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Supporting Information

Parameterization and atomistic simulations of biomimetic membranes

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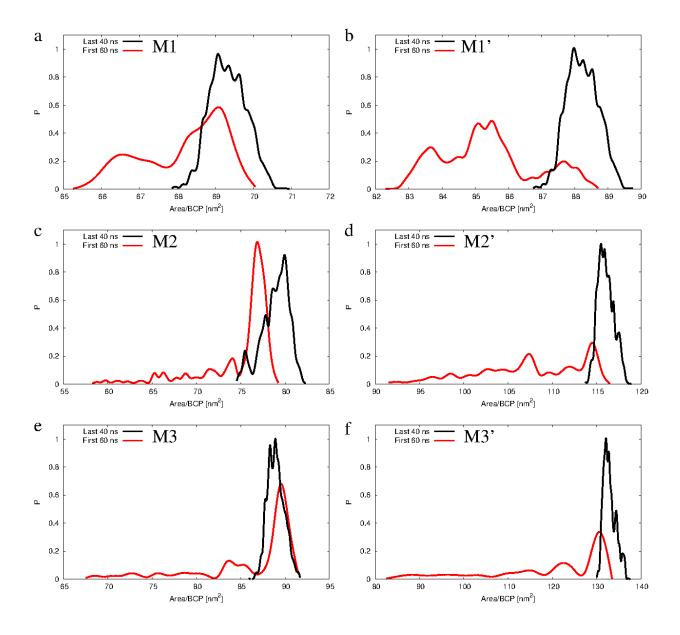


Fig. S1: Distributions of area per BCP (nm²) from the first 60 ns (red traces) and the last 40 ns (black traces) of each 100 ns MD simulation for each of the six different membranes are shown. In each panel, data corresponding to Fig. 3 are plotted to demonstrate the convergence characteristics of area per BCP toward the end of each simulation in various membrane configurations. Narrow and sharply-peaked distributions from the final 40 ns of each simulation (black traces) indicate significantly decreased fluctuations and convergence of area per BCP in comparison to the first 60 ns of each simulation. The standard deviations are small and reported in Table 2.

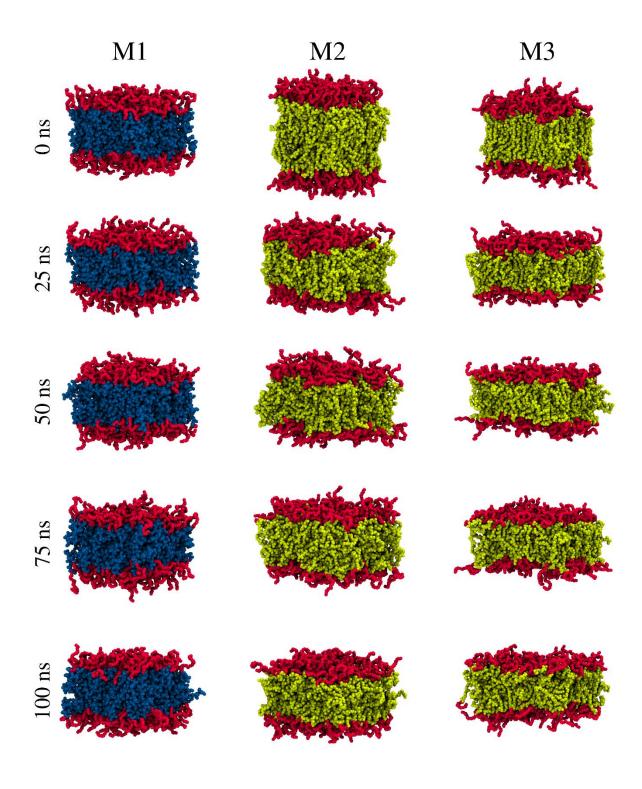


Fig. S2: Shown are snapshots of pristine membrane configurations at t = 0, 25, 50, 75, and 100 ns for membranes M1, M2, and M3. These data further enhance Fig. 3 where insets in each panel show only the final snapshots at t = 100 ns. All polymer chains are colored (PEO: red; PB: blue; PI: yellow).

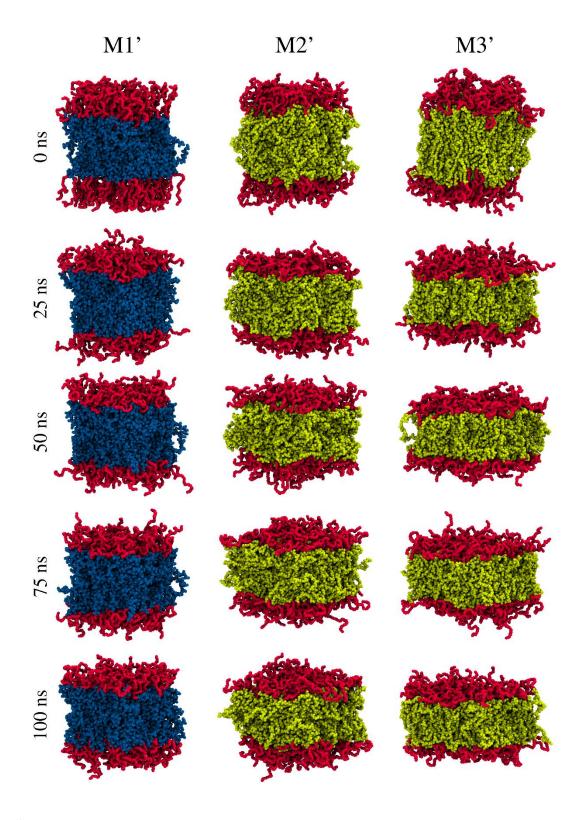


Fig. S3: Shown are snapshots of pristine membrane configurations at t = 0, 25, 50, 75, and 100 ns for membranes M1', M2', and M3'. These data further enhance Fig. 3 where insets in each panel show only the final snapshots at t = 100 ns. All polymer chains are colored (PEO: red; PB: blue; PI: yellow).