nAChr (pLGIC)'s have 20 potential lipid occupancy spots. In the outer leaflets PUFAs occupy the M4, saturated and chol occupy the inner subunits. In the inner leaflet charge plays a crucial role. Where anionic lipids will interact around the M1/M3 subunits (interaction with the chol/sat region), and PUFAs still occupy the M4.

Affinity for PUFA acyl chain. Where are they? Do they match our hypothesis?

1) Saturating Affinity table
2) Density sites

Does the inner leaflet follow suite? Does charge play a role? What is the stronger driver: PUFA or HG?

1) HG affinity table
2) Saturation - HG affinity table

Why PUFAs at the M4?

Why anionic in the inner membrane?

1) Saturation - HG affinity table
2) Simulation image showing TMD boundary anionic amino acids