in buffer (solid line), zwitterionic lipid vesicles (dotted lines), and anionic lipid vesicles (dashed lines). The CD spectrum of melittin as a tetramer in 2 M NaCl is also displayed (bold solid line).

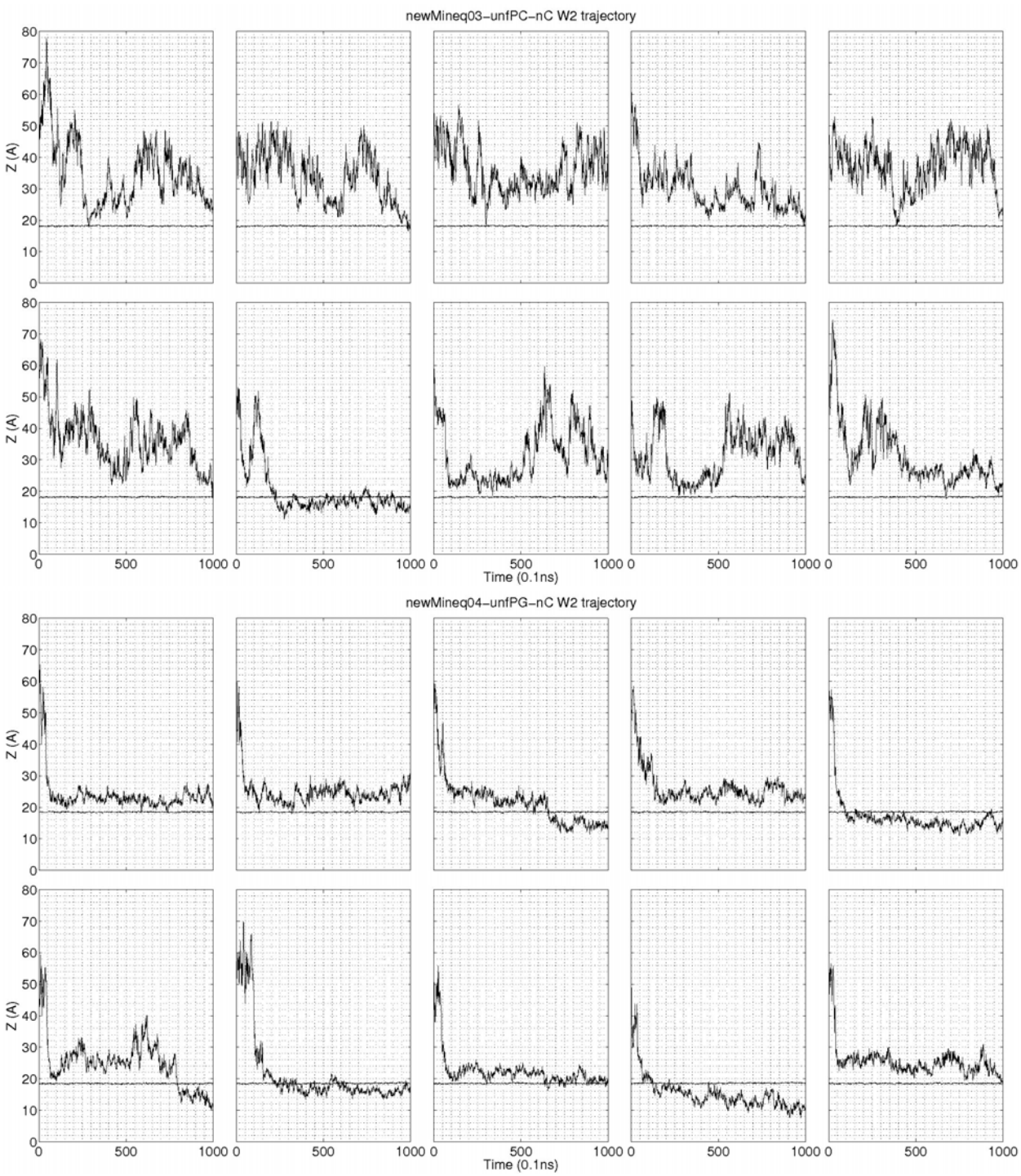

Figure S3: Trajectories of the tryptophan residue (W2) in CM15 during the ten 100-ns simulations in 100% POPC (zwitterionic lipids, top) and 2:1 POPC:POPG (anionic lipids, bottom). The horizontal solid line in each frame represents the average position of phosphorous atoms.

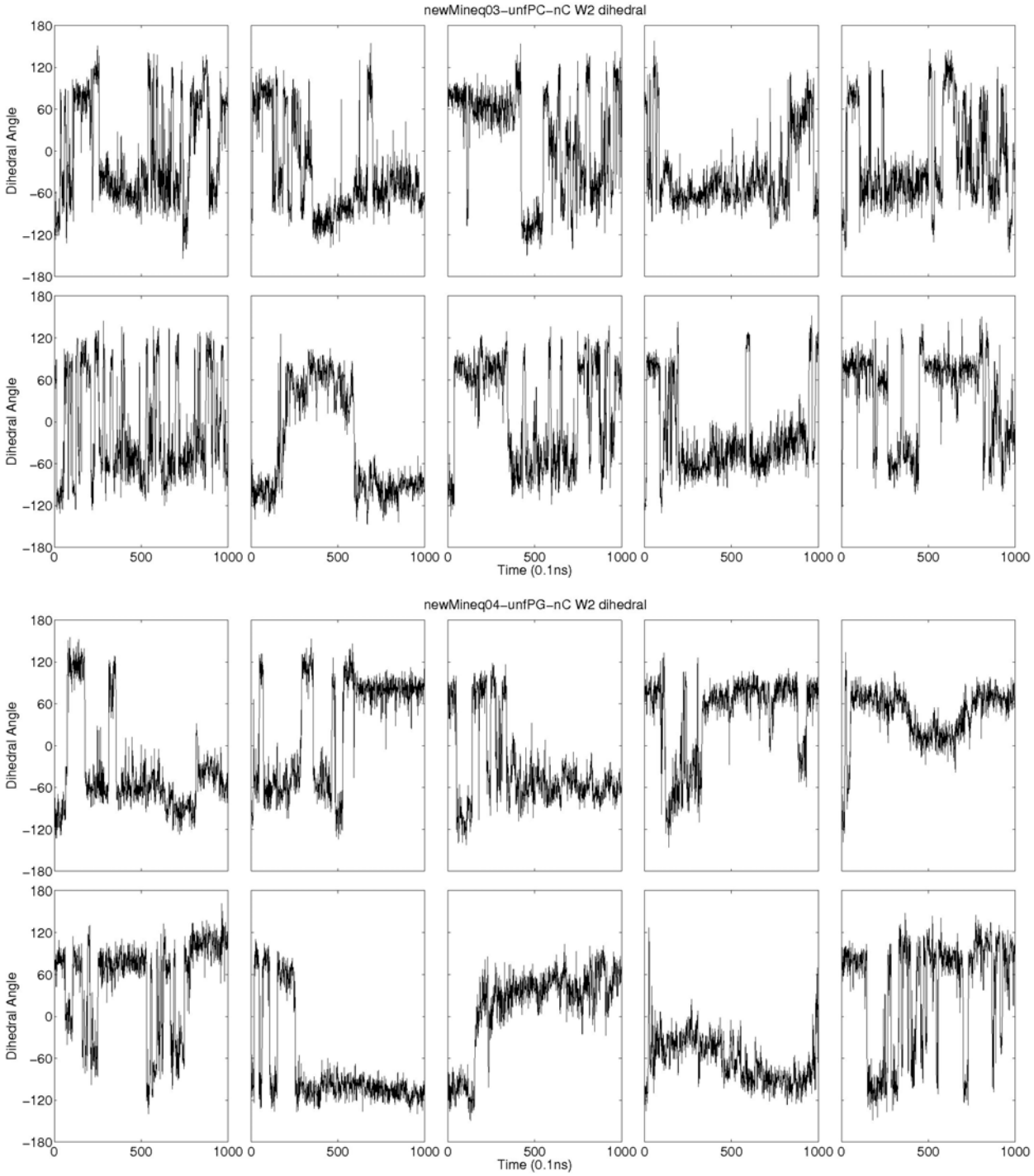

Figure S4: Side-chain dihedral angles of the tryptophan residue (W2) in CM15 during the ten 100-ns simulations in 100% POPC (zwitterionic lipids, top) and 2:1 POPC:POPG (anionic lipids, bottom).