

Supporting Information:

NMRlipids IV: Headgroup & glycerol backbone structures, and cation binding in bilayers with PE and PG lipids

Pavel Buslaev,[†] Fernando Favela-Rosales,[‡] Patrick Fuchs,[¶] Matti Javanainen,[§]
Jesper J. Madsen,^{||,⊥} Josef Melcr,^{§, #} Markus S. Miettinen,[@] O. H. Samuli
Ollila,^{*,△} Chris G. Papadopoulos,[∇] Antonio Peón,^{††} Thomas J. Piggot,^{‡‡} and
Pierre Poulain[¶]

[†]*University of Jyväskylä*

[‡]*Departamento de Investigación, Tecnológico Nacional de México, Campus Zacatecas
Occidente, México*

[¶]*Paris, France*

[§]*Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences,
Flemingovo nám. 542/2, CZ-16610 Prague 6, Czech Republic*

^{||}*Department of Chemistry, The University of Chicago, Chicago, Illinois, United States of
America*

[⊥]*Department of Global Health, College of Public Health, University of South Florida, Tampa,
Florida, United States of America*

[#]*Groningen Biomolecular Sciences and Biotechnology Institute and The Zernike Institute
for Advanced Materials, University of Groningen, 9747 AG Groningen, The Netherlands*

[@]*Department of Theory and Bio-Systems, Max Planck Institute of Colloids and Interfaces,
14424 Potsdam, Germany*

[△]*Institute of Biotechnology, University of Helsinki*

[∇]*I2BC - University Paris Sud
S2*

^{††}*Spain*

^{‡‡}*Chemistry, University of Southampton, Highfield, Southampton SO17 1BJ, United*

S1 R-PDLF and SDROSS experiments



Figure S1: (A) Chemical structure of POPE with the labeling of headgroup and glycerol backbone carbons. (B) INEPT spectra from POPE sample with the headgroup and glycerol backbone peaks labeled. (C) 2D R-PDLF spectra (D) Dipolar sliced from the 2D R-PDLF spectra with the resulting order parameters on top of figures. (E) Experimental S-DROSS curves giving signs of the order parameters.

1.A, B etc. labels to be put in the figure.



Figure S2: (A) Chemical structure of POPG with the labeling of headgroup and glycerol backbone carbons. (B) INEPT spectra from POPG sample with the headgroup and glycerol backbone peaks labeled. (C) 2D R-PDPLF spectra (D) Dipolar slices from the 2D R-PDPLF spectra with the resulting order parameters on top of figures. (E) Experimental S-DROSS curves giving signs of the order parameters.



Figure S3: Simpson simlaton of S-DROSS curve of β -carbon of POPG.

S2 Comparison of headgroup order parameters from different force fields to experiments

The quality of PE and PG headgroup conformational ensembles in different simulations against NMR experiments is evaluated in figures S4 and S5 using C-H bond order parameters as in our previous studies for PC and PS lipids.^{1,2} Conclusions are the same for all lipids: None of the force fields correctly captures the lipid headgroup conformational ensembles, but CHARMM36 gives results closest to experiments.

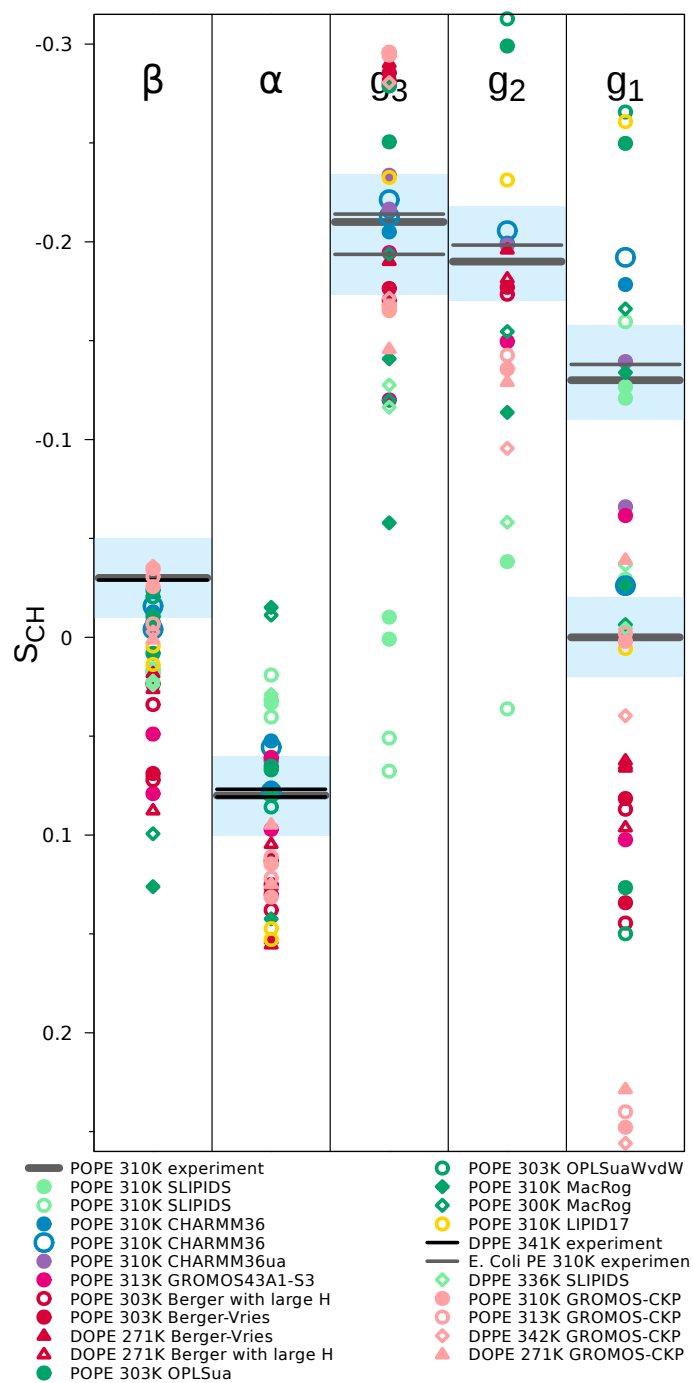


Figure S4: The headgroup and glycerol backbone order parameters of PE lipids from experiments (POPE and signs this work, DPPE from Ref. 3 and E.coliPE from Ref. 4) and simulations with different force fields.

2.This should be clarified as in NMRlipidsI and error bars should be added. Probably larger error bars for united atom models based on the report by Fuchs et al.

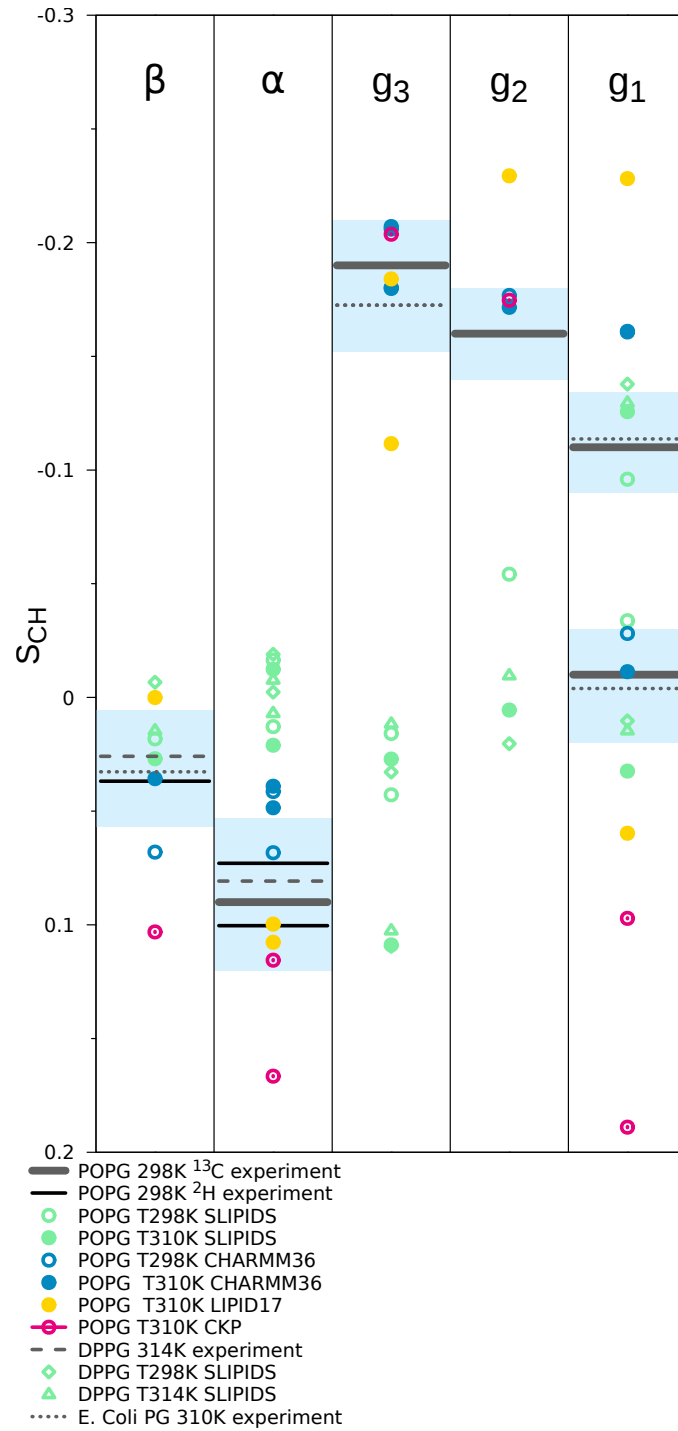


Figure S5: The headgroup and glycerol backbone order parameters of PG lipids from experiments (POPG and signs from this work and from Ref. 5, DPPG with 100mM NaCl from Ref. 6, and E. Coli PG results from Ref. 4). and simulations with different force fields.

S3 PC headgroup in mixtures with PE or PG lipids

Headgroup order parameters of PC lipids are unchanged upon addition of zwitterionic lipids or cholesterol in experiments, but increase upon addition of negatively charged PG or PS lipids because headgroup dipole tilts more parallel to the membrane plane after incorporation of negative charges into the membrane.^{7,10,11} The response of PC headgroup order parameters to the addition of PE or PG lipids from different simulations is compared with experiments in figure S6. None of the simulations reproduce neither the experimentally observed increase in PC headgroup order parameters with increasing amount of PG nor the related tilting of the headgroup more parallel with the membrane. Similar observations in our previous work for PS lipids were explained by the overestimated counterion binding affinity that neutralizes the effect of added negative charge.² All simulations except Berger-OPLS predict tilting of P-N headgroup outwards from the membrane and decrease of PC headgroup order parameters upon addition of PE lipids. These results are not in line with experiments where the PC headgroup order parameters are not affected by zwitterionic lipids.⁷ The good performance of Berger-OPLS simulations in here is surprising because headgroup conformational ensemble is not very close to experiments in this model and the response of headgroup order parameters to cholesterol was significantly overestimated by the Berger/Höltje force field in our previous work.¹

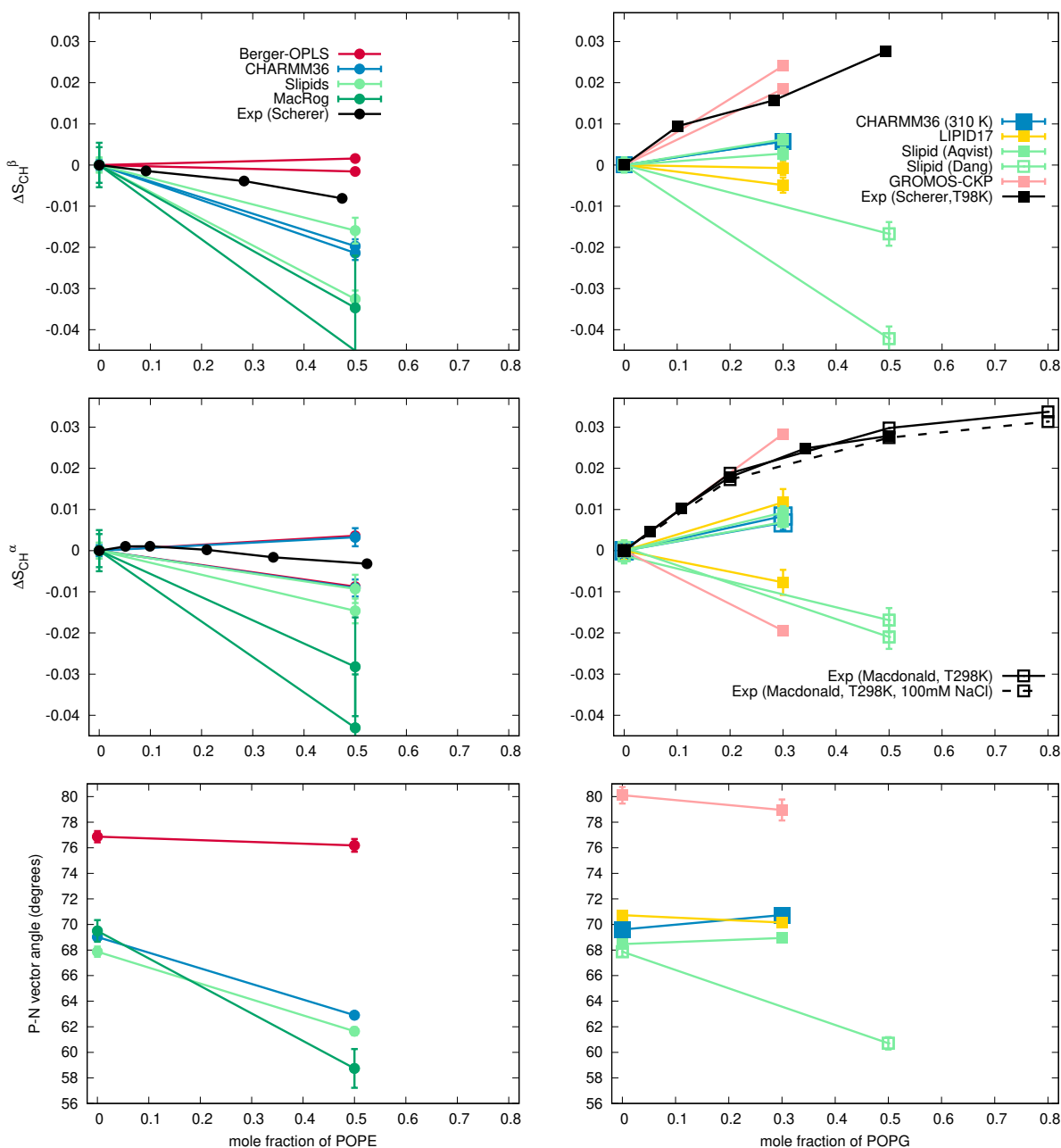


Figure S6: Modulation of POPC headgroup order parameters with increasing amount of POPE (left) and POPG (right) in bilayer from experiments^{7,8} and simulations with different force fields. Signs are determined as discussed in.^{1,9}

S4 PG headgroup in mixtures with PC lipids

Changes in other than PC lipid headgroup with changing membrane composition are less extensively characterized in the literature. The β -carbon order parameter in PG headgroup increases mildly⁸ or is unchanged⁵ upon increasing amount of PC lipids (Fig. S7), but experimental data from α -carbon is not available. Also the tested force fields predict very small changes for the β -carbon order parameter, while the P-N vector tilt and its response to the increased amount of PC varies significantly between force fields in figure S7. Therefore, more experimental data and more accurate force fields are still required to resolve the PG conformational ensembles in mixtures with other lipids.

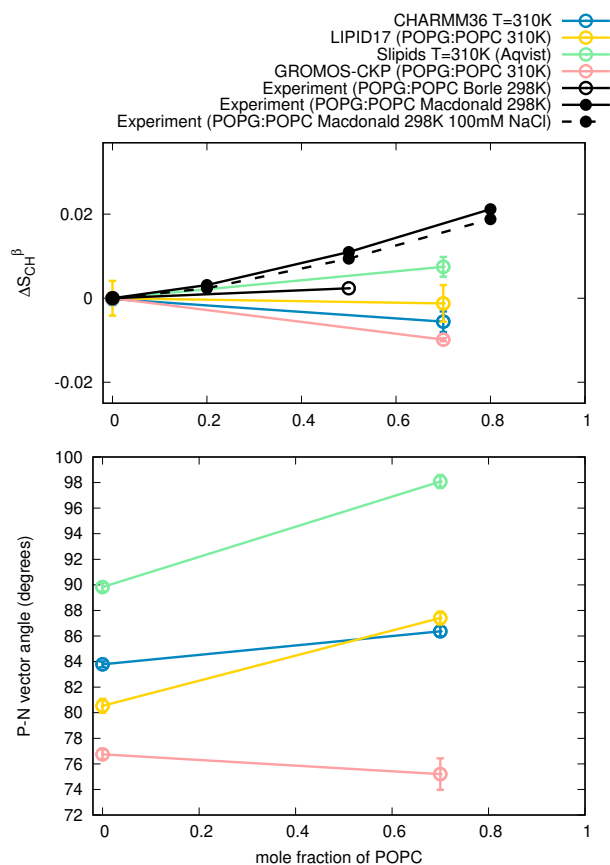


Figure S7: Modulation of PG lipid headgroup order parameters with the increasing amount of PC in lipid bilayer from experiments^{5,8} and simulations with different force fields.

S5 Calcium binding to POPC:POPG mixtures

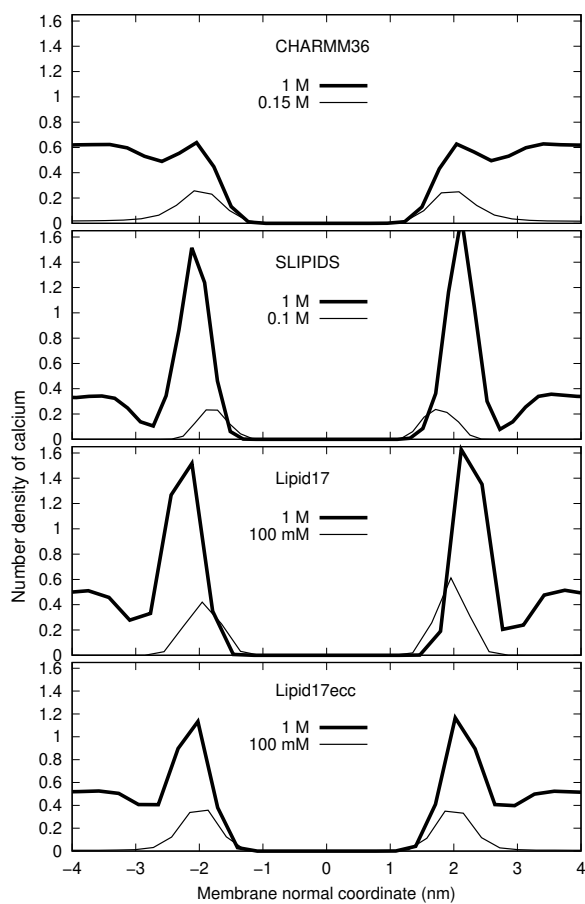
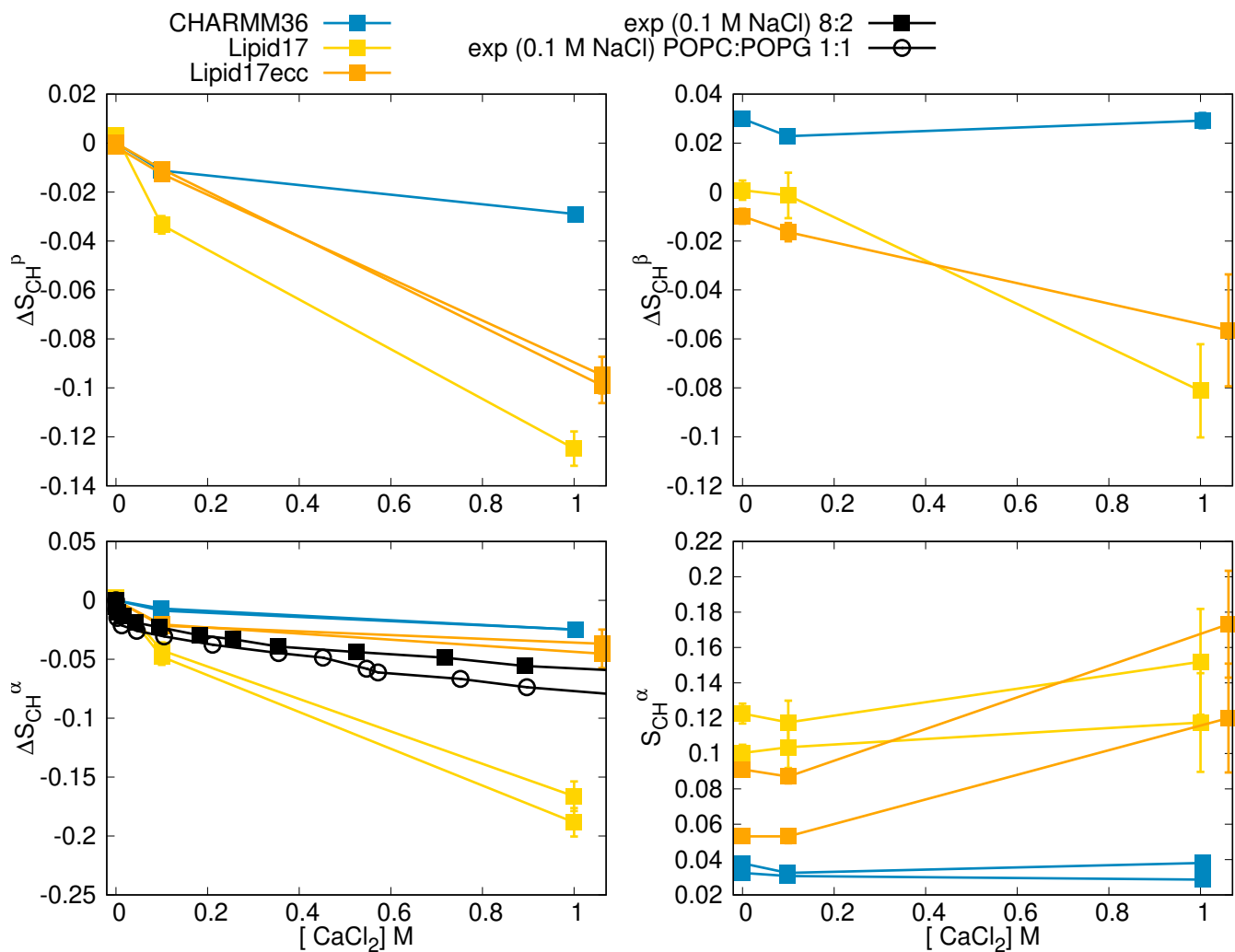


Figure S8: Calcium ion density profiles along membrane normal from simulations of POPC:POPG (1:1) mixtures with different force fields. The changes in the order parameters upon addition of CaCl_2 are compared with experiments in figure 4 in the main text.



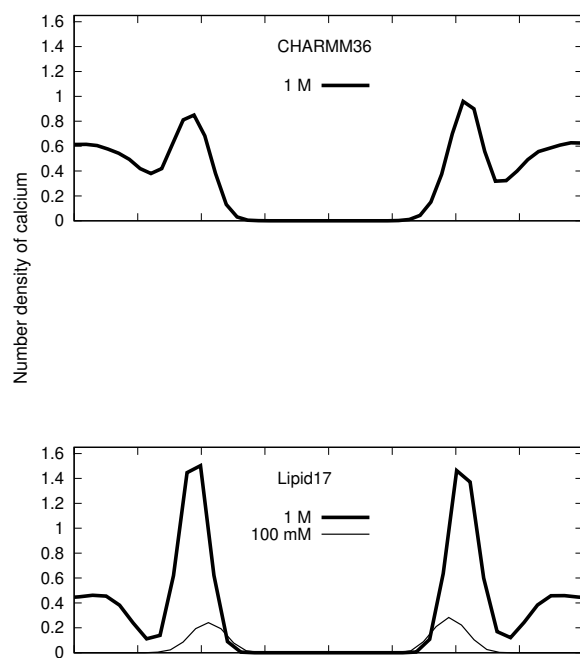


Figure S10: Calcium ion density profiles along membrane normal from simulations of POPC:POPG (4:1) mixtures with different force fields.

S6 Changes in headgroup conformations upon addition of CaCl_2

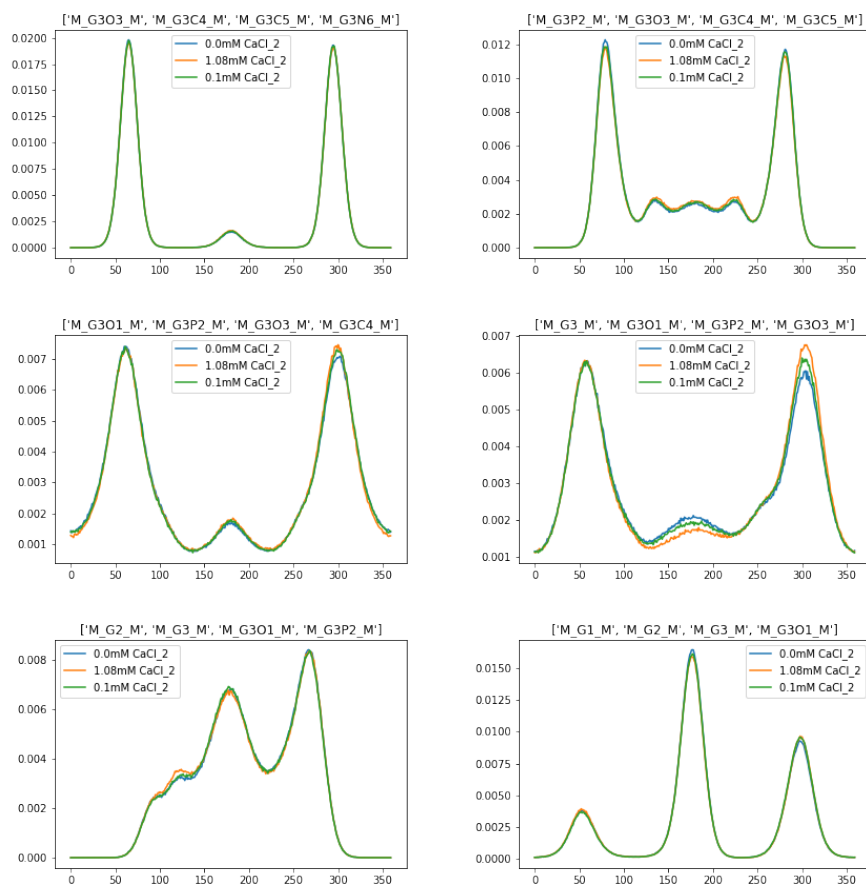


Figure S11: Changes in POPC CHARMM36 dihedrals with increasing amount of CaCl_2 .

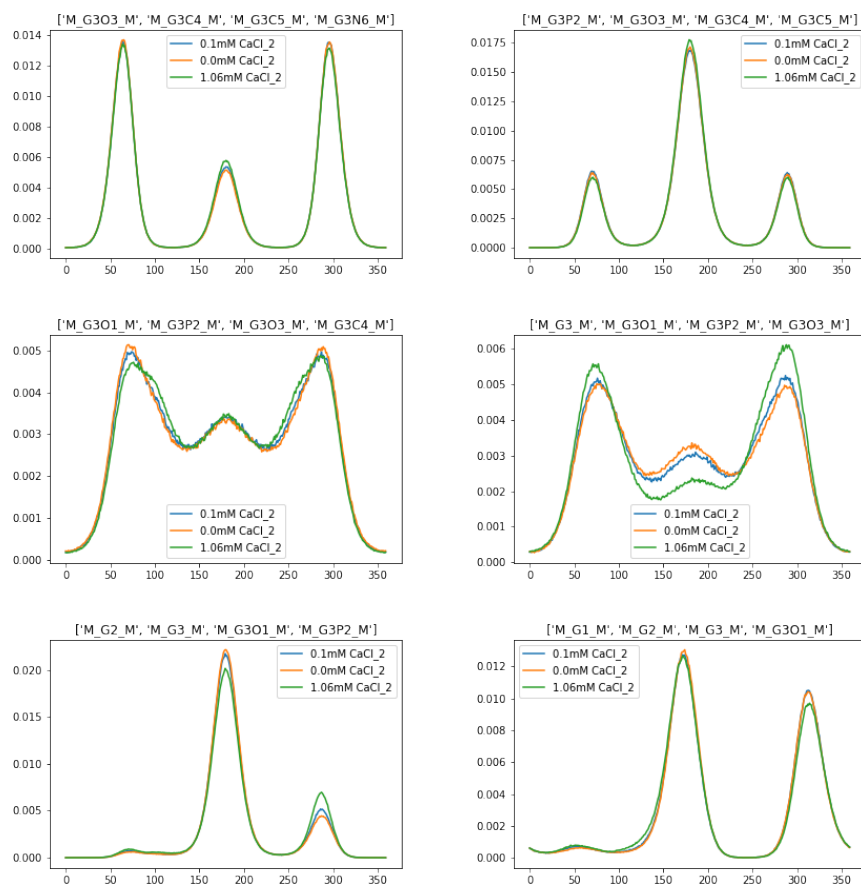


Figure S12: Changes in POPC lipid17ecc dihedrals with increasing amount of CaCl_2 .

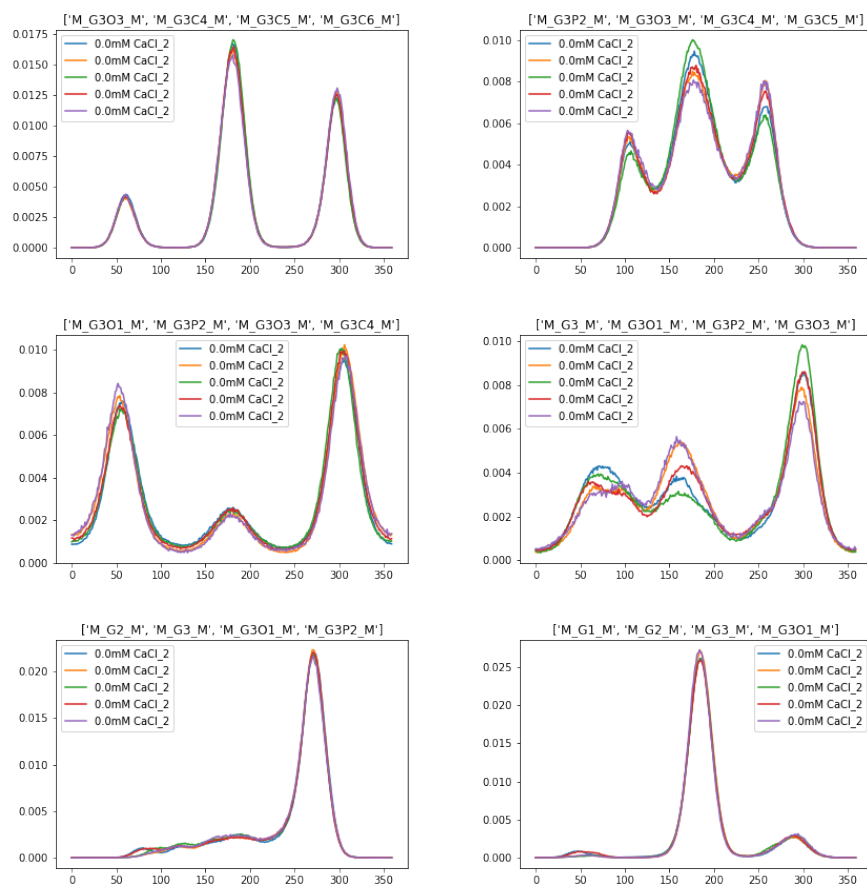


Figure S13: Changes in POPG lipids dihedrals with increasing amount of CaCl_2 .

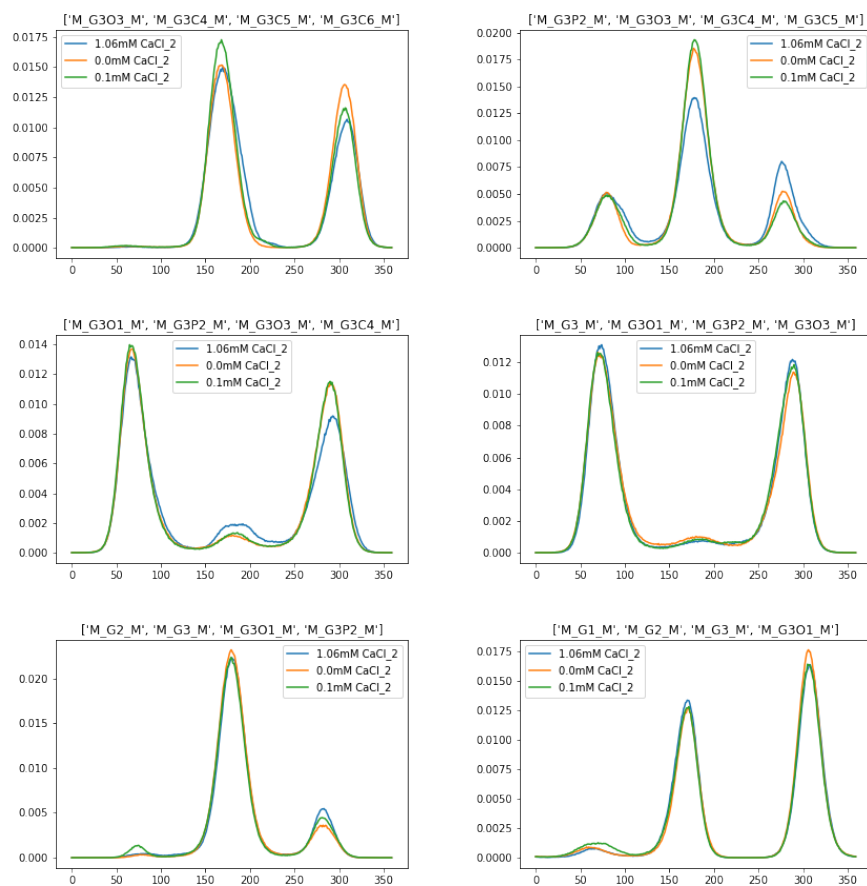


Figure S14: Changes in POPG lipid17 dihedrals with increasing amount of CaCl₂.

S7 Simulated systems

S7.1 CHARMM36

POPE [25.Simulation details by M. Javanainen.](#)

POPE with additional NaCl [26.Simulation details by A. Peon.](#)

POPG [27.Simulation details by Ollila.](#)

POPG with additional NaCl [28.Simulation details by A. Peon.](#)

POPC:POPE mixtures Data is available at.^{62,63} 300 K with v-rescale ($\tau=0.1$ ps), 1 bar with PR semiisotropic ($\tau=4$ ps, compressibility= $4.5\text{e-}5$ bar⁻¹), PME order 4 and space 0.12, rcoulomb and rvdw 1.0, 128 lipids per leaflet, no ion [29.Full simulation details by Fuchs et al.](#)

POPC:POPG mixture with additional calcium [30.Simulation details by A. Kiirikki.](#)

POPC and POPC:POPG (7:3) mixture [31.Simulation details by A. Peon.](#)

S7.2 CHARMM36ua

POPE Data is available at.¹⁵ [32.Simulation details by T. Piggot.](#)

S7.3 Slipids

POPE Data is available at.¹⁸ [33.Simulation details by T. Piggot.](#)

POPE with additional NaCl [34.Simulation details by A. Peon.](#) I have assumed that ion parameters are default Slipids, i.e., Åqvist, please correct if this is not true.

DPPE Data is available at.¹⁷ [35.Simulation details by F. Favela.](#)

POPG Data is available at.⁴⁴ [36.Simulation details by F. Favela.](#) I have assumed that ion parameters are default Slipids, i.e., Åqvist, please correct if this is not true.

POPG with additional NaCl [37.Simulation details by A. Peon.](#) I have assumed that ion parameters are default Slipids, i.e., Åqvist, please correct if this is not true.

DPPG Data in 298 K is available at⁴⁶ and in 314 K at.⁴⁵ [38.Simulation details by F. Favela.](#) I have assumed that ion parameters are default Slipids, i.e., Åqvist, please correct if this is not true.

Table S1: List of MD simulations with PE lipids.

lipid/counter-ions	force field for lipids / ions	NaCl (M)	^a N _l	^b N _w	^c N _c	^d T (K)	^e t _{sim} (ns)	^f t _{anal} (ns)	^g files
POPE	CHARMM36 [?]	0	144	5760	0	310	500	400	12
POPE	CHARMM36 [?]	0	500	25000	0	310	500	100	13
POPE	CHARMM36 [?]	0.11	500	25000	50	310	500	100	14
POPE	CHARMM36ua [?]	0	336	15254	0	310	2×200	2×100	15
DPPE	Slipids ¹⁶	0	288	9386	0	336	200	100	17
POPE	Slipids ¹⁶	0	336	?	0	310	2×200	2×100	18
POPE	Slipids ¹⁶	0	500	25000	0	310	500	100	19
POPE	Slipids / Åqvist ^{16,20}	0.11	500	25000	50	310	500	100	21
DPPE	GROMOS-CKP [?]	0	128	3655	0	342	2×500	2×400	22
POPE	GROMOS-CKP [?]	0	128	3552	0	313	2×500	2×400	23
POPE	GROMOS-CKP [?]	0	500	25000	0	310	500	100	24
POPE	GROMOS-CKP [?]	0.11	500	25000	50	310	500	100	25
DOPE	GROMOS-CKP [?]	0	128	4789	0	271	2×500	2×400	26
POPE	GROMOS 43A1-S3 [?]	0	128	3552	0	313	2×200	2×100	27
POPE	OPLS-UA vdW on H [?]	0	128	3328	0	303	2×200	2×100	28
POPE	OPLS-UA [?]	0	128	3328	0	303	2×200	2×100	29
POPE	OPLS-MacRog ³⁰	0	144	5760	0	310	500	350	31
POPE	OPLS-MacRog ³⁰	0	128	5120	0	300	500	300	32
POPE	Berger-Vries [?]	0	128	3552	0	303	2×200	2×100	33
POPE	Berger-largeH [?]	0	128	3552	0	303	2×200	2×100	34
DOPE	Berger-Vries [?]	0	128	4789	0	271	2×200	2×100	35
DOPE	Berger-largeH [?]	0	128	4789	0	271	2×300	2×100	36
POPE	LIPID17 ³⁷	0	500	25000	50	310	500	100	38
POPE	LIPID17 ³⁷	0.11	500	25000	50	310	500	100	39

^aNumber of lipid molecules with largest mole fraction

^bNumber of water molecules

^cNumber of additional cations

^dSimulation temperature

^eTotal simulation time

^fTime used for analysis

^gReference for simulation files

3. Simulations with added NaCl are not currently used here, maybe should be removed from the table?

4. Citation for CHARMM36 PE?

5. Which ion model is used in ¹⁴?

6. Citation for GROMOS-CKP?

7. Citation for GROMOS 43A1-S3?

8. Citation for OPLS-UA models?

9. Citations for Berger-* simulations?

10. LIPID17 simulations with correct dihedrals still coming

Table S2: List of MD simulations with PG lipids.

lipid/counter-ions	force field for lipids / ions	NaCl (M)	^a N _l	^b N _w	^c N _c	^d T (K)	^e t _{sim} (ns)	^f t _{anal} (ns)	^g files
POPG/K ⁺	CHARMM36 [?] 11.	0	118	4110	0	298	100	100	40
POPG	CHARMM36 [?]	0.11	500	25000	49	310	500	100	41
POPG	CHARMM36 [?]	0	500	25000	0	310	500	100	42
POPG/Na ⁺	Slipids / Åqvist ^{20,43}	0	288	10664	0	298	250	100	44
DPPG/Na ⁺	Slipids / Åqvist ^{20,43}	0	288	11232	0	314	200	100	45
DPPG/Na ⁺	Slipids / Åqvist ^{20,43}	0	288	11232	0	298	400	100	46
POPG	Slipids / Åqvist ^{20,43}	0	500	25000	0	310	500	100	47
POPG	Slipids / Åqvist ^{20,43}	0.11	500	25000	49	310	500	100	48
POPG	LIPID17 / Dang ^{37,49}	0	500	25000	0	310	500	100	50
POPG	LIPID17 [?]	0.11	500	25000	49	310	500	100	51
POPG	GROMOS-CKP [?]	0	500	25000	0	310	500	100	52
POPG	GROMOS-CKP [?]	0.11	500	25000	49	310	500	100	53

^aNumber of lipid molecules with largest mole fraction

^bNumber of water molecules

^cNumber of additional cations

^dSimulation temperature

^eTotal simulation time

^fTime used for analysis

^gReference for simulation files

12.Simulations with added NaCl are not currently used here, maybe should be removed from the table?

13.Citations and ion model for CHARMM36?

14.Lipid17 simulation with ions with correct dihedral potentials still coming?

15.Citation and ion model for GROMOS-CKP?

Table S3: List of MD simulations with PE and PG lipids mixed with PC.

lipid/counter-ions	force field for lipids / ions	NaCl (M)	CaCl ₂ (M)	^a N _l	^b N _w	^c N _c	^d T (K)	^e t _{sim} (ns)	^f t _{anal} (ns)	^g files
POPC	CHARMM36 [?]	0	0	500	25000	0	310	500	100	54
POPC:POPG (7:3)	CHARMM36 [?]	0	0	350	25000	0	310	500	100	55
POPC:POPG (1:1)	CHARMM36 [?]	0	0	150:150	31500	0	298	500	400	56
POPC:POPG (1:1)	CHARMM36 [?]	0	0.1	150:150	31329	57	298	400	300	57
POPC:POPG (1:1)	CHARMM36 [?]	0	1.08	150:150	29766	578	298	500	400	58
POPC:POPG (4:1)	CHARMM36 [?]	0	0	350:88	26280	0	298	500	400	59
POPC:POPG (4:1)	CHARMM36 [?]	0	0.1	350:88	26280	47	298	500	400	60
POPC:POPG (4:1)	CHARMM36 [?]	0	1.0	350:88	24927	451	298	500	400	61
POPC	CHARMM36 [?]	0	0	256	8704	0	300	300	250	62
POPC:POPE (1:1)	CHARMM36 [?]	0	0	128	8704	0	300	300	250	63
POPC	OPLS-MacRog ³⁰	0	0	128	5120	0	300	500	300	64
POPC:POPE (1:1)	OPLS-MacRog ³⁰	0	0	128	5120	0	300	500	300	65
POPC	Slipid ¹⁶	0	0	512	23943	0	298	170	100	66
POPC:POPE (1:1)	Slipid ¹⁶	0	0	128	5120	0	298	500	300	67
POPC	GROMOS-CKP / ?? [?] ?	0	0	500	25000	0	310	500	100	68
POPC:POPG (7:3)	GROMOS-CKP / ?? [?] ?	0	0	350:150	25000	0	310	500	100	69
POPC	Slipid ¹⁶	0	0	500	25000	0	310	500	100	70
POPC:POPG (7:3)	Slipid / Åqvist ^{16,20}	0	0	350:150	25000	0	310	500	100	71
POPC:POPG (1:1)	Slipid / Dang ^{16,49,72,73}	0	0	128:128	12800	0	298	500	400	74
POPC:POPG (1:1)	Slipid / Dang ^{16,49,72,73}	0	0.1	128:128	12800	23	298	500	400	74
POPC:POPG (1:1)	Slipid / Dang ^{16,49,72,73}	0	0.2	128:128	12800	46	298	1500	500	74
POPC:POPG (1:1)	Slipid / Dang ^{16,49,72,73}	0	0.5	128:128	12800	115	298	1500	500	74
POPC:POPG (1:1)	Slipid / Dang ^{16,49,72,73}	0	1.0	128:128	12800	230	298	1500	500	74

^aNumber of lipid molecules with largest mole fraction

^bNumber of water molecules

^cNumber of additional cations

^dSimulation temperature

^eTotal simulation time

^fTime used for analysis

^gReference for simulation files

16. Citation and ion model for GROMOS-CKP?

17. Upcoming Lipid17ecc with POPC:POPS (4:1) mixture simulations to be added.

Table S4: List of MD simulations with PE and PG lipids mixed with PC.

lipid/counter-ions	force field for lipids / ions	NaCl (M)	CaCl ₂ (M)	^a N _l	^b N _w	^c N _c	^d T (K)	^e t _{sim} (ns)	^f t _{anal} (ns)	^g files
POPC:POPG (4:1)	Lipid17 / Dang ^{37,49,73}	0	0	350:88	26265	0	298	400	350	75
POPC:POPG (4:1)	Lipid17 / Dang ^{37,49,73}	0	0.1	350:88	26124	47	298	400	250	76
POPC:POPG (4:1)	Lipid17 / Dang ^{37,49,73}	0	1.0	350:88	24840	475	298	1200	200	77
POPC:POPG (1:1)	Lipid17 / Dang ^{37,49,73}	0	0	150:150	31572	0	298	320	200	78
POPC:POPG (1:1)	Lipid17 / Dang ^{37,49,73}	0	0.1	150:150	31401	57	298	718	198	79
POPC:POPG (1:1)	Lipid17 / Dang ^{37,49,73}	0	1.0	150:150	29865	569	298	720	200	80
POPC:POPG (4:1)	Lipid17ecc / ECC-ions ⁸¹⁻⁸³	0	0	350:88	26265	0	298	400	300	84
POPC:POPG (4:1)	Lipid17ecc / ECC-ions ⁸¹⁻⁸³	0	0.1	350:88	26124	47	298	400	300	85
POPC:POPG (4:1)	Lipid17ecc / ECC-ions ⁸¹⁻⁸³	0	1.0	350:88	24840	475	298	400	300	86
POPC:POPG (1:1)	Lipid17ecc / ECC-ions ⁸¹⁻⁸³	0	0	150:150	31572	0	298	347.8	333	87
POPC:POPG (1:1)	Lipid17ecc / ECC-ions ⁸¹⁻⁸³	0	0.1	150:150	29865	54	298	400	300	88
POPC:POPG (1:1)	Lipid17ecc / ECC-ions ⁸¹⁻⁸³	0	1.0	150:150	29865	569	298	600	400	89
POPC	Berger [?] 18.	0	0	256	10240	0	300	300	200	90
POPC:POPE (1:1)	Berger [?] 19.	0	0	128	11008	0	300	300	200	91
POPC:DOPE (1:1)	Berger [?] 20.	0	0	128	10240	0	300	300	200	92
DOPC	Berger [?] 21.	0	0	256	11008	0	300	300	200	93
DOPC:DOPE (1:1)	Berger [?] 22.	0	0	128	11008	0	300	300	200	94

^aNumber of lipid molecules with largest mole fraction

^bNumber of water molecules

^cNumber of additional cations

^dSimulation temperature

^eTotal simulation time

^fTime used for analysis

^gReference for simulation files

23. Citation and description for "Berger" model?

24. Upcoming Lipid17ecc with POPC:POPS (4:1) mixture simulations to be added.

POPC:POPG mixture with additional NaCl [39.Simulation details by A. Peon.](#) I have assumed that ion parameters are default Slipids, i.e., Åqvist, please correct if this is not true.

POPC:POPG mixture with additional CaCl [40.Simulation details by M. Javanainen.](#)

S7.4 Berger

POPE Data is available at. ^{33,34} [41.Simulation details by T. Piggot.](#)

DOPE Data is available at. ^{35,36} [42.Simulation details by T. Piggot.](#)

POPC:POPE, POPC:DOPE and DOPC:DOPE mixtures Data is available at. ^{90,91} 300 K with v-rescale ($\tau=0.1$ ps), 1 bar with PR semiisotropic ($\tau=4$ ps, compressibility= $4.5\text{e-}5$ bar⁻¹), PME order 4 and space 0.12, rcoulomb and rvdw 1.0, 128 lipids per leaflet, no ion [43.Simulation details by Fuchs et al.](#)

S7.5 GROMOS 43A1-S3

POPE Data is available at. ²⁷ [44.Simulation details by T. Piggot.](#)

S7.6 OPLS-UA

POPE Data is available at. ²⁹ [45.Simulation details by T. Piggot.](#)

POPE with vdW interaction in H Data is available at. ²⁸ [46.Simulation details by T. Piggot.](#)

S7.7 GROMOS-CKP and GROMOS-CKPM

POPE Data is available at. ²³ [47.Simulation details by T. Piggot.](#)

DOPE Data is available at. ²⁶ [48.Simulation details by T. Piggot.](#)

DPPE Data is available at. ²² [49.Simulation details by T. Piggot.](#)

POPG [50.Simulation details by A. Peon.](#)

POPC:POPG mixture [51.Simulation details by A. Peon.](#)

S7.8 OPLS-MacRog

POPE 52.Simulation details by M. Javanainen and P. Fuchs.

POPC:POPE mixtures 53.Simulation details by P. Fuchs.

S7.9 Lipid17

POPE 54.Simulation details by A. Peon.

POPG 55.Simulation details by A. Peon.

POPC:POPG 56.Simulation details by S. Virtanen or O. H. S. Ollila.

S7.10 Lipid17ecc

57.This is to be finished and POPC:POPG mixtures to be described In ECC-lipid models, electronic continuum correction (ECC) is applied to implicitly include the missing electronic polarizability into the force field description.^{95,96} In practise, this is implemented by scaling the charges and Lennard-Jones σ s of headgroup, glycerol backbone, and carbonyl regions of Amber Lipid14/17 models are scaled by constant factors. Here, we follow the approach that previously improved ion binding to bilayers containing negatively charged PS lipids:⁹⁶ ECC-POPC parameters (scaling factors $f_q=0.8$ and $f_\sigma=0.89$ applied to Lipid14 POPC parameters)⁹⁵ were used for POPC and scaling factors of $f_q=0.75$ and $f_\sigma=0.89$ were applied to the charges and Lennard-Jones σ s of headgroup, glycerol backbone, and carbonyl regions of Amber Lipid17 POPG parameters. The Lipid17 parameters (described above) and initial configurations were taken from Ref.⁵⁰ with the correct dihedral type, and the resulting parameters are available from Ref. ? . ECC-ion parameters with the scaled charges,⁸¹⁻⁸³ downloaded from bitbucket.org/hseara/ions/src/master/, were used in these simulations.

References

- (1) Botan, A.; Favela-Rosales, F.; Fuchs, P. F. J.; Javanainen, M.; Kanduč, M.; Kulig, W.; Lamberg, A.; Loison, C.; Lyubartsev, A.; Miettinen, M. S. et al. Toward Atomistic Resolution Structure of Phosphatidylcholine Headgroup and Glycerol Backbone at Different Ambient Conditions. *J. Phys. Chem. B* **2015**, *119*, 15075–15088.
- (2) Antila, H. S.; Buslaev, P.; Favela-Rosales, F.; Mendes Ferreira, T.; Gushchin, I.; Javanainen, M.; Kav, B.; Madsen, J. J.; Melcr, J.; Miettinen, M. S. et al. Headgroup Structure and Cation Binding in Phosphatidylserine Lipid Bilayers. *The Journal of Physical Chemistry B* **2019**, acs.jpcc.9b06091.
- (3) Seelig, J.; Gally, H. U. Investigation of phosphatidylethanolamine bilayers by deuterium and phosphorus-31 nuclear magnetic resonance. *Biochemistry* **1976**, *15*, 5199–5204.
- (4) Gally, H. U.; Pluschke, G.; Overath, P.; Seelig, J. Structure of Escherichia coli membranes. Glycerol auxotrophs as a tool for the analysis of the phospholipid head-group region by deuterium magnetic resonance. *Biochemistry* **1981**, *20*, 1826–1831.
- (5) Borle, F.; Seelig, J. Ca²⁺ binding to phosphatidylglycerol bilayers as studied by differential scanning calorimetry and 2H- and 31P-nuclear magnetic resonance. *Chemistry and Physics of Lipids* **1985**, *36*, 263 – 283.
- (6) Wohlgemuth, R.; Waespe-Sarcevic, N.; Seelig, J. Bilayers of phosphatidylglycerol. A deuterium and phosphorus nuclear magnetic resonance study of the head-group region. *Biochemistry* **1980**, *19*, 3315–3321.
- (7) Scherer, P.; Seelig, J. Structure and dynamics of the phosphatidylcholine and the phosphatidylethanolamine head group in L-M fibroblasts as studied by deuterium nuclear magnetic resonance. *EMBO J.* **1987**, *6*.

- (8) Macdonald, P. M.; Seelig, J. Calcium binding to mixed phosphatidylglycerol-phosphatidylcholine bilayers as studied by deuterium nuclear magnetic resonance. *Biochemistry* **1987**, *26*, 1231–1240.
- (9) Ollila, O. S.; Pabst, G. Atomistic resolution structure and dynamics of lipid bilayers in simulations and experiments. *Biochimica et Biophysica Acta (BBA) - Biomembranes* **2016**, *1858*, 2512 – 2528.
- (10) Seelig, J.; MacDonald, P. M.; Scherer, P. G. Phospholipid head groups as sensors of electric charge in membranes. *Biochemistry* **1987**, *26*, 7535–7541.
- (11) Antila, H. S.; Buslaev, P.; Favela-Rosales, F.; Mendes Ferreira, T.; Gushchin, I.; Javanainen, M.; Kav, B.; Madsen, J. J.; Melcr, J.; Miettinen, M. S. et al. Headgroup Structure and Cation Binding in Phosphatidylserine Lipid Bilayers. *The Journal of Physical Chemistry B* **0**, *0*, null.
- (12) Javanainen, M. Simulation of a POPE bilayer at 310K with the CHARMM36 force field. 2019; <https://doi.org/10.5281/zenodo.2641987>.
- (13) PEON, CHARMM36 POPE Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3237461>.
- (14) PEÄŞN, A. CHARMM36 POPE Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.2577454>.
- (15) Piggot, T. CHARMM36-UA POPE Simulations (versions 1 and 2) 310 K (NOTE: hexagonal membrane and POPE is called PEUA). 2018; <https://doi.org/10.5281/zenodo.1293774>.
- (16) Jämbeck, J. P. M.; Lyubartsev, A. P. An Extension and Further Validation of an All-Atomistic Force Field for Biological Membranes. *J. Chem. Theory Comput.* **2012**, *8*, 2938–2948.

- (17) Favela-Rosales, F. MD simulation trajectory of a fully hydrated DPPE bilayer: SLIPIDS, Gromacs 5.0.4. 2017. 2017; <https://doi.org/10.5281/zenodo.495247>.
- (18) Piggot, T. Slipids POPE Simulations (versions 1 and 2) 310 K (NOTE: hexagonal membrane). 2018; <https://doi.org/10.5281/zenodo.1293813>.
- (19) Peon, A. SLIPID POPE Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3231342>.
- (20) Åqvist, J. Ion-water interaction potentials derived from free energy perturbation simulations. *J. Phys. Chem.* **1990**, *94*, 8021–8024.
- (21) PEĂŞN, A. SLIPID POPE Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.2578069>.
- (22) Piggot, T. GROMOS-CKP DPPE Simulations (versions 1 and 2) 342 K. 2018; <https://doi.org/10.5281/zenodo.1293957>.
- (23) Piggot, T. GROMOS-CKP POPE Simulations (versions 1 and 2) 313 K. 2018; <https://doi.org/10.5281/zenodo.1293932>.
- (24) PEON, A. GROMOS POPE Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3237754>.
- (25) PEĂŞN, A. Gromos POPE Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.2574491>.
- (26) Piggot, T. GROMOS-CKP DOPE Simulations (versions 1 and 2) 271 K. 2018; <https://doi.org/10.5281/zenodo.1293941>.
- (27) Piggot, T. GROMOS 43A1-S3 POPE Simulations (versions 1 and 2) 313 K (NOTE: anisotropic pressure coupling). 2018; <https://doi.org/10.5281/zenodo.1293762>.

- (28) Piggot, T. OPLS-UA POPE Simulations (versions 1 and 2) 303 K with vdW on H atoms. 2018; <https://doi.org/10.5281/zenodo.1293853>.
- (29) Piggot, T. OPLS-UA POPE Simulations (versions 1 and 2) 303 K. 2018; <https://doi.org/10.5281/zenodo.1293855>.
- (30) RÅsg, T.; OrÅĆowski, A.; Llorente, A.; Skotland, T.; SylvÅĎnne, T.; Kauhanen, D.; Ekroos, K.; Sandvig, K.; Vattulainen, I. Data including GROMACS input files for atomistic molecular dynamics simulations of mixed, asymmetric bilayers including molecular topologies, equilibrated structures, and force field for lipids compatible with OPLS-AA parameters. *Data in Brief* **2016**, *7*, 1171 – 1174.
- (31) Javanainen, M. Simulation of a POPE bilayer, lipid model based on OPLS-aa by Rog et al. 2019; <https://doi.org/10.5281/zenodo.3571071>.
- (32) Milan Rodriguez, P.; Fuchs, P. F. MacRog pure POPE MD simulation (300 K - 500ns - 1 bar). 2020; <https://doi.org/10.5281/zenodo.3725670>.
- (33) Piggot, T. Berger POPE Simulations (versions 1 and 2) 303 K - de Vries repulsive H. 2018; <https://doi.org/10.5281/zenodo.1293889>.
- (34) Piggot, T. Berger POPE Simulations (versions 1 and 2) 303 K - larger repulsive H. 2018; <https://doi.org/10.5281/zenodo.1293891>.
- (35) Piggot, T. Berger DOPE Simulations (versions 1 and 2) 271 K - de Vries repulsive H. 2018; <https://doi.org/10.5281/zenodo.1293928>.
- (36) Piggot, T. Berger DOPE Simulations (versions 1 and 2) 271 K - larger repulsive H. 2018; <https://doi.org/10.5281/zenodo.1293905>.
- (37) Gould, I.; Skjevik, A.; Dickson, C.; Madej, B.; Walker, R. Lipid17: A Comprehensive AMBER Force Field for the Simulation of Zwitterionic and Anionic Lipids. 2018; In preparation.

- (38) PEON, A. LIPID17 POPE Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3378970>.
- (39) PEĂȘN, A. LIPID17 POPE Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.2577305>.
- (40) Ollila, O. H. S. POPG lipid bilayer simulation at T298K ran with MODEL_CHARMM_GUI force field and Gromacs. 2017; <https://doi.org/10.5281/zenodo.1011096>.
- (41) PEĂȘN, A. CHARMM36 POPG Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.2573531>.
- (42) ANTONIO, CHARMM36 POPG Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3237463>.
- (43) Jämbeck, J. P. M.; Lyubartsev, A. P. Implicit inclusion of atomic polarization in modeling of partitioning between water and lipid bilayers. *Phys. Chem. Chem. Phys.* **2013**, *15*, 4677–4686.
- (44) Favela-Rosales, F. MD simulation trajectory of a fully hydrated POPG bilayer: SLIPIDS, Gromacs 5.0.4. 2017. 2017; <https://doi.org/10.5281/zenodo.546133>.
- (45) Favela-Rosales, F. MD simulation trajectory of a fully hydrated DPPG bilayer @314K: SLIPIDS, Gromacs 5.0.4. 2017. 2017; <https://doi.org/10.5281/zenodo.546136>.
- (46) Favela-Rosales, F. MD simulation trajectory of a fully hydrated DPPG bilayer @298K: SLIPIDS, Gromacs 5.0.4. 2017. 2017; <https://doi.org/10.5281/zenodo.546135>.
- (47) PeĂșn, A. LIPID17 POPG Bilayer Simulation (Last 100 ns, 310 K) using dihedral type 9. 2019; <https://doi.org/10.5281/zenodo.3832274>.
- (48) PEĂȘN, A. SLIPID POPG Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.2633773>.

- (49) Smith, D. E.; Dang, L. X. Computer simulations of NaCl association in polarizable water. *J. Chem. Phys* **1994**, *100*, 3757–3766.
- (50) PEON, A. LIPID17 POPG Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3247659>.
- (51) PEÅŞN, A. LIPID17 POPG Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.2573905>.
- (52) PEON, A. GROMOS POPG Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3266166>.
- (53) PEÅŞN, A. Gromos POPG Bilayer Simulation (Last 100 ns, 150 mM NaCl, 310 K). 2019; <https://doi.org/10.5281/zenodo.3257649>.
- (54) PEON, A. CHARMM36 POPC Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3247813>.
- (55) PEON, A. CHARMM36 POPC-POPG 7:3 Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3248689>.
- (56) Kiirikki, A. M.; Ollila, O. H. S. POPC:POPG 1:1 MD simulation with CHARMM36 in water and Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.3997116>.
- (57) Kiirikki, A. M.; Ollila, O. H. S. POPC:POPG 1:1 MD simulation with CHARMM36 in 0.1 M CaCl solution and Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.4005515>.
- (58) Kiirikki, A. M.; Ollila, O. H. S. POPC:POPG 1:1 MD simulation with CHARMM36 in 1 M CaCl solution and Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.3997135>.
- (59) Kiirikki, A. M.; Ollila, O. H. S. POPC:POPG 4:1 MD simulation with CHARMM36 in water with Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.3996952>.

- (60) Kiirikki, A. M.; Ollila, O. H. S. POPC:POPG 4:1 MD simulation with CHARMM36 in 0.1 M CaCl₂ solution with Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.3997019>.
- (61) Kiirikki, A. M.; Ollila, O. H. S. POPC:POPG 4:1 MD simulation with CHARMM36 in 1 M CaCl₂ solution with Na⁺ counterions. 2020; <https://doi.org/10.5281/zenodo.3997037>.
- (62) Papadopoulos, C.; Fuchs, P. F. CHARMM36 pure POPC MD simulation (300 K - 300ns - 1 bar). 2018; <https://doi.org/10.5281/zenodo.1306800>.
- (63) Papadopoulos, C.; Fuchs, P. F. CHARMM36 POPC/POPE (50%-50%) MD simulation (300 K - 300ns - 1 bar). 2018; <https://doi.org/10.5281/zenodo.1306821>.
- (64) Milan Rodriguez, P.; Fuchs, P. F. MacRog pure POPC MD simulation (300 K - 500ns - 1 bar). 2020; <https://doi.org/10.5281/zenodo.3741793>.
- (65) Milan Rodriguez, P.; Fuchs, P. F. MacRog POPC/POPE 1:1 MD simulation (300 K - 500ns - 1 bar). 2020; <https://doi.org/10.5281/zenodo.3725637>.
- (66) Favela-Rosales, F. MD simulation trajectory of a lipid bilayer: Pure POPC in water. SLIPIDS, Gromacs 4.6.3. 2016. 2016; <https://doi.org/10.5281/zenodo.166034>.
- (67) Javanainen, M. Simulation of POPC:POPE 1:1 membrane with the Slipids force field. 2020; <https://doi.org/10.5281/zenodo.3605386>.
- (68) PEON, A. GROMOS-CKP POPC Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3247435>.
- (69) PEON, A. GROMOS-CKP POPC-POPG 7:3 Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3266240>.
- (70) PEON, A. SLIPID POPC Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3235552>.

- (71) PeON, A. SLIPID POPC-POPG 7:3 Bilayer Simulation (Last 100 ns, 310 K). 2019; <https://doi.org/10.5281/zenodo.3240156>.
- (72) Jämbeck, J. P.; Lyubartsev, A. P. Another piece of the membrane puzzle: extending slipids further. *Journal of chemical theory and computation* **2012**, *9*, 774–784.
- (73) Dang, L. X.; Schenter, G. K.; Glezakou, V.-A.; Fulton, J. L. Molecular simulation analysis and X-ray absorption measurement of Ca²⁺, K⁺ and Cl⁻ ions in solution. *J. Phys. Chem. B* **2006**, *110*, 23644–54.
- (74) Javanainen, M. Simulations of POPC:POPG 1:1 membranes with varying levels of CaCl₂ using the Slipids force field. 2020; <https://doi.org/10.5281/zenodo.3613573>.
- (75) Virtanen, S.; Ollila, O. H. S. LIPID17 POPC-POPG 80:20 MD simulation, Na⁺ counterions, 298K. 2019; <https://doi.org/10.5281/zenodo.3693681>.
- (76) Virtanen, S.; Ollila, O. H. S. LIPID17 POPC-POPG 80:20 MD simulation, Na⁺ counterions and 100mM CaCl₂, 298K. 2019; <https://doi.org/10.5281/zenodo.3833725>.
- (77) Virtanen, S.; Ollila, O. H. S. LIPID17 POPC-POPG 80:20 MD simulation, Na⁺ counterions and 1000mM CaCl₂, 298K. 2019; <https://doi.org/10.5281/zenodo.3874378>.
- (78) Virtanen, S.; Ollila, O. H. S. LIPID17 POPC-POPG 50:50 MD simulation, Na⁺ counterions, 298K. 2019; <https://doi.org/10.5281/zenodo.3857816>.
- (79) Virtanen, S.; Ollila, O. H. S. LIPID17 POPC-POPG 50:50 MD simulation, Na⁺ counterions and 100mM CaCl₂, 298K. 2019; <https://doi.org/10.5281/zenodo.3871590>.
- (80) Virtanen, S.; Ollila, O. H. S. LIPID17 POPC-POPG 50:50 MD simulation, Na⁺ counterions and 1000mM CaCl₂, 298K. 2019; <https://doi.org/10.5281/zenodo.3864993>.

- (81) Pluhařová, E.; Fischer, H. E.; Mason, P. E.; Jungwirth, P. Hydration of the chloride ion in concentrated aqueous solutions using neutron scattering and molecular dynamics. *Mol. Phys.* **2014**, *112*, 1230–1240.
- (82) Kohagen, M.; Mason, P. E.; Jungwirth, P. Accounting for Electronic Polarization Effects in Aqueous Sodium Chloride via Molecular Dynamics Aided by Neutron Scattering. *J. Phys. Chem. B* **2016**, *120*, 1454–1460.
- (83) Martínek, T.; Duboué-Dijon, E.; Timr, Š.; Mason, P. E.; Baxová, K.; Fischer, H. E.; Schmidt, B.; Pluhařová, E.; Jungwirth, P. Calcium ions in aqueous solutions: Accurate force field description aided by ab initio molecular dynamics and neutron scattering. *J. Chem. Phys.* **2018**, *148*, 222813.
- (84) Kiirikki, A. M.; Ollila, O. H. S. Lipid17ecc POPC:POPG 4:1 MD simulation in water with Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.3997154>.
- (85) Kiirikki, A. M.; Ollila, O. H. S. Lipid17ecc POPC:POPG 4:1 bilayer simulation in 0.1 M CaCl₂ solution and Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.3997176>.
- (86) Kiirikki, A. M.; Ollila, O. H. S. Lipid17ecc POPC:POPG 4:1 bilayer simulation in 1 M CaCl₂ solution and Na⁺ counter ions. 2020; <https://doi.org/10.5281/zenodo.3997184>.
- (87) Ollila, O. H. S.; Virtanen, I. S. ECC-LIPID17 POPC-POPG 50:50 MD simulation, Na⁺ counterions, 298K. 2020; <https://doi.org/10.5281/zenodo.3859339>.
- (88) Ollila, O. H. S.; Virtanen, I. S. ECC-LIPID17 POPC-POPG 50:50 MD simulation, Na⁺ counterions and 100mM CaCl₂, 298K. 2020; <https://doi.org/10.5281/zenodo.3855729>.

- (89) Ollila, O. H. S.; Virtanen, I. S. ECC-LIPID17 POPC-POPG 50:50 MD simulation, Na⁺ counterions and 1000mM CaCl₂, 298K. 2020; <https://doi.org/10.5281/zenodo.3862036>.
- (90) AmÄllie, B.; F.J., F. P. Berger pure POPC MD simulation (300 K - 300ns - 1 bar). 2018; <https://doi.org/10.5281/zenodo.1402417>.
- (91) AmÄllie, B.; F.J., F. P. Berger POPC/POPE (50:50 ratio) MD simulation (300 K - 400ns - 1 bar). 2018; <https://doi.org/10.5281/zenodo.1402449>.
- (92) AmÄllie, B.; F.J., F. P. Berger POPC/DOPE (50:50 ratio) MD simulation (300 K - 300ns - 1 bar). 2018; <https://doi.org/10.5281/zenodo.1402441>.
- (93) AmÄllie, B.; F.J., F. P. Berger pure DOPC MD simulation (300 K - 300ns - 1 bar). 2018; <https://doi.org/10.5281/zenodo.1402411>.
- (94) AmÄllie, B.; F.J., F. P. Berger DOPC/DOPE (50:50 ratio) MD simulation (300 K - 300ns - 1 bar). 2018; <https://doi.org/10.5281/zenodo.1402437>.
- (95) Melcr, J.; Martinez-Seara, H.; Nencini, R.; Kolafa, J.; Jungwirth, P.; Ollila, O. H. S. Accurate Binding of Sodium and Calcium to a POPC Bilayer by Effective Inclusion of Electronic Polarization. *The Journal of Physical Chemistry B* **2018**, *122*, 4546–4557.
- (96) Melcr, J.; Ferreira, T.; Jungwirth, P.; Ollila, O. H. S. Improved Cation Binding to Lipid Bilayer with Negatively Charged POPS by Effective Inclusion of Electronic Polarization. https://github.com/ohs011lila/ecc_lipids/blob/master/Manuscript/manuscript.pdf, Submitted.