Simulation protocol

All simulations were performed using gromacs version 3.3 (www.gromacs.org).[1] The GROMOS96 (43a2) united-atom force field and the simple point charge (SPC) water model were used.[2, 3] dipalmitoyl-phosphatidylcholin (DPPC) and dimyristoyl-phosphatidylcholine (DMPC) lipid parameters were taken from.[4] An electrostatic twin-range cut-off of 10/14 Å were used and hydrogen-bonds were restrained using LINCS.[5] Simulations were run with a 2 fs integration time-step and neighbor lists were updated every 5 steps. SPC, DPPC, and protein were each coupled separately to a heat bath with a temperature of 353 K and time constant τ_T = 0.1 ps using weak temperature coupling.[6] Simulations at a lower temperature of 323 K led to a gel-like phase of the bilayer, with the increased ordering of the lipids inhibiting the sampling required for folding. Atmospheric pressure of 1 bar was maintained using weak semi-isotropic pressure coupling with compressibility $\kappa_z = \kappa_{xy} = 4.6 \cdot 10^{-5}$ bar^{-1} and time constant τ_P = 1 ps.

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