Supplementary Information

Deformation of a Two-domain Lipid Bilayer due to Asymmetric Insertion of Lipid-modified Ras Peptides

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S1. Summary of simulation systems.

In table S1, we summarized the simulation system information including peptide/lipid ratio, box lengths and domain boundary direction.

Table S1. System information and box lengths after equilibration. Standard deviations of simulation box lengths (X, Y) were all less than 0.5%. p/l is the peptide to lipid (including cholesterol) mole ratio.

Peptide	**N_p (p/l)**	**X [nm]**	**Y [nm]**	**Domain boundary direction**
no	-	22.78	22.88	X
tH	16 (0.008)	22.02	24.09	Y
tH	32 (0.017)	22.16	24.25	X
tH	48 (0.025)	22.34	24.44	Y
tH	64 (0.033)	24.59	22.48	Y
de-Pa181	64 (0.042)	22.31	24.41	X
de-Pa184	64 (0.042)	22.31	24.41	X
de-Pa181/184	64 (0.042)	22.19	24.28	Y
de-Fa186	64 (0.042)	22.23	24.32	X

S2. Bilayer density profile.

To characterize the distribution of lipids and peptides in different domains, we calculated the number density profiles of the lipid headgroups and the peptide backbones.

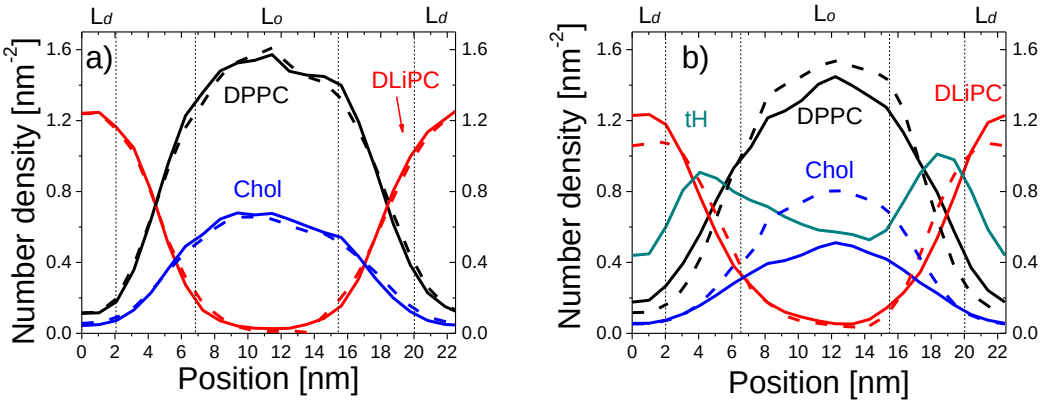

Fig. S1 *Bilayer density profiles along the direction perpendicular to the domain boundary. (a) Number density profiles of the phosphate group of DPPC and DLiPC, and the hydroxyl group of cholesterol, for the upper (dash line) and lower (solid line) monolayer of the tH-free bilayer. (b) Number density profiles of the phosphate bead of DPPC and DLiPC, and the hydroxyl group of cholesterol, for the upper (dash line) and lower (solid line) monolayer of the bilayer containing 64 tH peptides. The number density profile of the tH backbone beads is also shown.*

S3. Shape of bilayers with peptides.

To analyze the effect of peptide concentration and lipid modification on bilayer structure, we calculated the shape of the bilayer. Detailed discussion can be found in the main text.

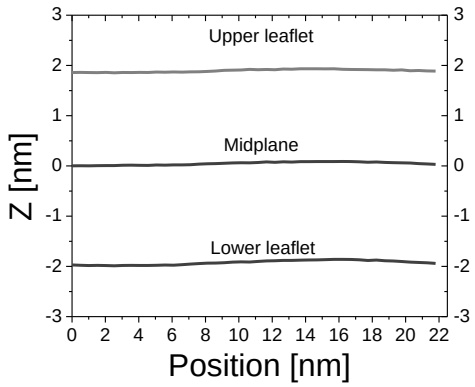

Fig. S2 *The shape of a bilayer (DPPC/DUPC=5/3, without cholesterol) with 64 tH peptides in the lower leaflet.*

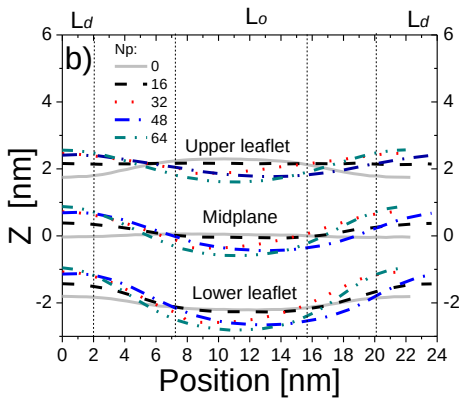

Fig S3: *Shape of bilayers containing different amounts of tH peptides (N_p=0: solid line, N_p=16: dashed line, N_p=32: dotted line, N_p=48: dash dot line, N_p=64: dash dot dot line).*

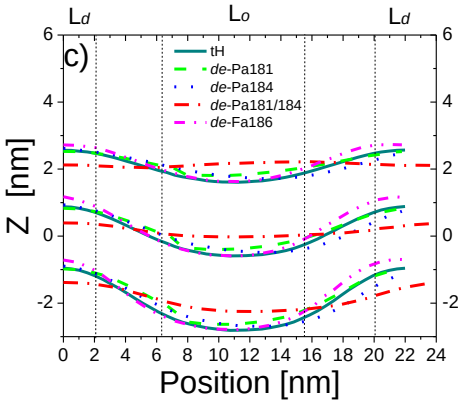

Fig. S4: *Shape of bilayers containing the same amount (N_p=64) of peptides that differ in lipid modification.*

S4. Time evolution of inter-leaflet cholesterol number difference

To monitor the monolayer composition difference induced by peptide insertion, we monitored the inter-leaflet cholesterol number difference over time. The equilibrium portion (t>16 μs) was used to estimate the average cholesterol number difference at equilibrium.

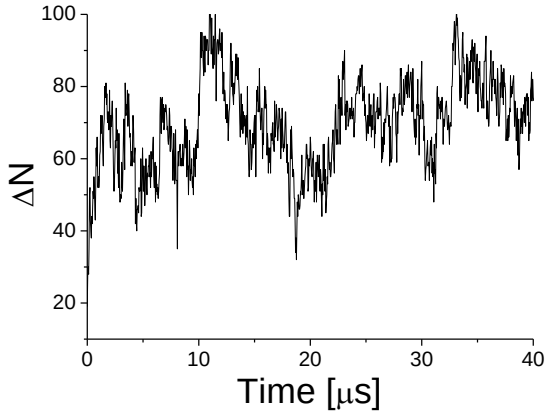

Fig. S5 *Time-dependent cholesterol number difference between the upper leaflet and the lower leaflet of the bilayer containing 64 tH peptide during the entire simulation.*