Supplementary Information: Self-diffusion is temperature independent on active membranes

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I. CG-MD SIMULATION PROTOCOL

a. Energy minimization and equilibration: The system's energy was minimized using the steepest descent and the conjugate gradients methods in the next step. We ran at least 5000 steps of energy minimization to ensure proper geometry and to minimize steric clashes. Following energy minimization, all systems were subjected to a six-step equilibration protocol (Table: SI), where the stiffness of the positional restraint on the lipid head groups (PO_4 bead of DPPC and DAPC) was in gradually decreased to avoid collapse of the system. Five different temperatures (298, 302, 306, 310, and 314 K) were controlled by velocity-rescale thermostats [1] with a coupling constant of 0.1 ps, which was used. For the equilibration, we used Berendsen barostat [2] with the compressibility of 4.5 $\times 10^{-5}$ bar^{-1} semi-isotropic scaling [3, 4].

Step	Restraint ($KJmol^{-1}s^{-1}$)	Timestep (fs)	Time (ns)
1	200	2	1
2	100	5	1
3	50	10	1
4	20	15	0.75
5	10	20	1
6	2	20	50
Total			54.75

TABLE SI. Equilibration Details

b. Production runs: For these simulations velocity rescale temperature bath was applied [1]. The pressure was controlled with the Parrinello-Rahman barostat [5] with a 12 ps coupling constant, and the compressibility of 3 $\times 10^{-4}$ bar^{-1} [6]. However, due to the longer spatial scale during production, the chance of undulation increases, which was significantly reduced by using a mild positional restraint (2 $kJmol^{-1}nm^{-1}$) on the PO_4 beads in the Z-direction [7, 8]. All the production simulation was conducted for 5 μs, except two pure DPPC systems that were run for 30 μs using GROMACS-2022.2 [9–11] with 20 fs timestep where each 100 ps snapshots were stored for analysis. The cumulative simulation time was 1 ms.

II. LATTICE MODEL SIMULATION PARAMETERS

Simulation parameters	Values
Lattice size ($L \times L$)	100×100
Radius of aster (R_a)	8
Areal density of asters (A_{frac})	0.2
Mean lifetime of aster remodeling (τ_a)	10
Equilibration steps	500 steps
Time to reach steady state	1000 steps
Production run	18500 steps
No. of replicas for each (T)	40
Probability to move towards aster core (passive lipids) (p)	0.8
Temperatures (T)	281 - 321K (spacing = 3K)
Binding probability of ACS to PM (p_b)	0.0 - 1.0 (spacing = 0.2)
Interaction strength of LJ (J/k_BT at T=293 K)	1/1.43 (like lipids) & 0 (unlike lipids)
LJ interaction cutoff radius	2.5σ
1 lattice unit	$2^{1/6}\sigma$

TABLE SII. The mesoscopic lattice model simulation is performed on a 2D square lattice of size $L \times L$ with periodic boundary conditions. The lattice sites are occupied with either passive or inert lipids in equal ratios. All spatial parameters are in the units of lattice constant and time scales are in the units of MC steps. 1 lattice unit (σ_d)= 2.5/100 μm [12] and 1 MC step (τ_d) = $\frac{\sigma_d^2}{4D}$ = 0.446 ms, where D $\sim$ 14 $\mu m^2 s^{-1}$ is the typical diffusivity value from our CG-MD simulations.

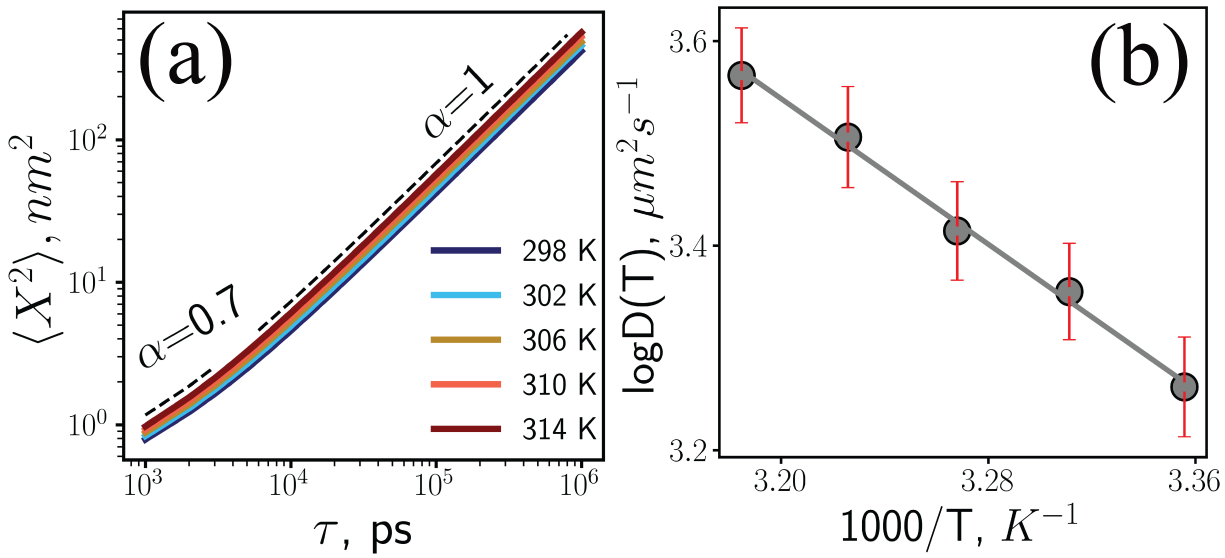

FIG. S1. **In equilibrium, DAPC lipids show diffusive behavior, and the diffusion coefficient follows Arrhenius kinetics**. (a-b) MSD ($\langle X^2 \rangle$) and diffusivity (semilog scale) of pure DAPC membrane at different T (298 K - 314 K). All the results from long-timescale simulations. Error bars are the standard deviation of 10 replicates.

III. MOVIE DETAILS

Movie: "displace_with_activity.mp4" shows the active dynamics of lipids on a lattice at 311 K. The passive lipid densities are shown in red and the inert lipid densities are shown in blue. Passive tracer lipid tracks are shown in maroon and inert tracer lipid tracks are in blue. Asters are marked by black circles.

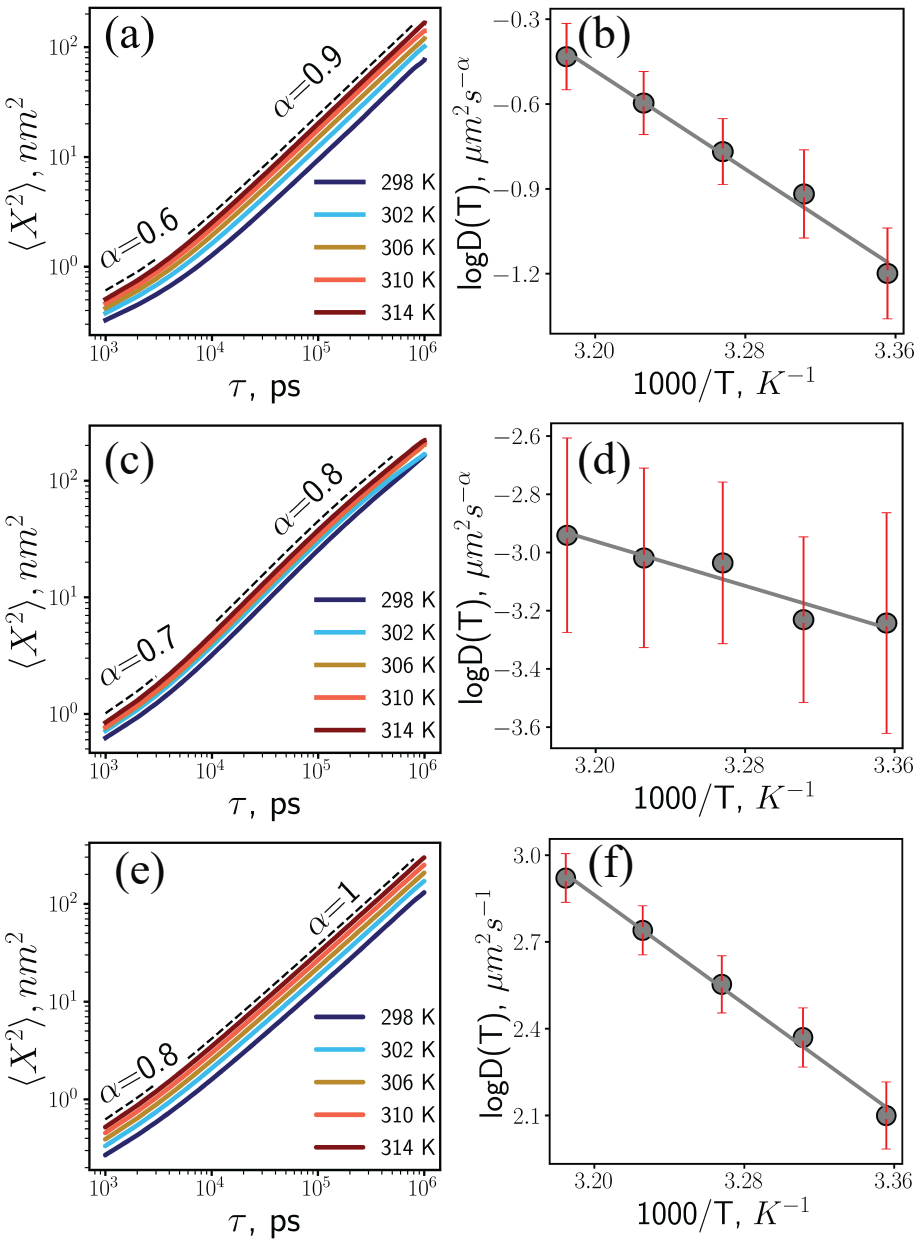

FIG. S2. **In equilibrium, mixed model PC lipids show subdiffusive behavior (For DPPC, α = 0.9 and DAPC, α = 0.8) and CHOL shows diffusive behavior**. MSD ($\langle X^2 \rangle$) and transport coefficient (semilog scale) of DPPC (a-b), DAPC (c-d), and for CHOL (e-f) in the mixed model membrane at different T (298 K - 314 K). All the results from long-timescale simulations. Error bars are the standard deviation of 12 replicates.

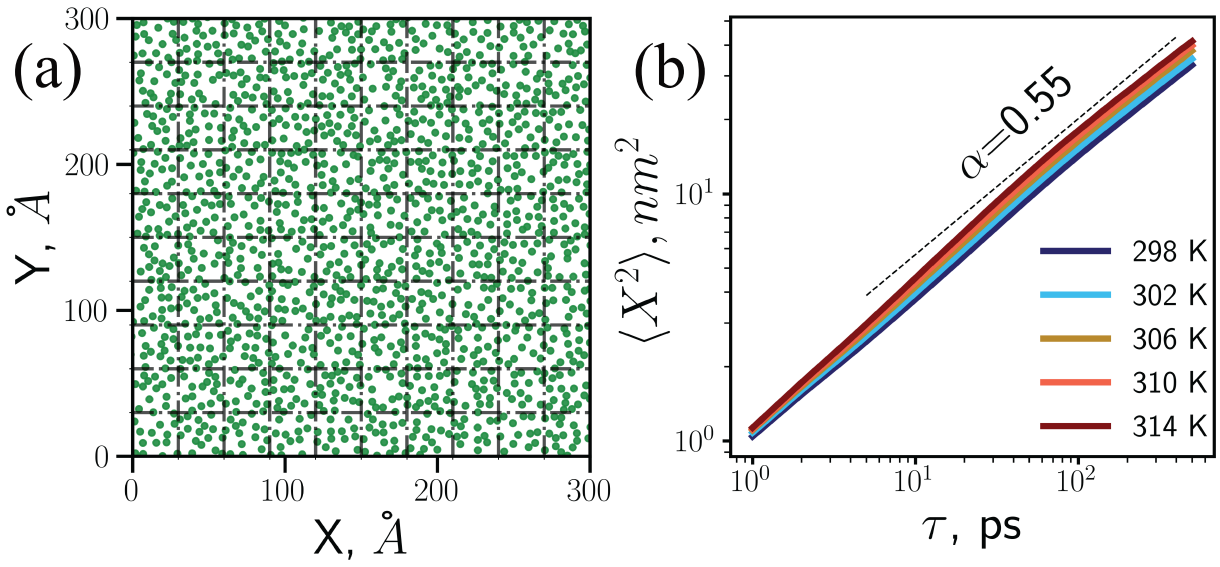

FIG. S3. Nanoscale simulation system snapshot and MSD. (a) Snapshot PO_4 groups of DPPC at 314 K (each grid = 3×3 nm). (b) MSD ($\langle X^2 \rangle$) averaged over grids at different T (298 K - 314 K).

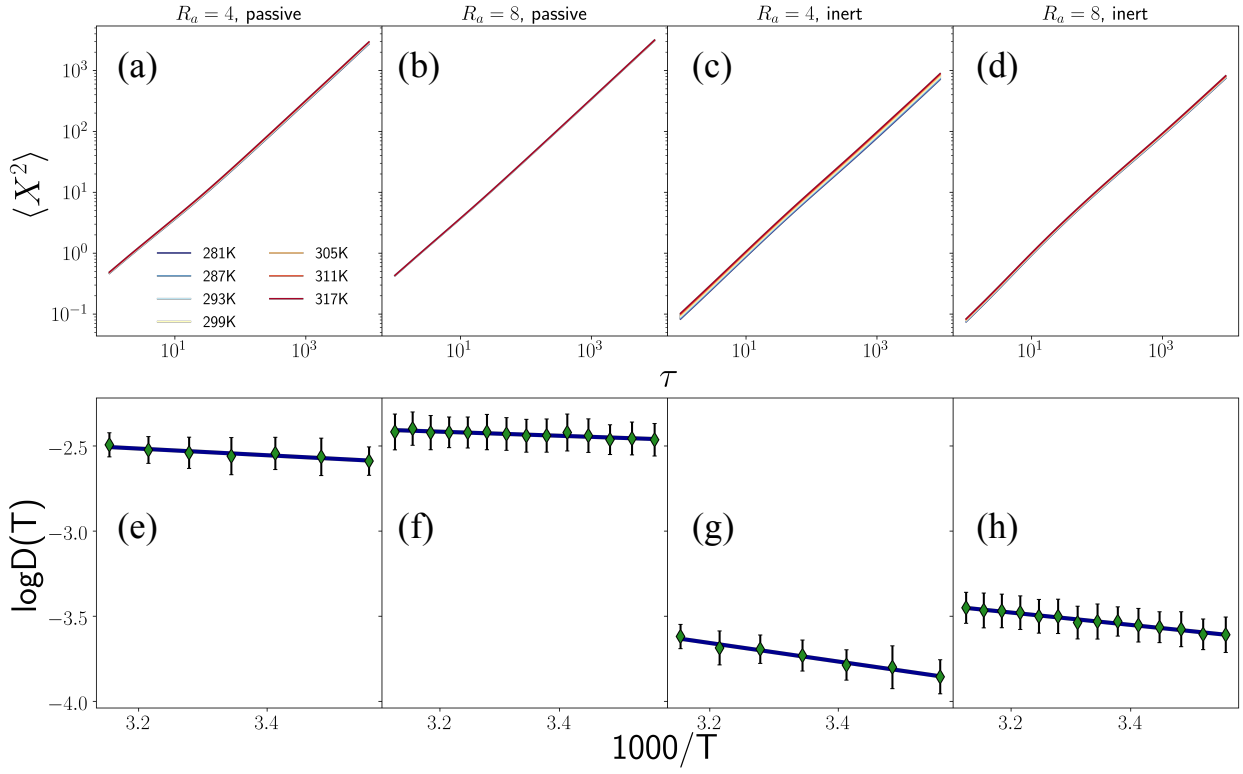

FIG. S4. Change in aster radius has no effect on diffusive behavior of lipids. The data from two different sizes of asters ($R_a = 4$ and 8) is compared in (a)-(h) for passive and inert lipids.

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