

(#99) In Silico Design and Molecular Dynamics Simulation of Glycophorin A Transmembrane Dimer, in Pure DPPC and Mixed DPPC-DMPC Phospholipid Bilayers

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We simulated the pure (**DPPC**) bilayer, with 128 molecules and specified how this system responds to:

- 1) The insertion of (**DMPC**) molecules (**DPPC 60% - DMPC 40%**) and
- 2) The simultaneous presence of DMPC molecules and **Glycophorin A** transmembrane. (**Residues 62 to 101 of human GPA**)

The initial phospholipid bilayer structures: **Membuilder** web server.

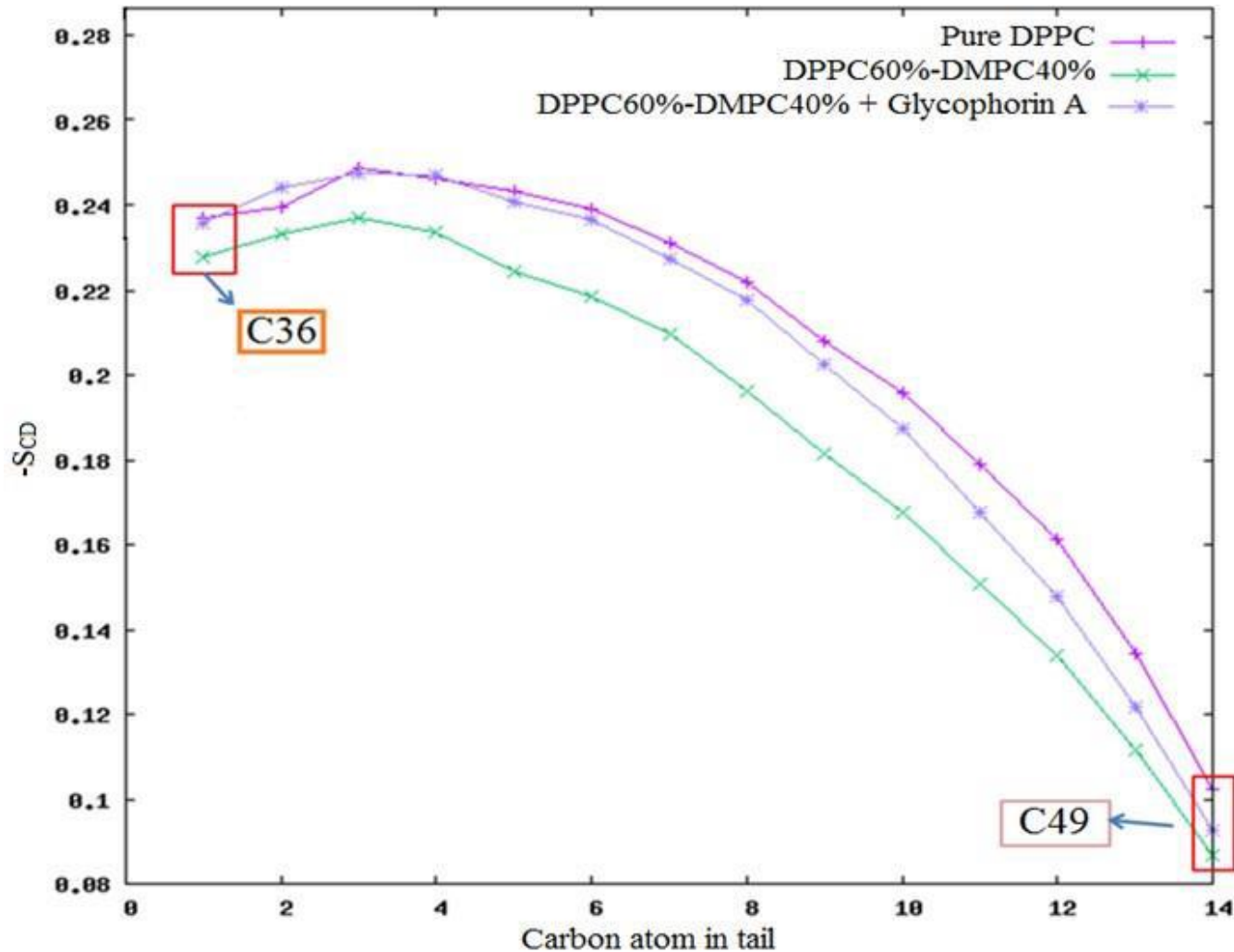
Starting structure of GpAtm: (**OPM**) database.

- 10 ns MD simulations were performed on pure and mixed bilayers. (Berger forcefield for lipids), (Gromacs 4.5.4)
- The **g_membed** program: inserting the **GpAtm** into bilayers.

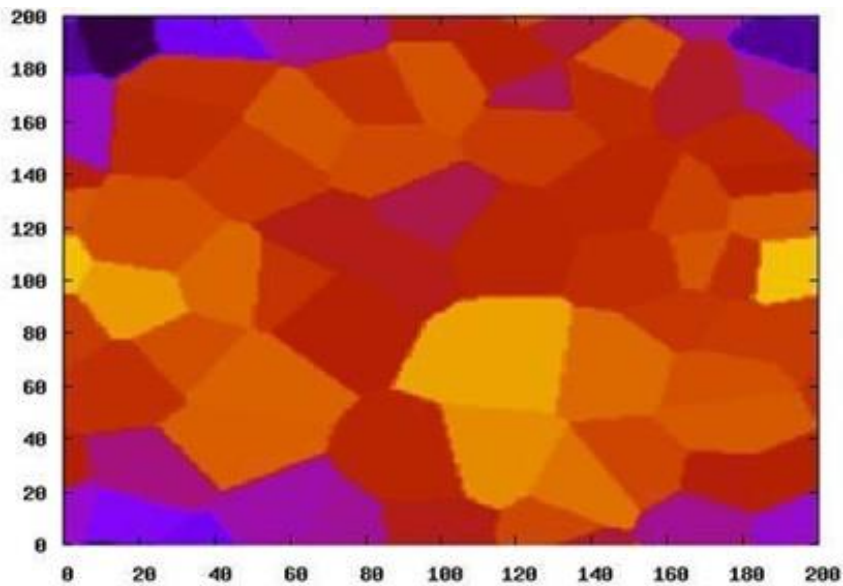
➤ Resulting systems were simulated for **100 ns. (Temperature: 323 K)**

➤ **RMSD and Box-x length** of different molecules (**Equilibration?**)

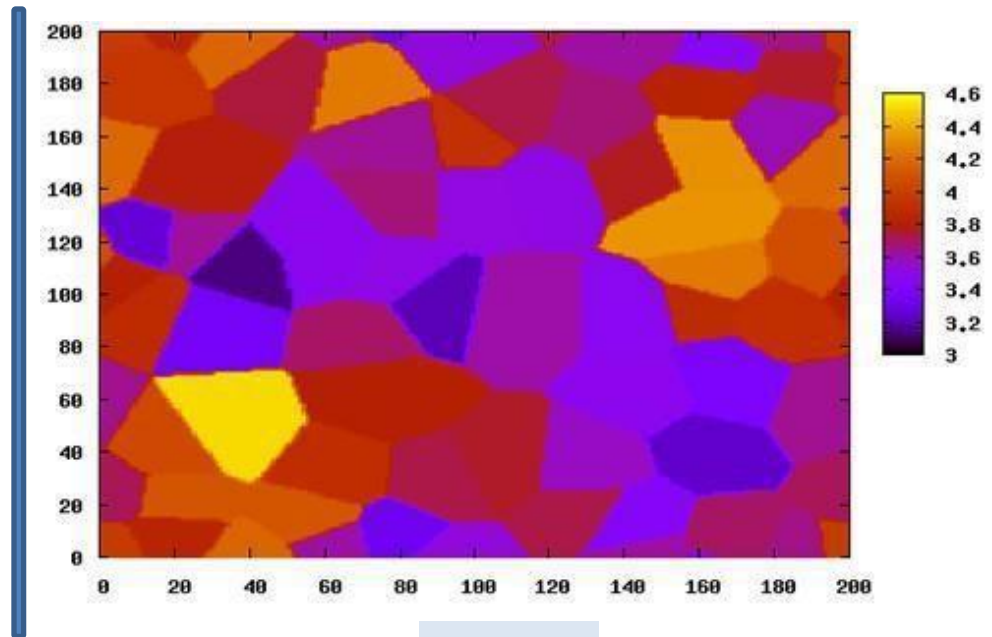
100 ns simulation of mixed bilayer containing GpAtm



- ❑ After insertion of DMPC molecules: **Clear decrease in DOP.**
- ❑ Later insertion of **GpAtm**, gives rise to the more ordered hydrocarbon chains.



0 ns



100 ns

The **membrane thickness** contour plots for the mixed DPPC-DMPC bilayer including GpAtm, at the first (**0ns**) and last (**100 ns**) MD configurations.

- The bilayer thickness decreases around the **box-center**, where the GpAtm is inserted.
- It is an indication of the **negative hydrophobic mismatch**.

In order to **maximize** favorable interactions between the hydrophobic length of the integral protein, with the hydrophobic bilayer thickness, **DPPC molecules shorten their chain lengths**, which results in less bilayer thickness.