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

Pavel Buslaev,[†] Rebeca García Fandiño,[‡] Fernando Favela-Rosales,[§] Patrick Fuchs,[‖] Matti Javanainen,[⊥] Jesper J. Madsen,[#,@] Josef Melcr,[⊥,△] Paula Milan Rodriguez,[‖] Markus S. Miettinen,[▽] O. H. Samuli Ollila,[*,††] Chris G. Papadopoulos,[‡‡] Antonio Peón,[¶¶] Thomas J. Piggot,[§§] Ángel Piñeiro,[‖‖] and Pierre Poulain[‖]

†*University of Jyväskylä*

‡*Center for Research in Biological Chemistry and Molecular Materials (CiQUS), Universidade de Santiago de Compostela, E-15782 Santiago de Compostela, Spain*

¶*CIQUP, Centro de InvestigaÃğÃčo em QuÃŋmica, Departamento de QuÃŋmica e BioquÃŋmica, Faculdade de CiÃłncias, Universidade do Porto, Porto, Portugal*

§*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*

S1 R-PDLF and SDROSS experiments

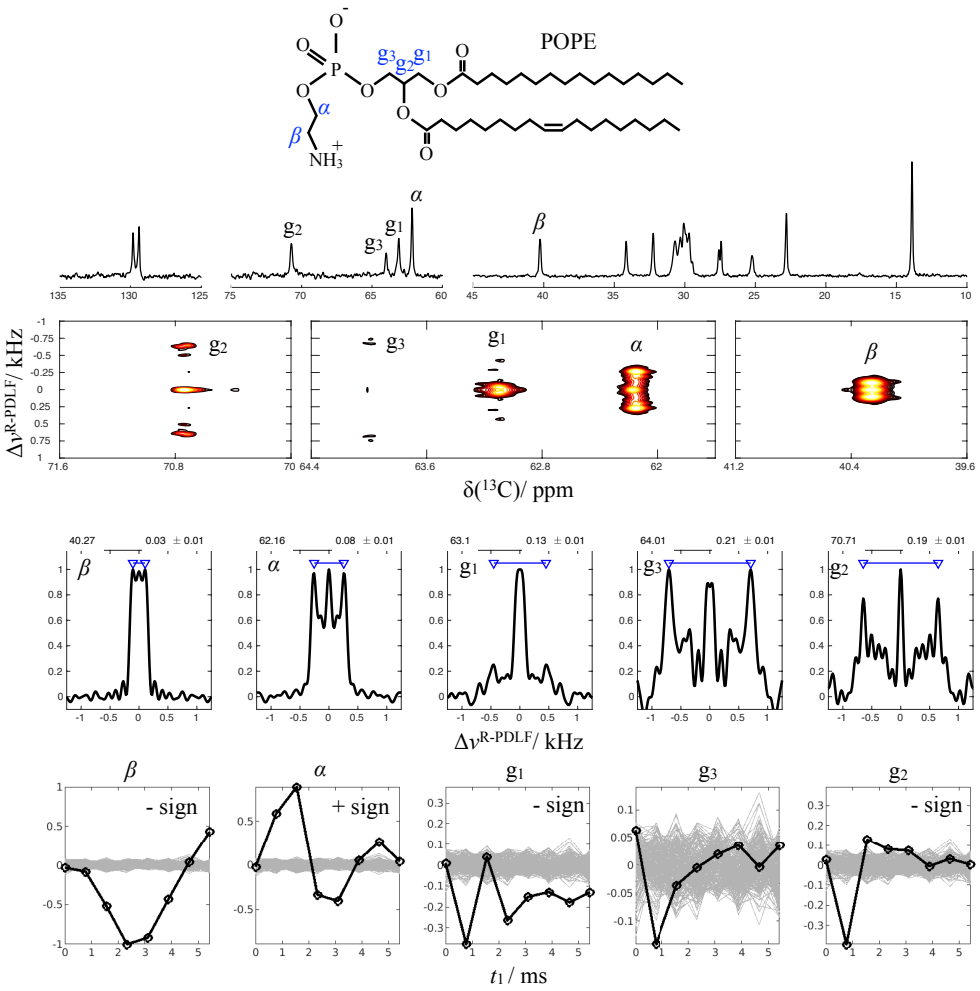

Figure S1: (A) Chemical structure of POPE with the labeling of headgroup and glycerol backbone carbons. (B) INEPT spectra from POPE sample with the headgroup and glycerol backbone peaks labeled. (C) 2D R-PDLF spectra (D) Dipolar sliced from the 2D R-PDLF spectra with the resulting order parameters on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

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

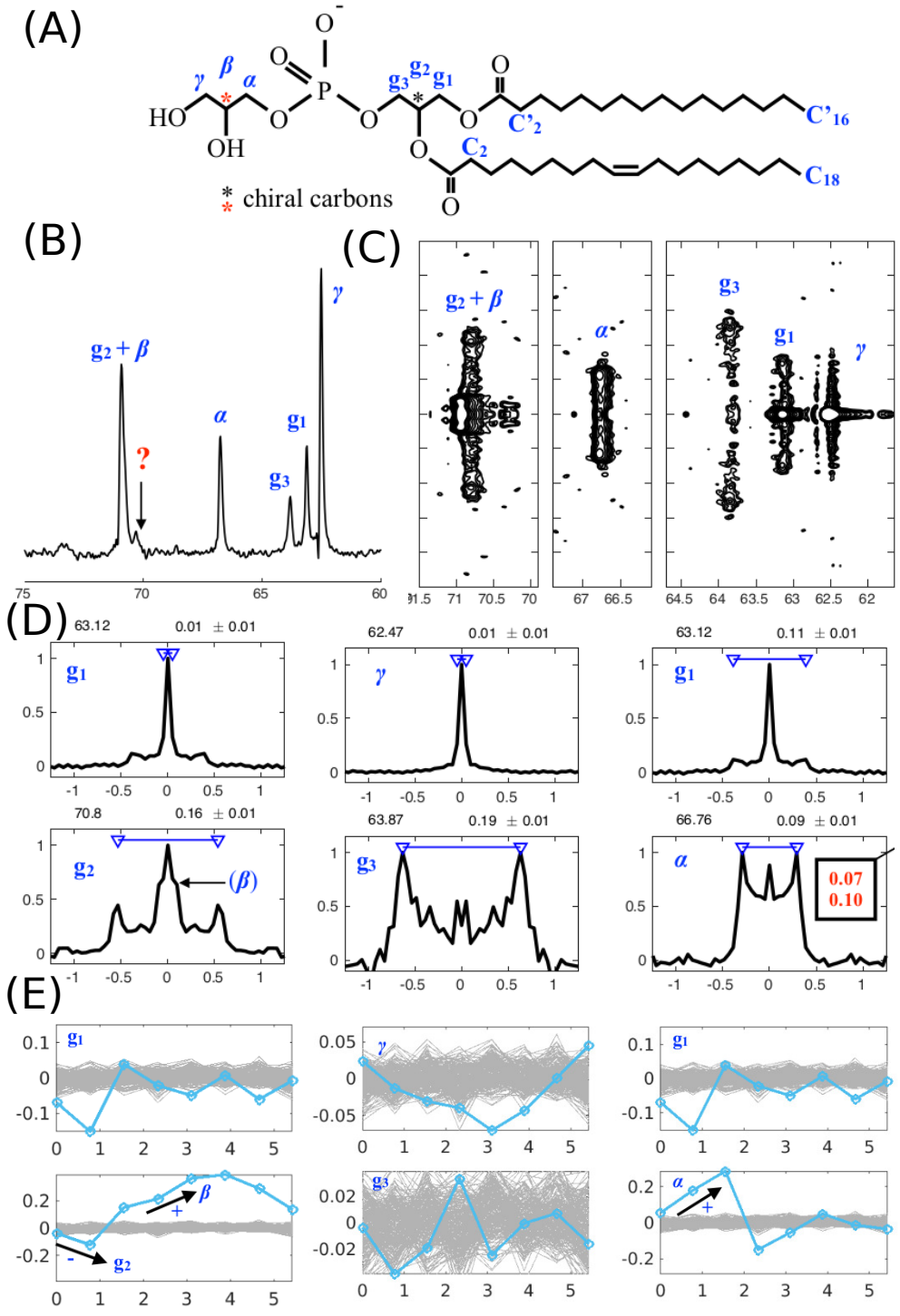

Figure S2: (A) Chemical structure of POPG with the labeling of headgroup and glycerol backbone carbons. (B) INEPT spectra from POPG sample with the headgroup and glycerol backbone peaks labeled. (C) 2D R-PDLF spectra (D) Dipolar sliced from the 2D R-PDLF spectra with the resulting order parameters on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

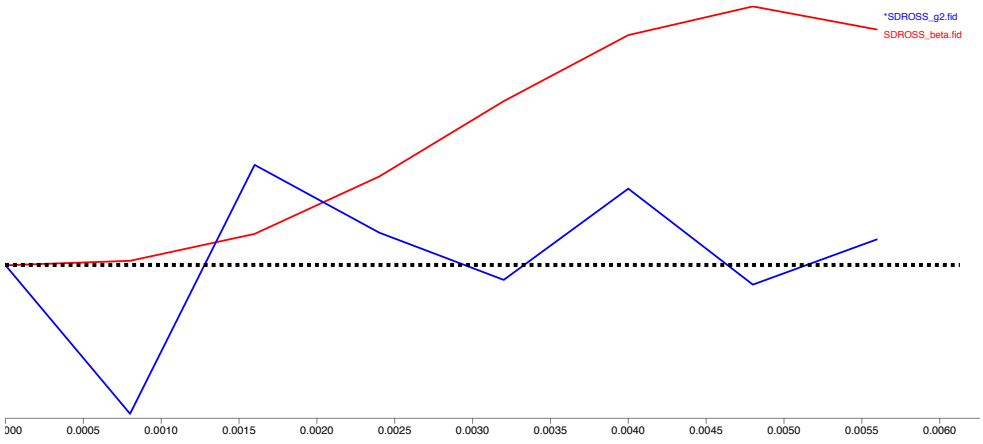

Figure S3: Simpson simulaton of S-DROSS curve of β-carbon of POPG.

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.

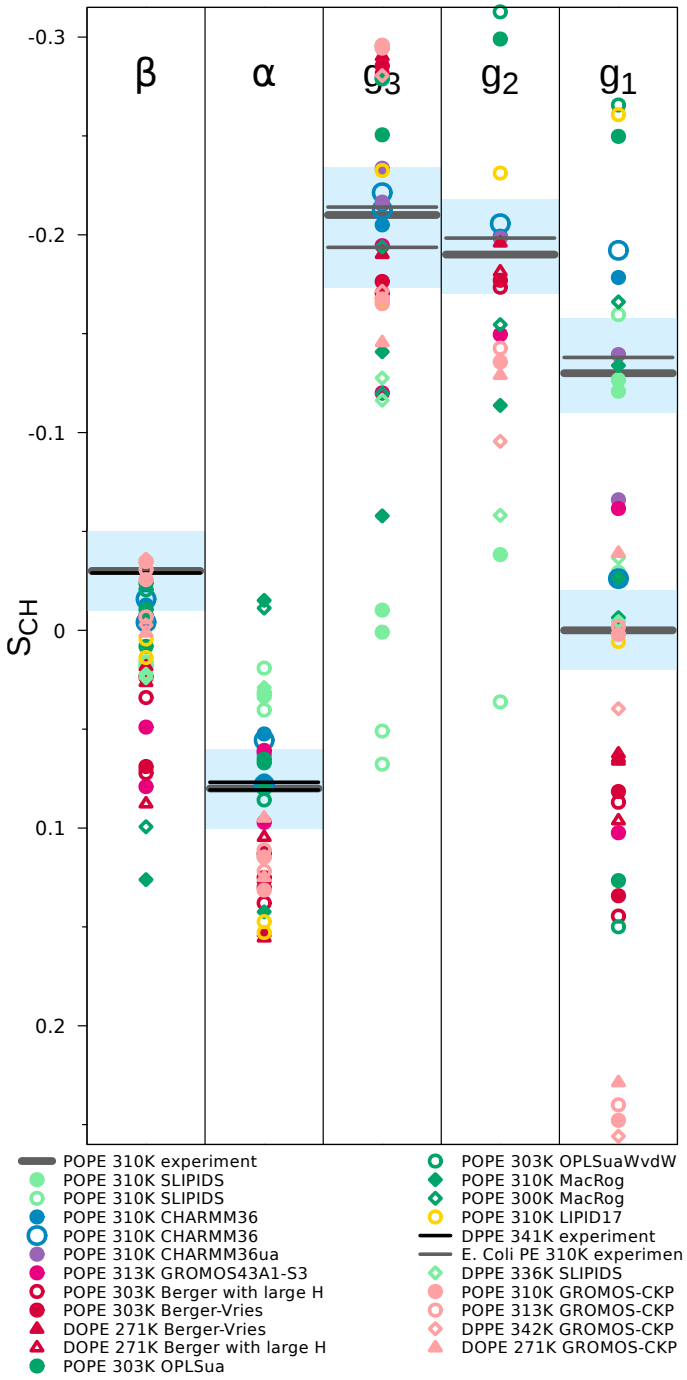

Figure S4: The headgroup and glycerol backbone order parameters of PE lipids from experiments (POPE and signs this work, DPPE from Ref. 3 and E.coliPE from Ref. 4) and simulations with different force fields.

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.

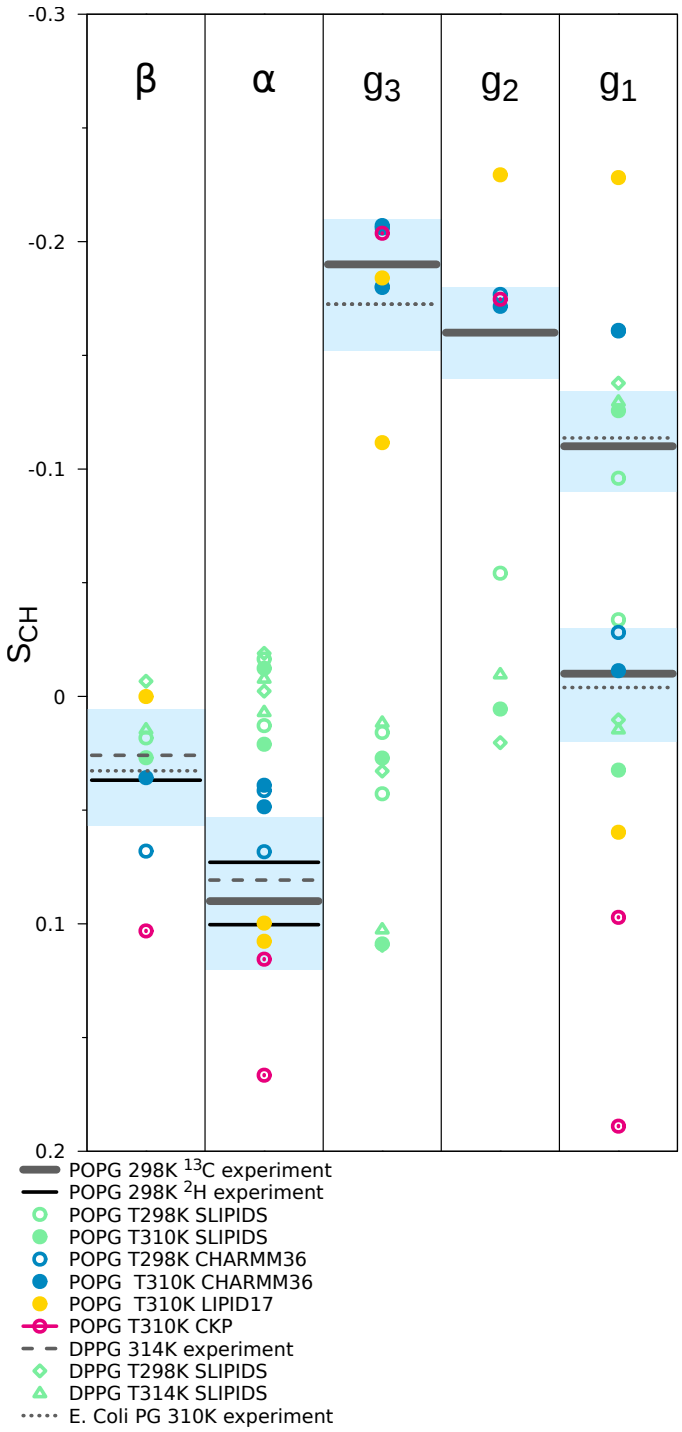

Figure S5: The headgroup and glycerol backbone order parameters of PG lipids from experiments (POPG and signs from this work and from Ref. 5, DPPG with 100mM NaCl from Ref. 6,and E.Coli PG results from Ref. 4) and simulations with different force fields.

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 neturalizes the effect of added negative charge.[2] **3.Difference between ÃĚqvist and Dang in Slipids results probably supports this, but this has to checked from density profiles.** 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 enemble 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]

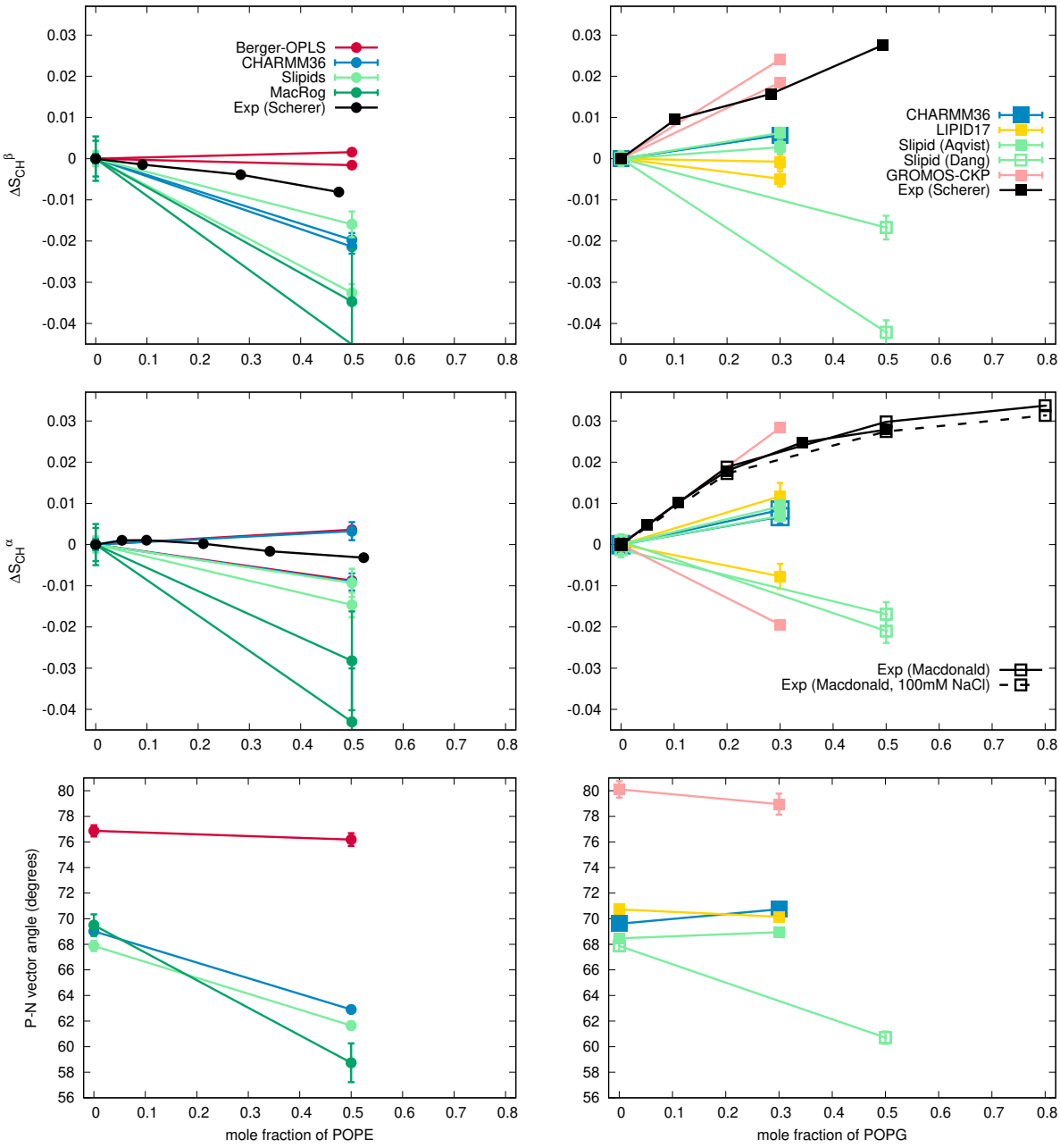

Figure S6: Modulation of POPC headgroup order parameters with increasing amount of POPE (left) and POPG (right) in bilayer from experiments at 298 K[7,8] and simulations with different force fields (temperatures listed in tables S3 and S4 are between 298-310 K). Signs are determined as discussed in Refs. 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 mildly[8] or is unchanged[5] 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.

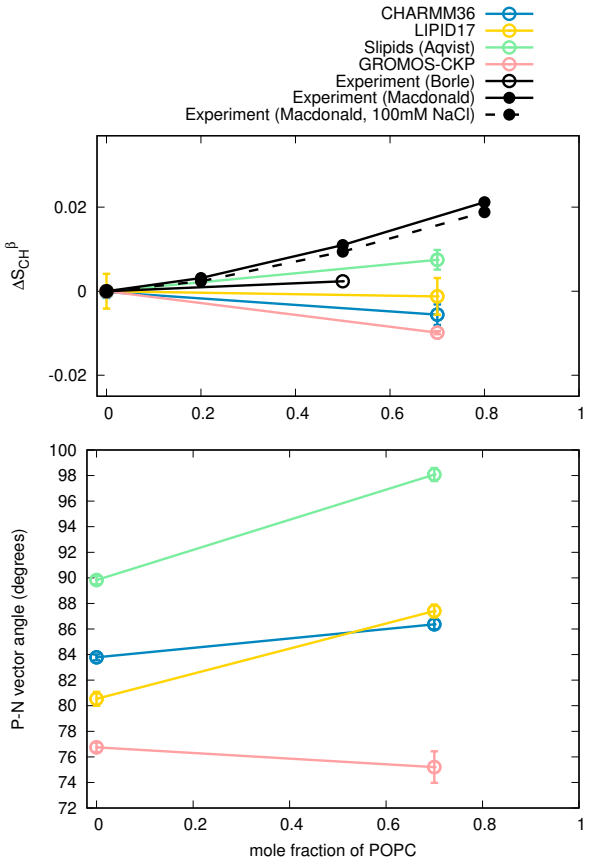

Figure S7: Modulation of PG lipid headgroup order parameters with the increasing amount of PC in lipid bilayer from experiments at 298 K[5,8] and simulations with different force fields at 310 K.

S5 Calcium binding to POPC:POPG mixtures

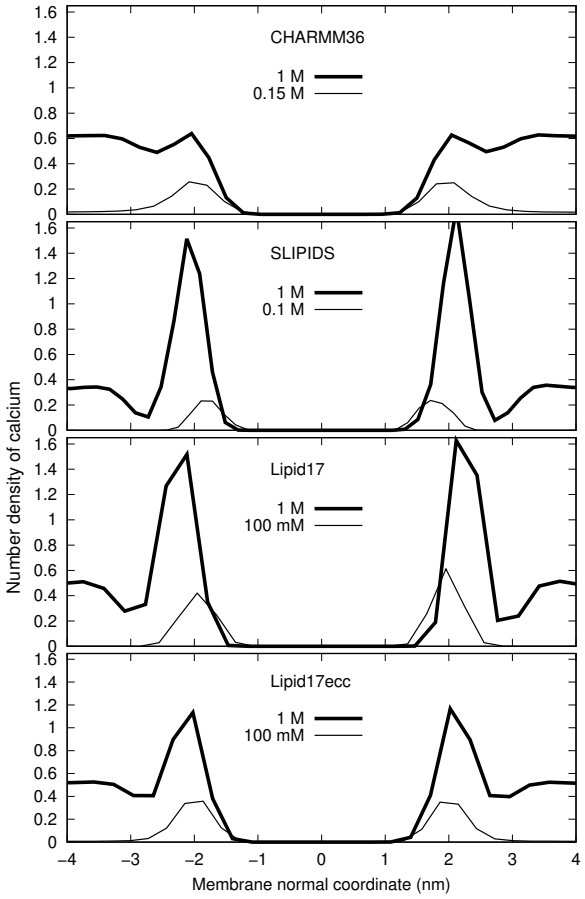

Figure S8: Calcium ion density profiles along membrane normal from simulations of POPC:POPG (1:1) mixtures with different force fields. The changes in the order parameters upon addition of $CaCl_2$ are compared with experiments in figure 4 in the main text.

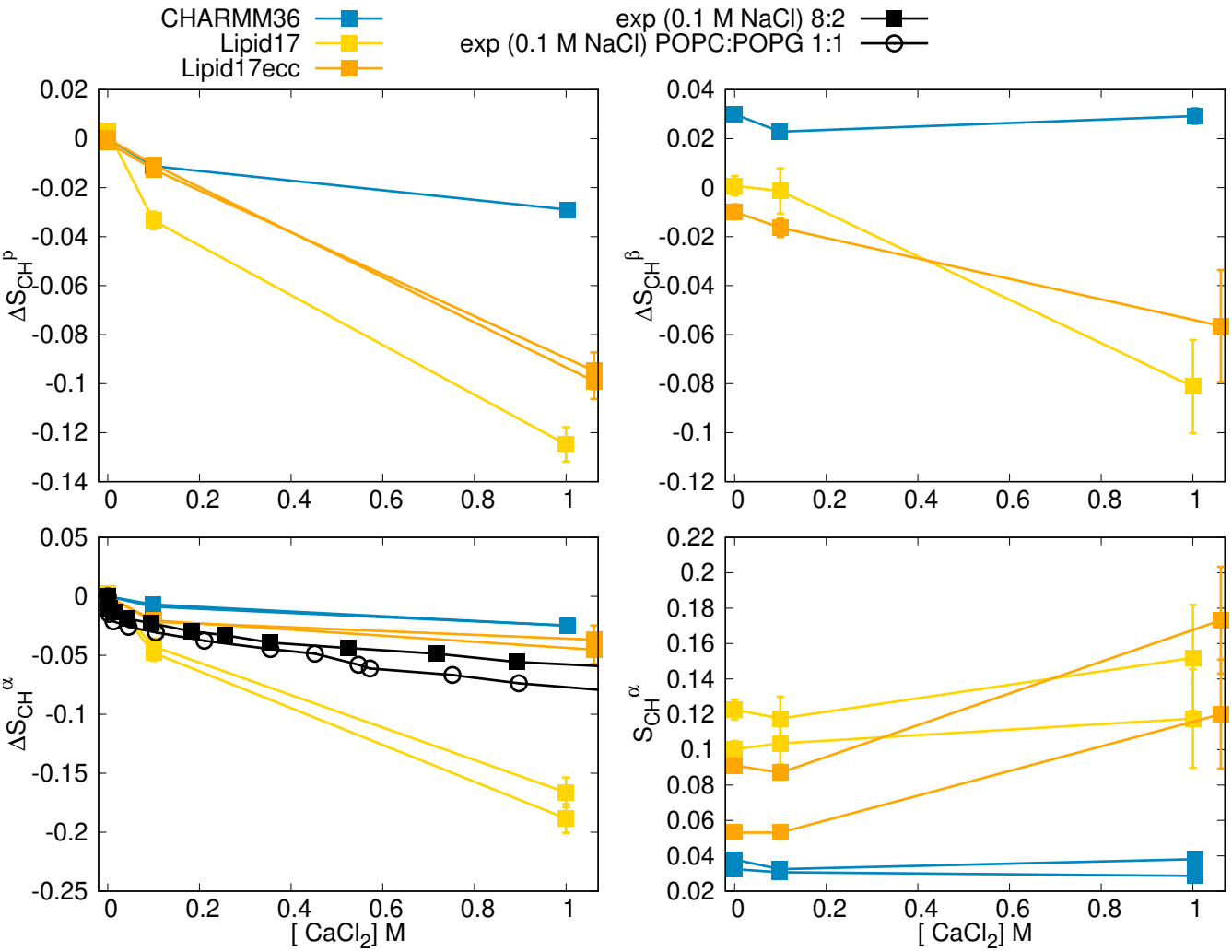

Figure S9: Modulation of headgroup order parameters of POPC (*left*) and POPG (*right*) in POPC:POPG (4:1) mixture upon addition of $CaCl_2$ in 298 K temperature from experiments[8] and simulations. The changes with respect to the systems without $CaCl_2$ are shown for other data than for the α-carbon of POPG for which experimental order parameter is not available.

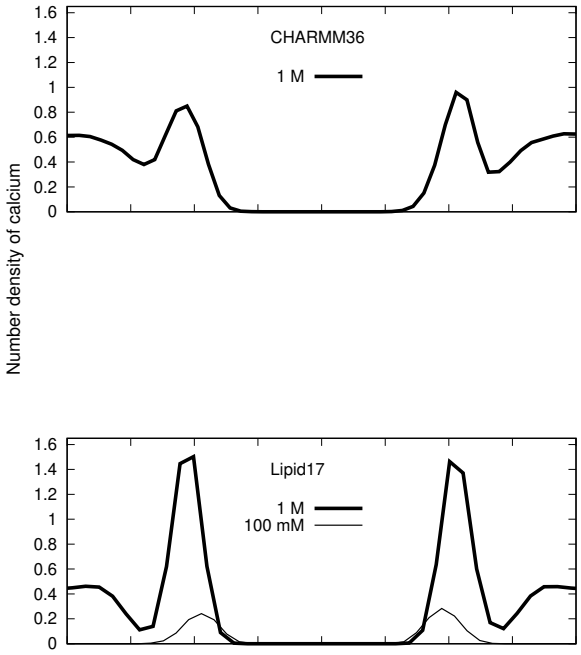

Figure S10: Calcium ion density profiles along membrane normal from simulations of POPC:POPG (4:1) mixtures with different force fields.

S6 Changes in headgroup conformations upon addition of $CaCl_2$

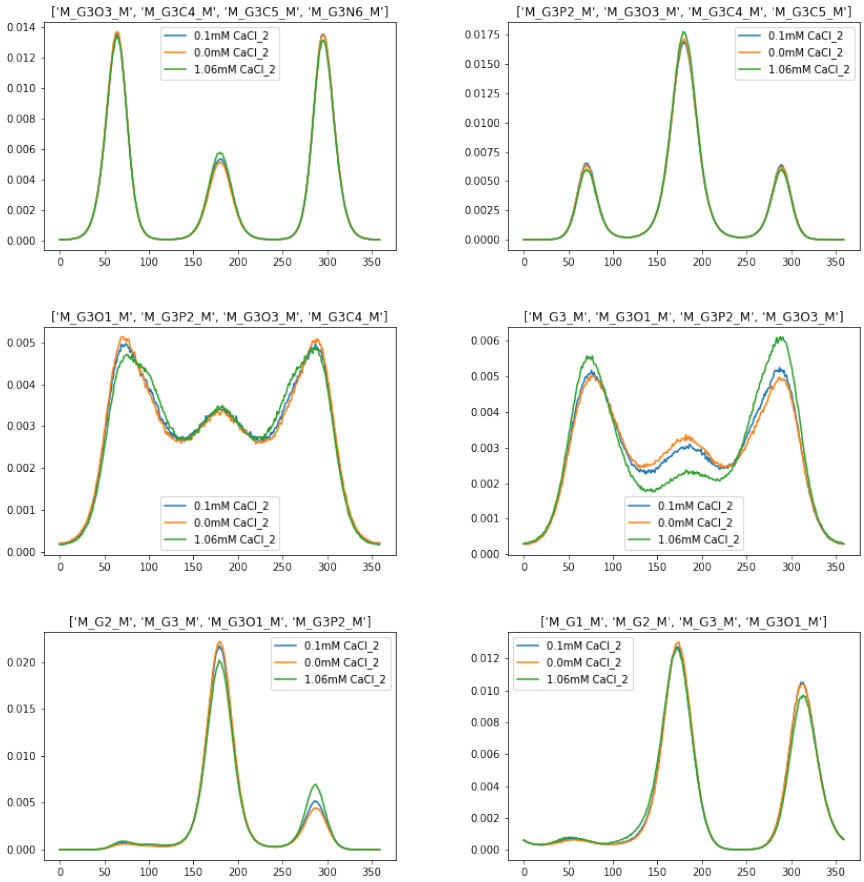

Figure S11: Changes in POPC lipid17ecc dihedrals with increasing amount of $CaCl_2$.

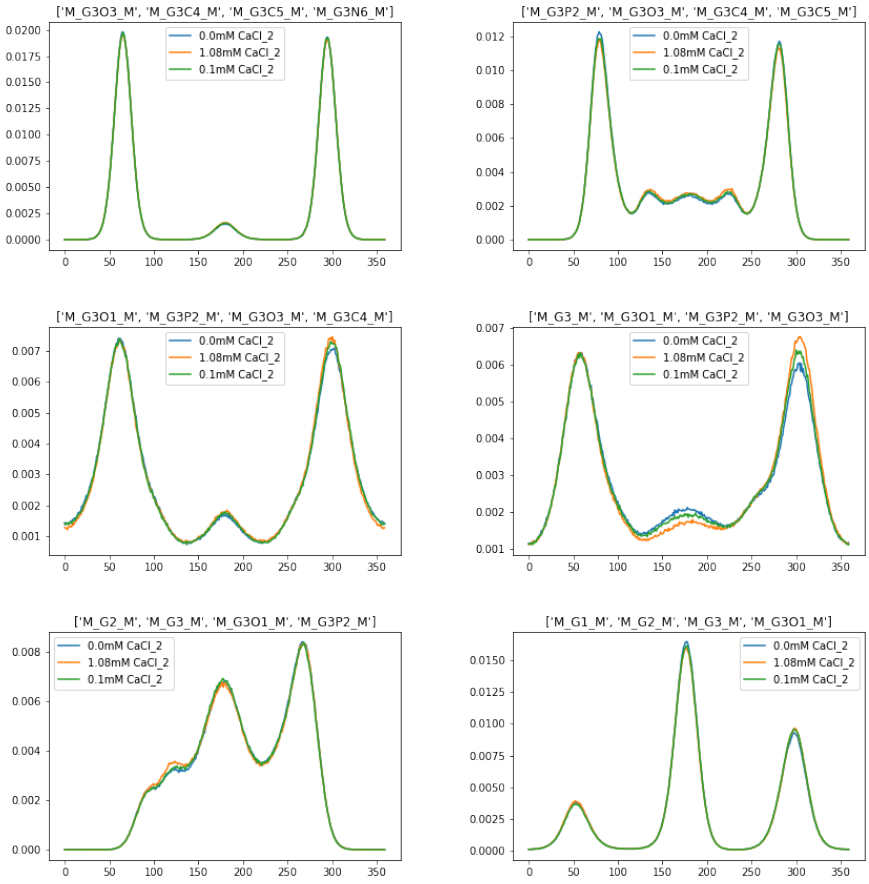

Figure S12: Changes in POPC CHARMM36 dihedrals with increasing amount of $CaCl_2$.

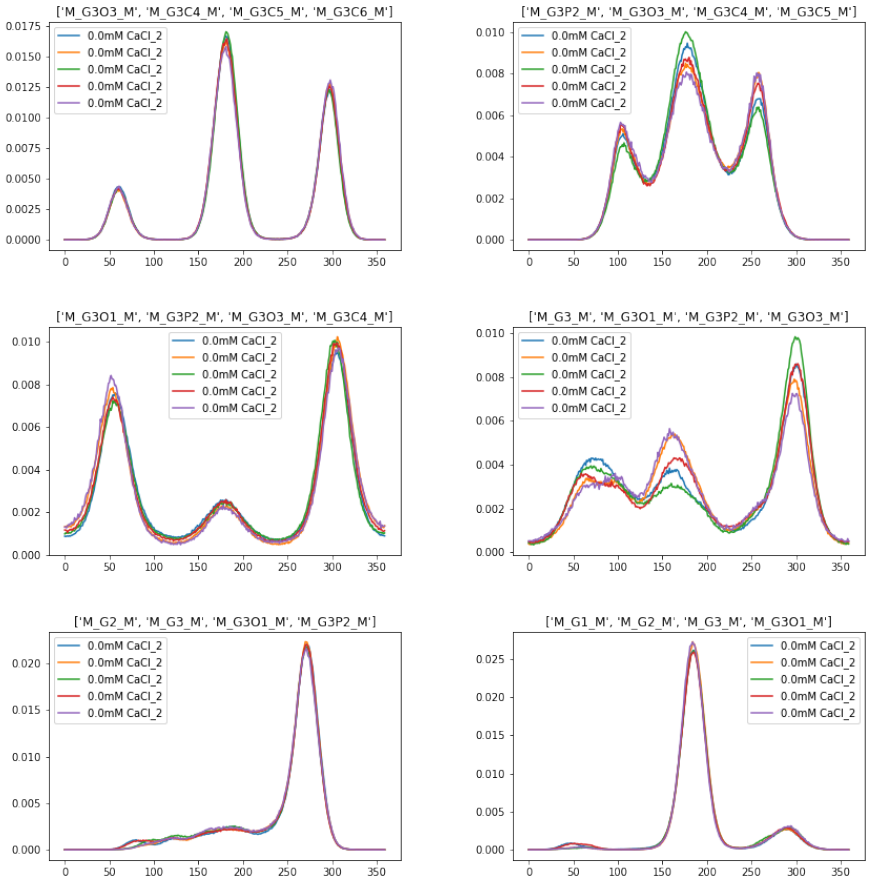

Figure S13: Changes in POPG Slipids dihedrals with increasing amount of $CaCl_2$.

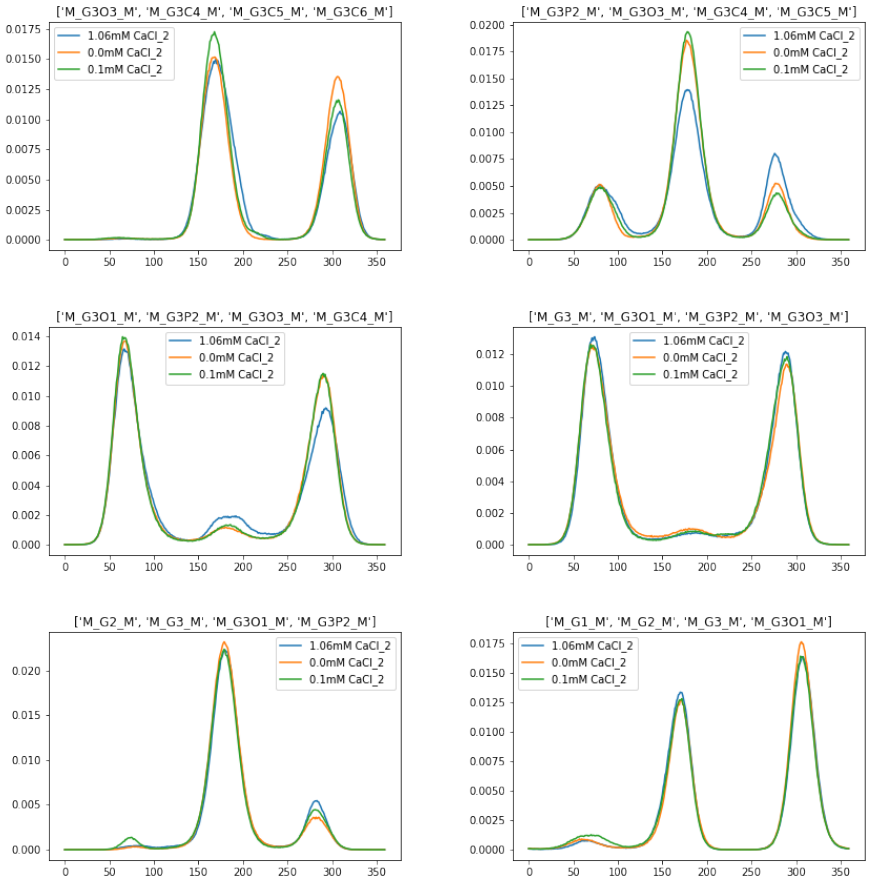

Figure S14: Changes in POPG lipid17 dihedrals with increasing amount of $CaCl_2$.

S7 Simulated systems

S7.1 CHARMM36

POPE **26.Simulation details by M. Javanainen.**

POPE with additional NaCl **27.Simulation details by A. Peon.**

POPG **28.Simulation details by Ollila.**

POPG with additional NaCl **29.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=4.5e-5 bar^{-1}), PME order 4 and space 0.12, rcoulomb and rvdw 1.0, 128 lipids per leaflet, no ion **30.Full simulation details by Fuchs et al.**

POPC:POPG mixture with additional calcium **31.Simulation details by A. Kiirikki.**

POPC and POPC:POPG (7:3) mixture **32.Simulation details by A. Peon.**

S7.2 CHARMM36ua

POPE Data is available at.[15] **33.Simulation details by T. Piggot.**

S7.3 Slipids

POPE Data is available at.[18] **34.Simulation details by T. Piggot.**

POPE with additional NaCl **35.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] **36.Simulation details by F. Favela.**

POPG Data is available at.[44] **37.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 **38.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 at[46] and in 314 K at.[45] **39.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]

[a]Number of lipid molecules with largest mole fraction
[b]Number of water molecules
[c]Number of additional cations
[d]Simulation temperature
[e]Total simulation time
[f]Time used for analysis
[g]Reference for simulation files

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

5.Citation for CHARMM36 PE?

6.Which ion model is used in[14]?

7.Citation for GROMOS-CKP?

8.Citation for GROMOS 43A1-S3?

9.Citation for OPLS-UA models?

10.Citations for Berger-* simulations?

11.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? 12.	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]

[a]Number of lipid molecules with largest mole fraction
[b]Number of water molecules
[c]Number of additional cations
[d]Simulation temperature
[e]Total simulation time
[f]Time used for analysis
[g]Reference for simulation files

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

14.Citations and ion model for CHARMM36?

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

16.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]

[a]Number of lipid molecules with largest mole fraction
[b]Number of water molecules
[c]Number of additional cations
[d]Simulation temperature
[e]Total simulation time
[f]Time used for analysis
[g]Reference for simulation files

17.Citation and ion model for GROMOS-CKP?

18.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[?] **19.**	0	0	256	10240	0	300	300	200	[90]
POPC:POPE (1:1)	Berger[?] **20.**	0	0	128	11008	0	300	300	200	[91]
POPC:DOPE (1:1)	Berger[?] **21.**	0	0	128	10240	0	300	300	200	[92]
DOPC	Berger[?] **22.**	0	0	256	11008	0	300	300	200	[93]
DOPC:DOPE (1:1)	Berger[?] **23.**	0	0	128	11008	0	300	300	200	[94]

[a]Number of lipid molecules with largest mole fraction
[b]Number of water molecules
[c]Number of additional cations
[d]Simulation temperature
[e]Total simulation time
[f]Time used for analysis
[g]Reference for simulation files

24.Citation and description for "Berger" model?

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

POPC:POPG mixture with additional NaCl **40.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 **41.Simulation details by M. Javanainen.**

S7.4 Berger

POPE Data is available at.[33,34] **42.Simulation details by T. Piggot.**

DOPE Data is available at.[35,36] **43.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=4.5e-5 bar^{-1}), PME order 4 and space 0.12, rcoulomb and rvdw 1.0, 128 lipids per leaflet, no ion **44.Simulation details by Fuchs et al.**

S7.5 GROMOS 43A1-S3

POPE Data is available at.[27] **45.Simulation details by T. Piggot.**

S7.6 OPLS-UA

POPE Data is available at.[29] **46.Simulation details by T. Piggot.**

POPE with vdW interaction in H Data is available at.[28] **47.Simulation details by T. Piggot.**

S7.7 GROMOS-CKP and GROMOS-CKPM

POPE Data is available at.[23] **48.Simulation details by T. Piggot.**

DOPE Data is available at.[26] **49.Simulation details by T. Piggot.**

DPPE Data is available at.[22] **50.Simulation details by T. Piggot.**

POPG **51.Simulation details by A. Peon.**

POPC:POPG mixture **52.Simulation details by A. Peon.**

S7.8 OPLS-MacRog

POPE **53.Simulation details by M. Javanainen and P. Fuchs.**

POPC:POPE mixtures **54.Simulation details by P. Fuchs.**

S7.9 Lipid17

POPE **55.Simulation details by A. Peon.**

POPG **56.Simulation details by A. Peon.**

POPC:POPG **57.Simulation details by S. Virtanen or O. H. S. Ollila.**

S7.10 Lipid17ecc

58.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?] In practise, this is implemented by scaling the charges and Lennard-Jones σs 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:[?] ECC-POPC parameters (scaling factors f_q=0.8 and f_σ=0.89 applied to Lipid14 POPC parameters)[95] were used for POPC and scaling factors of f_q=0.75 and f_σ=0.89 were applied to the charges and Lennard-Jones σs 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.jpcb.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) PEÃŞN, 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) PEÃŞN, 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) PEÃŞN, 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) RÃşg, T.; OrÅĆowski, A.; Llorente, A.; Skotland, T.; SylvÃďnne, 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) PEÃŞN, 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) PEÃŞN, 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) PeÃşn, A. LIPID17 POPG Bilayer Simulation (Last 100 ns, 310 K) using dihedral type 9. 2019; https://doi.org/10.5281/zenodo.3832274.

(48) PEÃŞN, 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) PEÃŞN, 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) PEÃŞN, 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 CaCl_2 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) AmÃľlie, B.; F.J., F. P. Berger pure POPC MD simulation (300 K - 300ns - 1 bar). 2018; https://doi.org/10.5281/zenodo.1402417.

(91) AmÃľlie, 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) AmÃľlie, 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) AmÃľlie, B.; F.J., F. P. Berger pure DOPC MD simulation (300 K - 300ns - 1 bar). 2018; https://doi.org/10.5281/zenodo.1402411.

(94) AmÃľlie, 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.