

Supplemental Material for

**The Curvature Induction of Surface-Bound Antimicrobial Peptides Piscidin 1 and
Piscidin 3 Varies With Lipid Chain Length**

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Supplemental Material

Movie S1-S4. Piscidin 1 (S1; top leaflet and S2; bottom leaflet) or 3 (S3; top leaflet and S4; bottom leaflet) in each of the four bilayers. Movies are for 10 to 100 ns of each simulation and include two views of the peptide. One view is along the helical axis while the other is from the midplane toward the membrane surface. Lipids within 10 Å of the peptide are shown. The peptide (orange), sn1 chain (gray), and sn2 chain (purple).

Fig. S1. Electron density (top-half) and pressure (bottom-half) profiles each system. Profiles for systems containing membrane and peptide have solid lines, while systems with only the membrane have dashed lines. Electron density profiles are shown for the peptides (orange), phosphates (green), acyl chains (grey), and terminal CH₃ (blue). Lateral pressure profiles for pure bilayer (black) and bilayer + p3 (orange) are shown. Error in $F'(0)$ is between 0.004 and 0.012 dyn/cm and are listed in Table 2.

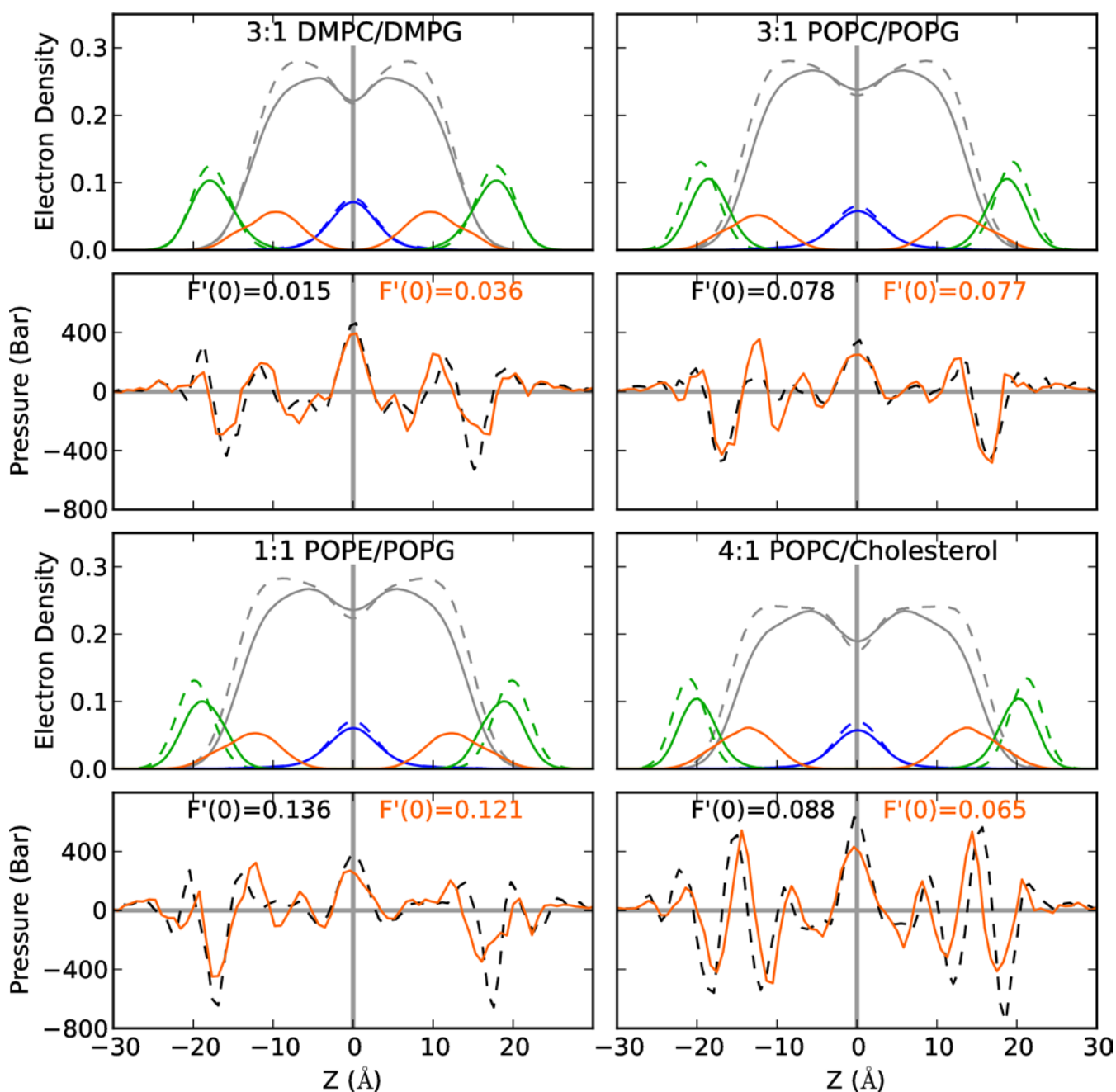


Fig. S2. S_{CD} for the pure bilayers (black) and with p1 (red). S_{CD} for the bilayer with p1 are further decomposed into those within 9 Å (green), 9-18 Å (blue), greater than 18 Å from the peptide.

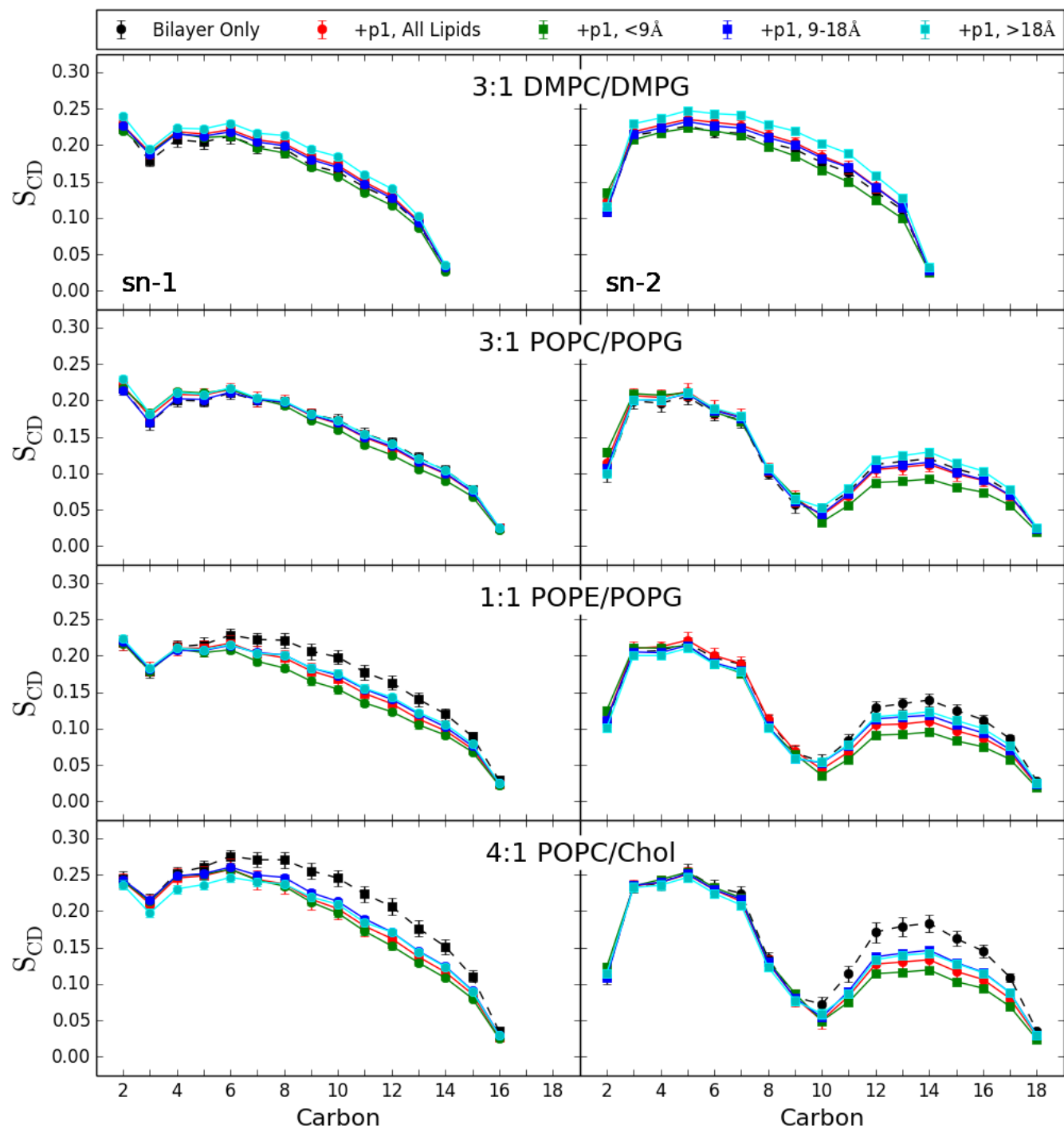


Fig. S3. Electron density peaks for CH₃. Total CH₃ peak (blue), upper leaflet (green), lower leaflet (red), and peptide density (orange).

