

Supplementary Materials

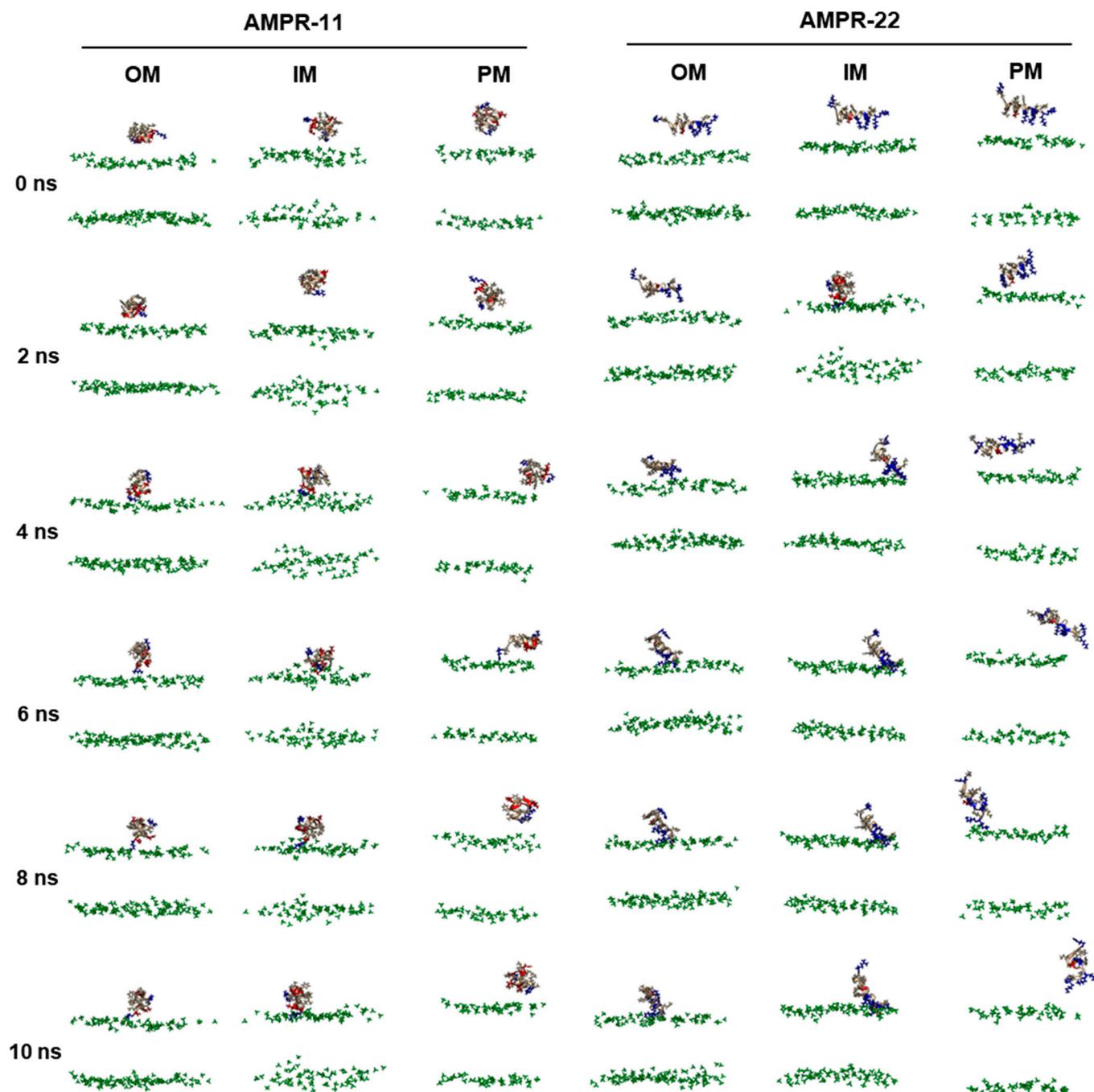


Figure S1. Representative structures of AMPR-11/22 interaction with Gram-negative bacterial outer/inner membrane and eukaryotic plasma membrane model. Phosphate group of the lipid is colored green. Hydrophobic (nonpolar), hydrophilic (polar), and cationic residues of AMPR-11 are shown in copper, red, and blue, respectively.

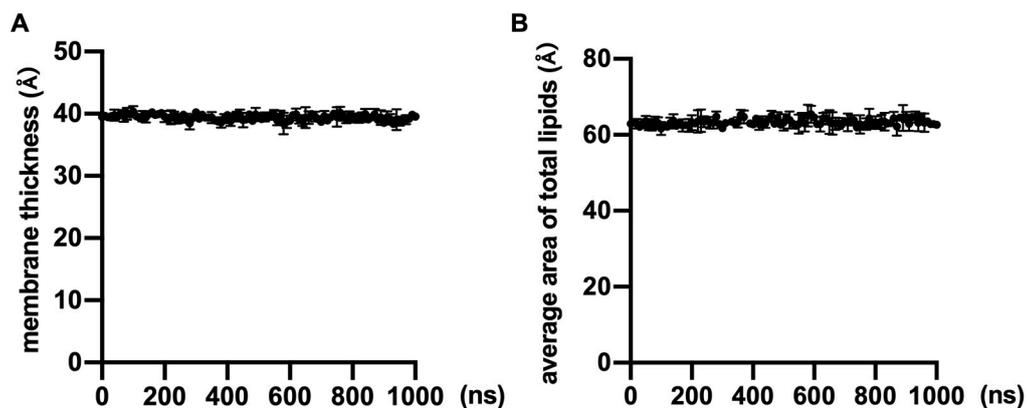


Figure S2. Average area of total lipids (A) and membrane thickness (B) of bacterial inner membrane during 1 μ s simulations were calculated with 3-carbon backbone (C1, C2, and C3) of glycerol in each lipid.

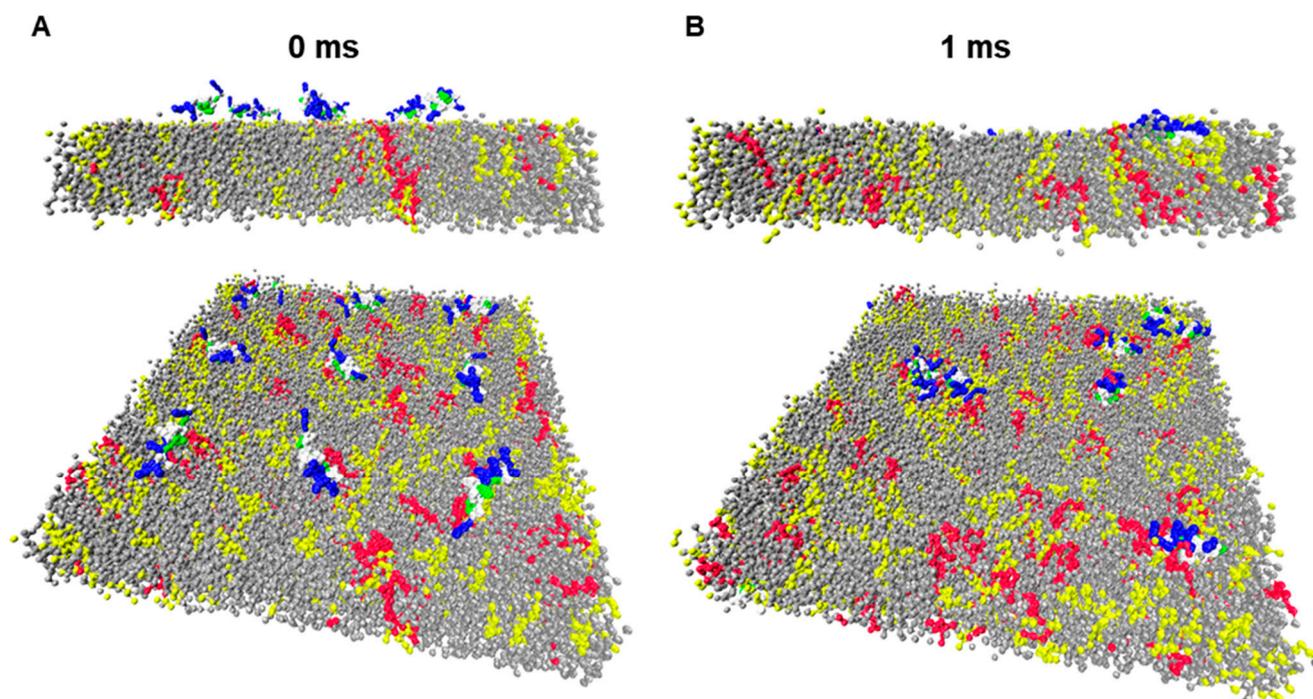


Figure S3. Coarse-grained MD simulation of AMPR-22. Nine AMPR-22 molecules were placed onto the bacterial inner membrane and simulated for 1 ms under a martini22p force field. POPG, POPE and CDL2 of the lipid are colored yellow, gray, and red, respectively. Hydrophobic (nonpolar), hydrophilic (polar), and cationic residues of AMPR-22 are shown in white, green, and blue, respectively.