Supporting Information

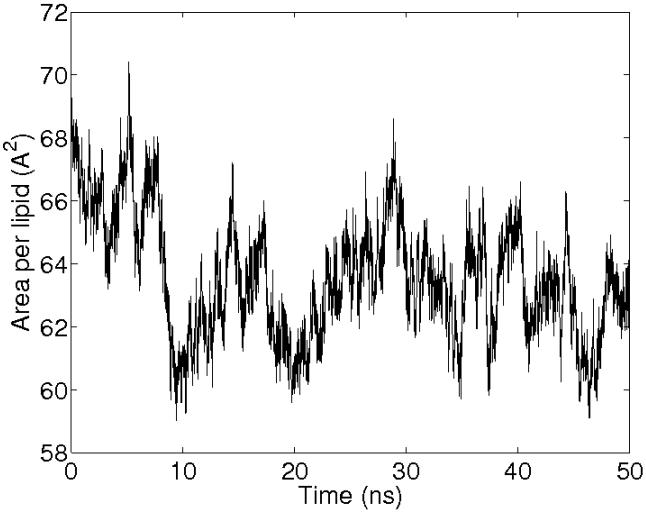

Figure S1: Area per lipid in a 50-ns NPT simulation of POPC. The x/y aspect ratio was allowed to change freely in the first 500 ps of simulation. The average area per lipid is 62.6 ± 1.3 Å^2 calculated using the last 10 ns of the trajectory.

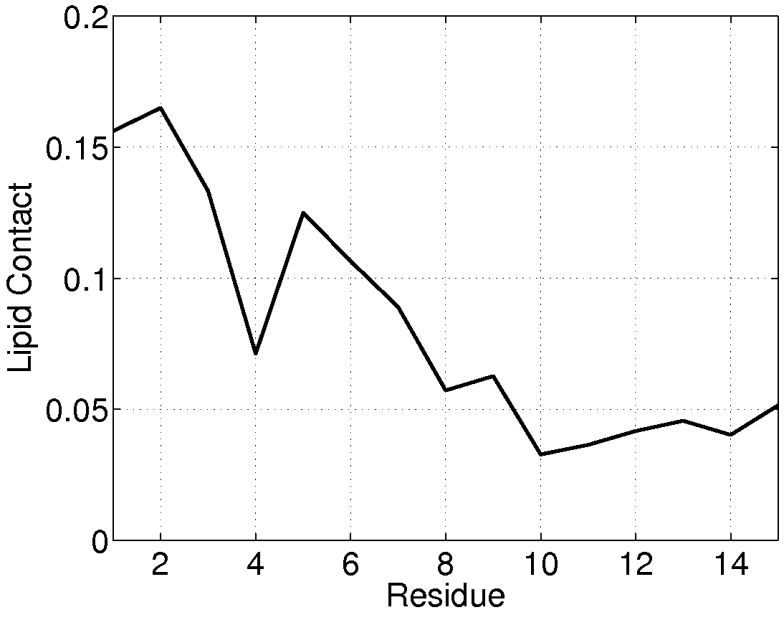

Figure S2: The number of peptide atoms in contact with lipid molecules in the CM15r-POPG:POPC simulation. See the Methods section and Fig 5 for calculation details.

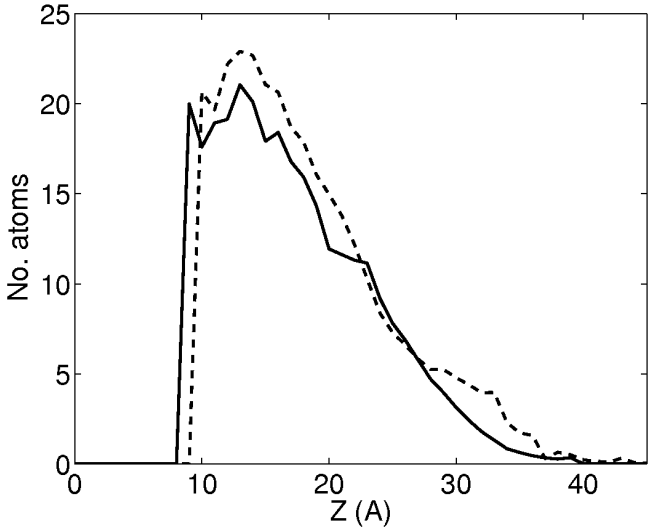

Figure S3: Total number of peptide atoms in contact with lipid molecules in the CM15r-POPC (solid) and CM15r-POPG:POPC (dashed) simulations.

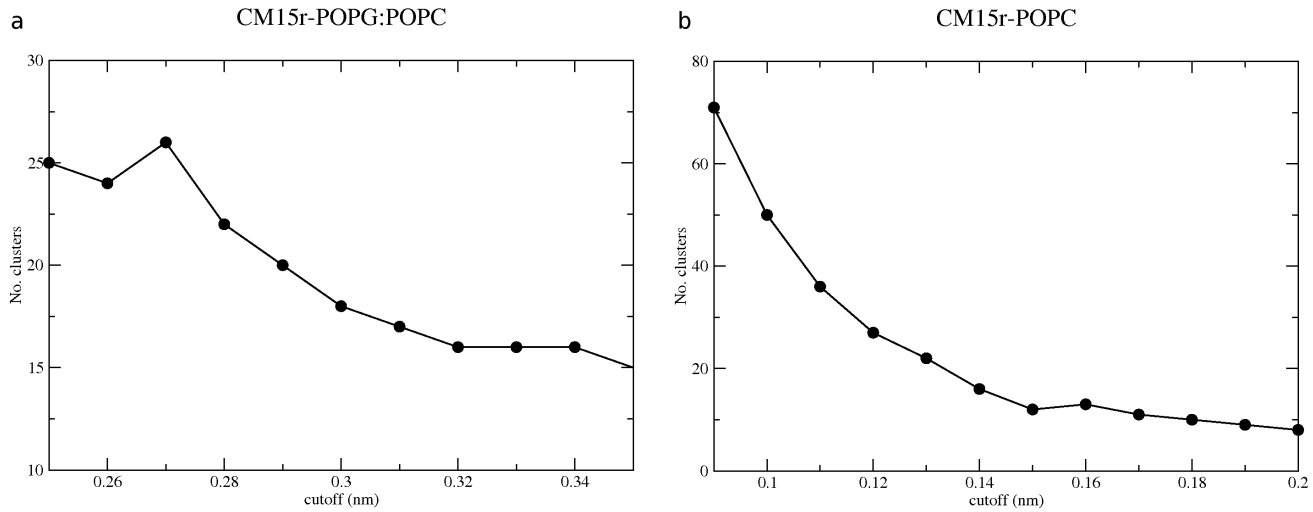

Figure S4: Parameter scan for the clustering analysis. The number of total clusters are plotted as a function of the cutoff used in the calculations. Cutoffs (0.32 nm for CM15r-POPG:POPC and 0.15 nm for CM15r-POPC) were chosen such that further increase in their values will not result in significant change in the number of clusters.

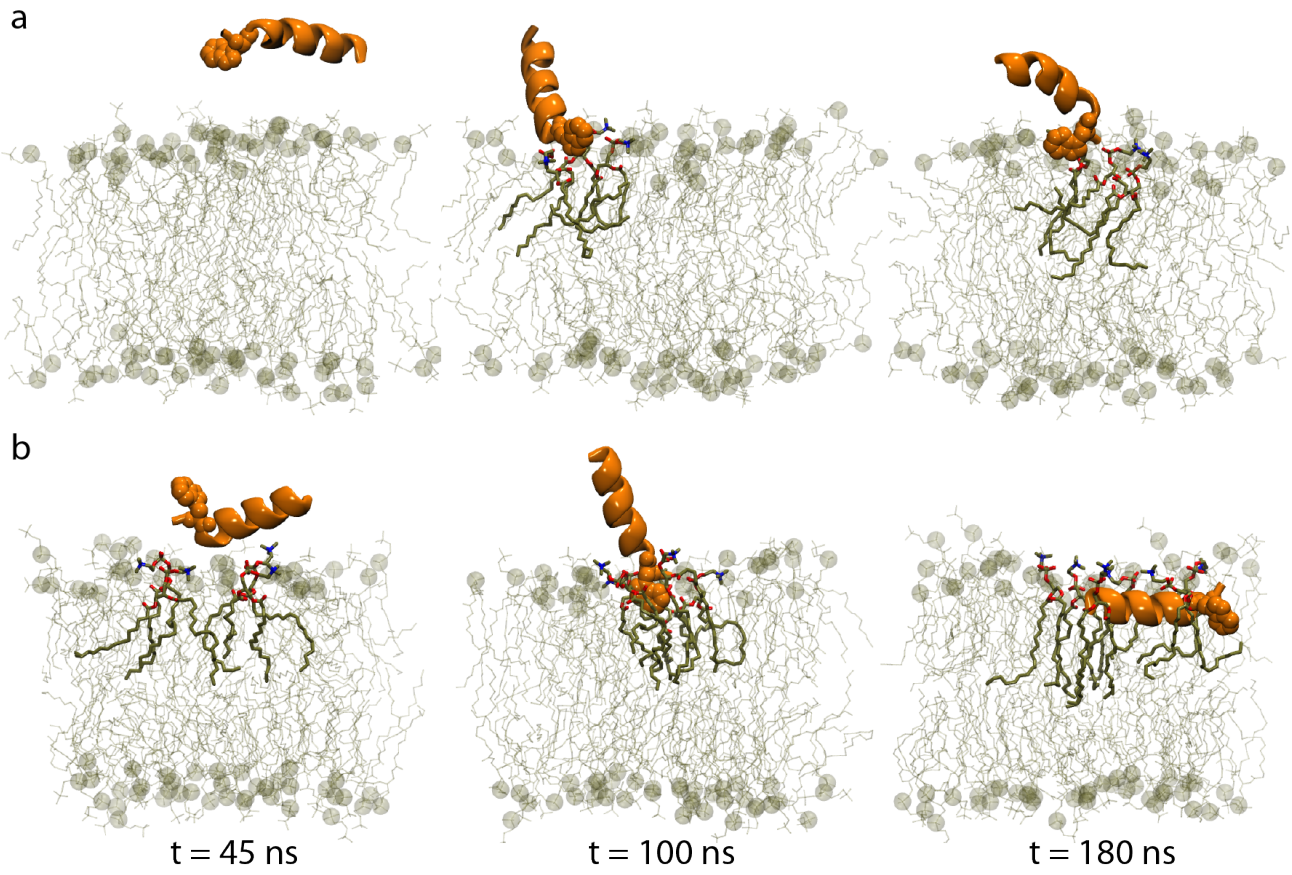

Figure S5: Snapshots of two 180-ns simulations of CM15H-POPC. Color scheme as Fig 3.

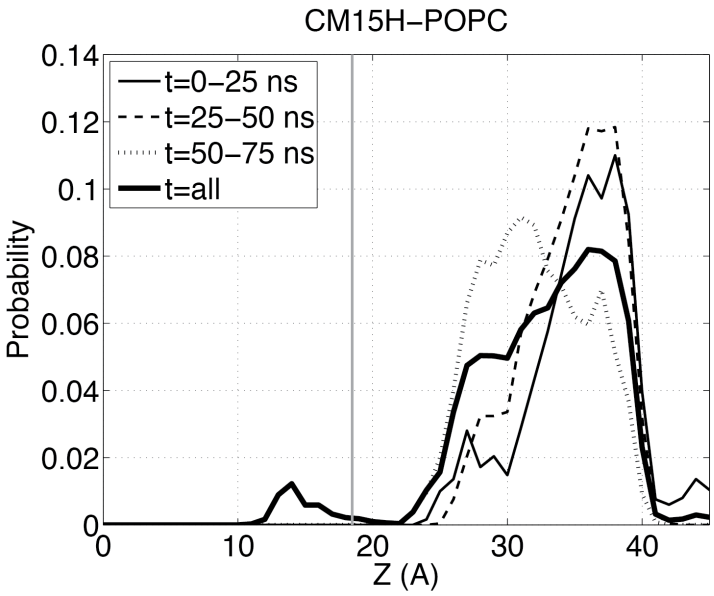

Figure S6: Center-of-mass distribution in the CM15H-POPC simulation.