

The electrometer concept and binding of cations to phospholipid bilayers

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Despite the vast amount of experimental and theoretical studies, the binding affinity of cations, especially the biologically relevant Na^+ and Ca^{2+} ions, into a phospholipid bilayer is not agreed on in the literature. Here we show that the ion binding affinity can be directly compared between simulations and experiments by using the choline headgroup order parameters according to the electrometer concept. Our results strongly support the traditional view that Na^+ ions and other monovalent ions (except Li^+) do not specifically bind to phosphatidylcholine lipid bilayers with mM concentrations, in contrast to Ca^{2+} and other multivalent ions. Especially the Na^+ binding affinity is overestimated by several molecular dynamics simulation models, leading to artificially positively charged lipid bilayer. Qualitatively correct headgroup order parameter response is observed with Ca^{2+} binding in all the tested models, however none of the tested models has sufficient quantitative accuracy to interpret the Ca^{2+} /lipid stoichiometry or induced atomistic resolution structural changes.

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I. INTRODUCTION

The interaction of cations with phospholipid membranes is important in many physiological processes, nerve cell signalling being the prime example. For this reason such interactions have been widely studied via experiments, simulations, and theory. While it is generally agreed that the relative binding affinity of different ions follows the Hofmeister series [1–9], no consensus emerges from the literature on the quantitative binding affinities of different ions to phospholipid bilayers. Two extensive reviews covering work done prior to 1990 [2, 3] concluded that monovalent cations interact only weakly with phospholipid bilayers (with the exception of Li^+), while for multivalent ions the interactions are significant. This conclusion has been supported by further studies showing that bilayer properties remain unaltered upon addition of millimolar concentrations of monovalent salt [4, 10, 11]. On the other hand, the weakness of interactions between phospholipids and monovalent ions has been questioned in several experimental and molecular dynamics

simulation studies [6–9, 12–18] suggesting stronger binding especially for Na^+ ions.

More specifically, millimolar concentrations of NaCl have a negligible effect on the choline head group order parameters [19], area per molecule [10], dipole potential [20], and lipid lateral diffusion [11]; in contrast, these properties are significantly affected by the presence of CaCl_2 or other multivalent ions. [reference to be added?] In addition, water sorption isotherms are very similar for POPC/NaCl system and NaCl in pure water —indicating only weak interaction between ion and lipids [4]. Further, only minor changes in POPC infrared spectra are observed in the presence of NaCl, while changes are significant in the presence of Ca^{2+} and other multivalent ions, also confirming that interaction between Na^+ and lipids are weak [4]. In contrast, the decrease in rotational and translational dynamics of fluorescent probes in lipid bilayers with mM NaCl concentrations suggests significant Na^+ binding [7, 9, 12]. However, the reduced lateral diffusion is not observed in noninvasive NMR experiments, suggesting that fluorescence results arise from Na^+ interactions with probes rather than with lipids [11]. Also the interpretation of calorimetric measurements has been controversial. The effect of monovalent ions (except for Li^+) on phase transition temperature is small, compared to the effect of multivalent ions; this was initially interpreted by Cevc as an indication that only multivalent ions and Li^+ specifically bind to phospholipid bilayers [2]; however, more recently such small effect was interpreted as an indication that also Na^+ binds to lipid membranes [8, 12]. In electrophoresis measurements on phosphatidylcholine vesicles, NaCl increases the (initially negative) zeta potential to about zero; however, positive zeta potentials can be generally reached only with multivalent ions or Li^+ [1, 8, 14, 15, 21]. The lack of significant positive electrophoretic mobility in the presence of NaCl suggests weak binding of Na^+ ; however, the same data can also be explained by the effect of Cl^- ions [22, 23]. Finally, changes in bilayer elasticity and area per lipid measured with Atomistic Force Microscopy (AFM) can be interpreted as Na^+ binding to phospholipids [14–18].

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Atomistic molecular dynamics (MD) simulations are a powerful tool to interpret experimental data in terms of atomic-level interactions. In atomistic MD simulations, the majority of commonly used models predicts binding of Na^+ ions to phosphatidylcholine lipid bilayers, but the strength of binding depends on the specific model used [12, 13, 22, 24–27]. Some simulation studies confirmed a reduction in lipid lateral diffusion due to Na^+ binding, in agreement with fluorescent probe measurements [7, 9, 12] but in contrast with NMR experiments [11]. Other simulations showed a reduction in area per lipid in the presence of NaCl, in agreement with AFM experiments [14–18]; however, the reduction in area was observed at excessively low Na^+ concentrations, compared to observations from scattering experiments [10]. Predictions of electrophoretic mobility in the presence of NaCl yielded positive values, higher than in experiments; however, this could be explained by the behaviour of Cl^- ions [22, 23].

In the present work we set out to solve the apparent contradictions between experiments and simulations on the binding of cations to phospholipid bilayers. To this aim, we use MD simulations to calculate the order parameters of the head group carbons α and β (see Fig. 1) as a function of cation concentration, and then we compare simulations with experiments. We perform simulations with a number of different force fields, and focus on the interpretation of NMR data reported as a function of NaCl and CaCl_2 concentrations. According to the “electrometer concept”, changes in order parameters of the α and β carbons in the phospholipid head group can be used to measure the ion affinity to the phosphatidylcholine (PC) lipid bilayer [19, 28–30]. Order parameters can be accurately measured in experiments and straightforwardly compared to simulations [31], therefore the electrometer concept allows the comparison of binding affinity between simulations and experiments. We show that the response of order parameters to penetrating cations is qualitatively correct in simulations, but the affinity of PC bilayers for Na^+ ions is significantly overestimated in several MD simulation models. Moreover, we show that the accuracy of tested models does not allow for an interpretation of lipid- Ca^{2+} interactions with atomistic resolution.

II. RESULTS AND DISCUSSION

The electrometer concept is originally based on the measured absolute value increase for β and decrease for α segment order parameters with bound cations [19, 28–30]. However, more recent experiments assigned negative sign to the order parameter of the β carbon, and positive to the α carbon [32–34]; thus both order parameter values are actually decreasing (becoming more negative) as the concentration of cations increases [31]. Figure 2 shows the head group order parameters values from H^2 NMR measures for DPPC and POPC bilayers [19, 28], with correct signs [32–34], as a function NaCl and CaCl_2 concentration. Only minor decreases are measured in the presence of NaCl, while the effect of CaCl_2 is an order of magnitude larger. Thus, according to the electrometer

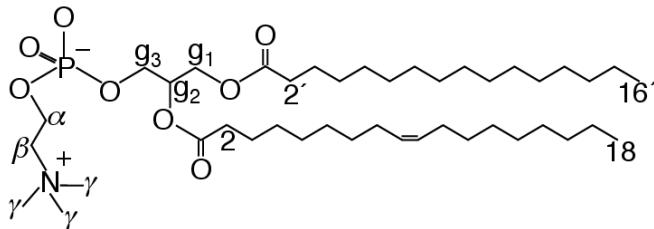


FIG. 1: Chemical structure of 1-palmitoyl-2-oleoylphosphatidylcholine (POPC).

eter concept, monovalent Na^+ ions have negligible affinity for PC lipid bilayers at concentrations up to 1 M, while binding of Ca^{2+} ions at the same concentration is significant [19, 28]. This conclusion is in agreement with several other experimental studies [2–4, 10, 11].

Figure 2 also reports order parameters calculated from MD simulations of DPPC and POPC lipid bilayers in the presence of NaCl or CaCl_2 . Details of the simulated systems are reported in Table I and in Supplementary Information. First of all, it should be noted that none of the models used here reproduces the order parameters within experimental uncertainty for pure PC bilayer without ions, indicating structural inaccuracies with varying severity for all models [35]. Second, all simulation models tested here show a decrease of choline order parameters, hence the structural response of the lipid head groups to the presence of Na^+ is qualitatively correct in all simulation models. Third, the order parameters in Fig. 2 with added NaCl show significantly different behavior for different simulation models, and such different behavior is related to differences in ion binding affinities. We can clarify the relationship between order parameters and Na^+ binding affinities by calculating Na^+ density profiles from the different simulation models (see Fig. 3). In the figure, simulation models are ordered according to the order parameter changes (reported Fig. 2), from the smallest to the largest. The Na^+ density peaks are larger for models with larger changes in order parameters, indicating a strong correlation between Na^+ binding affinities and choline order parameters and therefore supporting the validity of the electrometer concept [19, 28–30].

Let us now examine more in detail the response to the presence of NaCl predicted by the different simulation models tested here. The best agreement with experiments (i.e., lowest order parameter changes) is observed for the Orange, CHARMM36 and Lipid14 models (see Figs. 2). These also predict the lowest Na^+ densities in the proximity of the membrane (see Fig. 3). While the predicted changes in order pa-

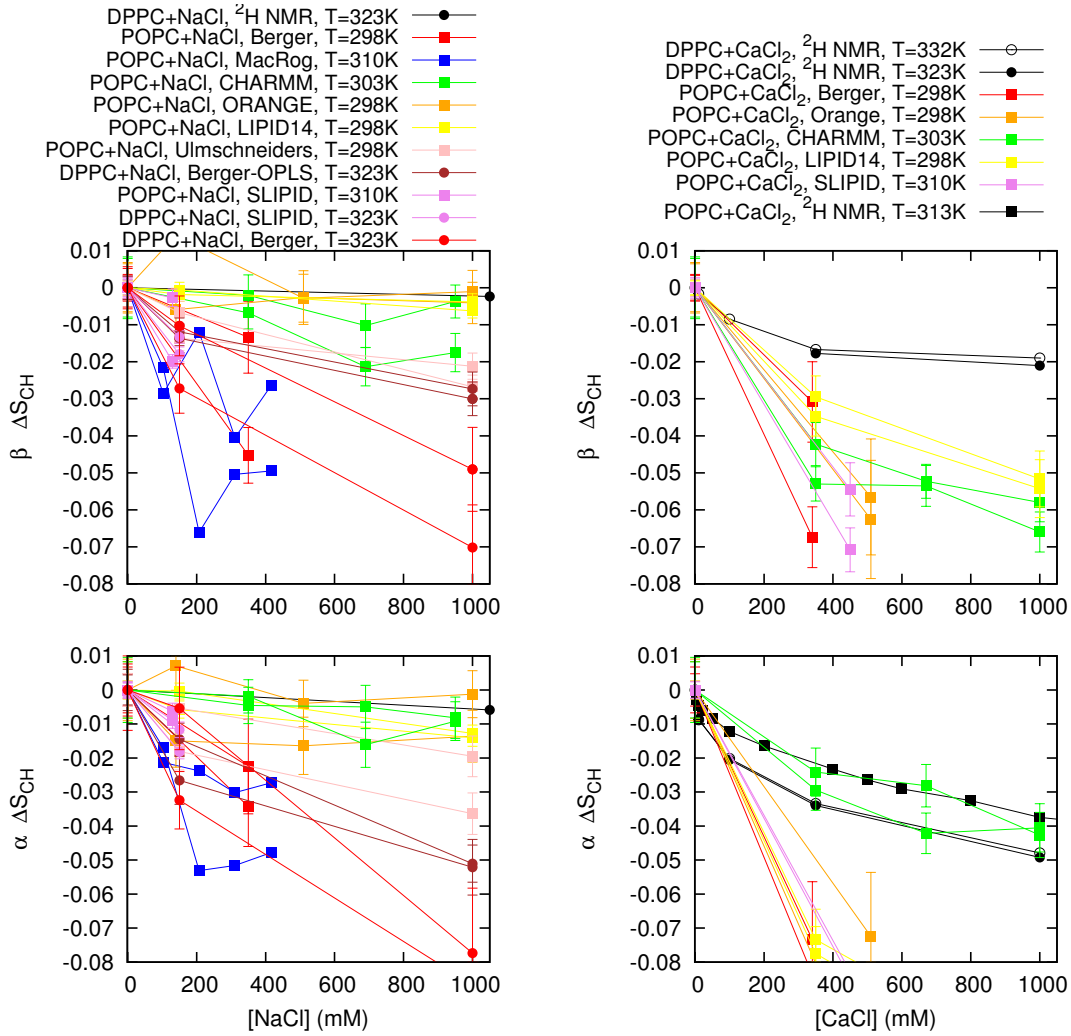


FIG. 2: The order parameter changes for β and α segments as a function of NaCl (left column) and CaCl₂ (right column) concentration, from simulations and experiments [19] (POPC with CaCl₂ from [28]). The signs of the experimental order parameters, taken from experiments without ions [32–34], can be assumed to be unchanged with concentrations represented here [28, 31].

rameters for these three models are very similar, the ion density profiles show differences in Na⁺ affinity, Orange having lowest affinity and CHARMM36 the highest. With the achieved accuracy for the order parameters we are not able to conclude which of these three models has the most realistic Na⁺ binding affinity, especially with physiological NaCl concentrations (~ 150 mM) which is relevant for most applications. On one hand, it is clear that models in better agreement with experimental data on order parameters show low Na⁺ binding affinity, as reported in a number of experiments. On the other hand, differences in ion binding affinities raise questions on the quantitative application of the electrometer concept in molecular simulations.

We notice that the choline order parameter changes with NaCl are clearly overestimated in all other tested models (see Fig. 2), related to unrealistically strong Na⁺ binding affinity to the bilayer (see Fig. 3). Such observation raises questions on the quality of the predictions reported in a number of sim-

ulation papers... [complete with examples]

The overestimated Na⁺ binding may originate, e.g., from incorrect choline structure [35], lack of polarizability [85], other discrepancies in the ion models [86–88] or from combination of these and other issues. Interestingly, the same ion model and non-bonded parameters are used in the Orange and BergerOPLS [45] simulations while Na⁺ ion binding affinity is realistic in the Orange model but overestimated in BergerOPLS model, showing that the binding affinity significantly depends on the used lipid parameters. On the other hand, Na⁺ binding with Berger, BergerOPLS and Slipid models is reduced but not yet in agreement with experiments when charges on the ions are reduced (to compensate for the lack of electronic polarizability [85, 89], see Supplementary Information). Further, the Slipid model gives similar binding affinity with two different ion parameters. Altogether, these results indicate that at least lipid models need improvement to correctly

TABLE I: List of simulations performed in this work. The ion concentrations are calculated as $[\text{ion}] = (N_{\text{ion}} \times [\text{water}]) / N_w$, where $[\text{water}] = 55.5 \text{ M}$. These correspond the concentrations reported in the experiments by Akutsu et al. [19]. The lipid force fields are named as in our previous work [35]. For ion force fields, specific ion parameters are cited when possible.

Force field (lipid, ion)	lipid	[Ion] mM	^a N _l	^b N _w	^c N _{Na}	^d N _{Ca}	^e N _{Cl}	^f T (K)	^g t _{sim} (ns)	^h t _{anal} (ns)	Files
Berger-POPC-07[36]	POPC	0	128	7290	0	0	0	298	270	240	[37]
Berger-POPC-07[36], ffgmx[38]	POPC	340 (NaCl)	128	7202	44	0	44	298	110	50	[39]
Berger-POPC-07[36], ffgmx[38]	POPC	340 (CaCl ₂)	128	7157	0	44	88	298	108	58	[40]
Berger-DPPC-97[41]	DPPC	0	72	2880	0	0	0	323	60	50	[42]
Berger-DPPC-97[41], ffgmx[38]	DPPC	150 (NaCl)	72	2880	8	0	8	323	120	60	[43]
Berger-DPPC-97[41], ffgmx[38]	DPPC	1000 (NaCl)	72	2778	51	0	51	323	120	60	[44]
BergerOPLS-DPPC-06[45]	DPPC	0	72	2880	0	0	0	323	120	60	[46]
BergerOPLS-DPPC-06[45], OPLS[47]	DPPC	150 (NaCl)	72	2880	8	0	8	323	120	60	[48]
BergerOPLS-DPPC-06[45], OPLS[47]	DPPC	1000 (NaCl)	72	2778	51	0	51	323	120	60	[49]
CHARMM36[50]	POPC	0	72	2242	0	0	0	303	30	20	[51]
CHARMM36[50], CHARMM36[52]	POPC	350 (NaCl)	72	2085	13	0	13	303	80	60	[53]
CHARMM36[50], CHARMM36[52]	POPC	690 (NaCl)	72	2085	26	0	26	303	73	60	[54]
CHARMM36[50], CHARMM36[52]	POPC	950 (NaCl)	72	2168	37	0	37	303	80	60	[55]
CHARMM36[50], CHARMM36	POPC	350 (CaCl ₂)	128	6400	0	35	70	303	200	100	[56]
CHARMM36[50], CHARMM36	POPC	670 (CaCl ₂)	128	6400	0	67	134	303	200	120	[57]
CHARMM36[50], CHARMM36	POPC	1000 (CaCl ₂)	128	6400	0	100	200	303	200	100	[58]
MacRog[59]	POPC	0	288	14400	0	0	0	310	90	40	[60]
MacRog[59], OPLS[47]	POPC	100 (NaCl)	288	14554	27	0	27	310	90	50	[61]
MacRog[59], OPLS[47]	POPC	210 (NaCl)	288	14500	54	0	54	310	90	50	[61]
MacRog[59], OPLS[47]	POPC	310 (NaCl)	288	14446	81	0	81	310	90	50	[61]
MacRog[59], OPLS[47]	POPC	420 (NaCl)	288	14392	108	0	108	310	90	50	[61]
Orange, OPLS[47]	POPC	0	72	2880	0	0	0	298	60	50	[62]
Orange, OPLS[47]	POPC	140 (NaCl)	72	2866	7	0	7	298	120	100	[63]
Orange, OPLS[47]	POPC	510 (NaCl)	72	2802	26	0	26	298	120	100	[64]
Orange, OPLS[47]	POPC	1000 (NaCl)	72	2780	50	0	50	298	120	80	[65]
Orange, OPLS	POPC	510 (CaCl ₂)	72	2802	0	26	52	298	120	60	[66]
Slipid[67]	DPPC	0	128	3840	0	0	0	323	150	100	[68]
Slipid[67], AMBER[69, 70]	DPPC	150 (NaCl)	600	18000	49	0	49	323	100	40	-
Slipid[71]	POPC	0	128	5120	0	0	0	303	200	150	[72]
Slipid[71], AMBER[73]	POPC	130 (NaCl)	200	9000	21	0	21	310	105	100	[74]
Slipid[71], AMBER[?]	POPC	450 (CaCl)	200	9000	0	73	146	310	600	100	[?]
Lipid14 [75], AMBER[47]	POPC	0	128	5120	0	0	0	298	205	200	[76]
Lipid14 [75], AMBER[47]	POPC	150 (NaCl)	128	5120	12	0	12	298	205	200	[77]
Lipid14 [75], AMBER[47]	POPC	1000 (NaCl)	128	5120	77	0	77	298	205	200	[78]
Lipid14 [75], AMBER[47]	POPC	350 (CaCl ₂)	128	6400	0	35	70	298	200	100	[79]
Lipid14 [75], AMBER[47]	POPC	1000 (CaCl ₂)	128	6400	0	100	200	298	200	100	[80]
Ulmschneiders [81], OPLS[47]	POPC	0	128	5120	0	0	0	298.15	205	200	[82]
Ulmschneiders [81], OPLS[47]	POPC	150 (NaCl)	128	5120	12	0	12	298.15	205	200	[83]
Ulmschneiders [81], OPLS[47]	POPC	1000 (NaCl)	128	5120	77	0	77	298.15	205	200	[84]

^a The number of lipid molecules

^b The number of water molecules

^c The number of Na⁺ molecules

^d The number of Ca²⁺ molecules

^e The number of Cl molecules

^f Simulation temperature

^g The total simulation time

^h Time frames used in the analysis

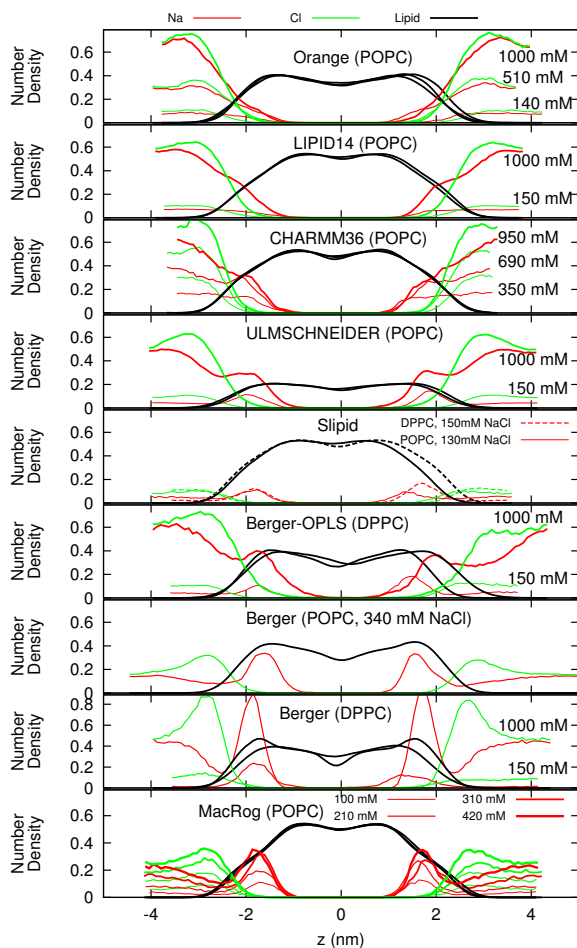


FIG. 3: Atom number density profiles along the membrane normal for lipids, Na^+ , and Cl^- ions from simulations with different force fields and different NaCl concentrations. The force fields are ordered according to the order parameter changes reported Fig. 2, from the smallest (top panel) to the largest (bottom panel). The lipid densities are scaled by 100 (united atom) or 200 (all atom model) to improve readability. Figure discussed in

https://github.com/NMRLipids/lipid_ionINTERACTION/issues/4.

predict the Na^+ binding affinity.

In contrast to Na^+ , Ca^{2+} binding and related order parameter decrease is seen in experiments [2, 3, 19, 28] and in all tested simulation models, see Figs. 2 and 4. While the significant Ca^{2+} binding affinity to a phosphatidylcholine bilayer at mM concentrations is agreed in the literature, the estimations for lipid/ Ca^{2+} stoichiometry vary between 17 and 0.24 [13, 21, 28]. The smallest number (0.24) indicating that one Ca^{2+} ion binds roughly four lipid molecules originates from simulation with Berger model [13]. **1. There is something wrong in these stoichiometry numbers.** The direct comparison of order parameters between different simulation models and experiments in Fig. 2 shows that Ca^{2+} binding induced changes are overestimated in all tested models. In contrast to Na^+ , clear correlation between Ca^{2+} binding affinity and order pa-

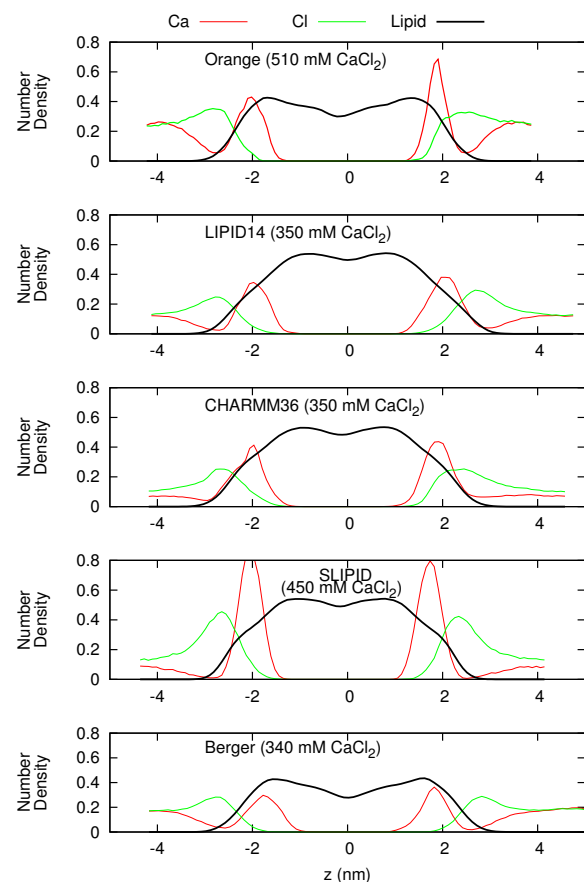


FIG. 4: Atom number density profiles along the membrane normal coordinate z for lipids, Ca^{2+} and Cl^- ions from simulations with different force fields. The profiles only with smallest available CaCl_2 concentration are shown for clarity.

Figure including all the available concentrations is shown in the Supplementary Information. The lipid densities are scaled with 100 (united atom) or 200 (all atom model) to make them visible with the used y-axis scale. Figure discussed in https://github.com/NMRLipids/lipid_ionINTERACTION/issues/4.

rameter changes is not found, thus the overestimation of order parameter change may arise, e.g. from overestimated binding, incorrect headgroup response to penetrating divalent cation or penetration depth. The ion model having scaled charges [?] used with CHARMM36 did not improve the results, see Supplementary Information.

The Berger model predicts deeper penetration depth (density maxima close to ± 1.8 nm) compared to other models (density maxima close to ± 2 nm). The latter value is probably more realistic since ^1H NMR and neutron scattering data indicates that Ca^{2+} interact mainly with the choline group [2, 90–92]. Further, the ^1H NMR experiments suggest that the N- β - α -O dihedral is only in gauche-conformation in the absence of ions, but in the presence of multivalent ions also anti-conformations would be present [91, 93]. However, the glycerol backbone and headgroup atomistic resolution structures [35] and their changes are not reproduced within exper-

imental error in the tested simulation models, thus the model development is needed before Ca^{2+} binding affinity, lipid/ion stoichiometry and concomitant structural changes can be interpreted. **2.The P-N vector tilting analysis should be considered**

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III. CONCLUSIONS

As suggested by the electrometer concept [19, 28–30], the headgroup α and β segment order parameter decrease in phosphatidylcholine lipid bilayers is related to the cation binding affinity in all tested simulation models, despite of inaccuracies in actual atomistic resolution structures [35]. The concept allows direct comparison of Na^+ binding affinity between simulations and NMR experiments by using the headgroup order parameter changes. The comparison reveals that most models overestimate the Na^+ binding, only Orange, Lipid14 and CHARMM36 predict realistic binding affinity. None of the tested models has the required accuracy to interpret the Ca^{2+} /lipid stoichiometry or induced atomistic resolution structural changes.

In general the results support the traditional view that Na^+ and other monovalent ions (except Li^+) do not specifically bind to the phospholipid bilayer with mM concentrations, in contrast to Ca^{2+} and other multivalent ions [1, 4, 10, 11, 19–21, 28]. The contradicting results from molecular dynamics simulations [12, 13], fluorescent probe dynamics [7, 9, 12], calorimetry [8, 12] and AFM [14–18] suggesting stronger Na^+ binding can be explained by simulation artefacts, direct interactions between Na^+ and fluorescent probes [11], alternative interpretation of significance of small phase transition temperature shift [2] and insufficient resolution of AFM for atomistic resolution interpretation.

The artificial specific Na^+ binding in simulations may lead to doubtful results since it leads effectively positively charged phosphatidylcholine lipid bilayer even in physiological NaCl concentration. Such a bilayer has distinctly different interactions with charged objects compared to the more realistic model without specific Na^+ binding. Furthermore, the overestimation of Na^+ binding affinity may extend also to other positively charged objects, e.g. membrane protein segments. This would affect lipid protein interactions and could explain contradicting results on electrostatic interactions between charged protein segments and lipid bilayer [94, 95]. In conclusion, more careful studies and model development on lipid bilayer-charged object interactions are needed to make molecular dynamics simulations straightforwardly usable in physiologically relevant electrostatic environment.

This work has been, and will be, progressed and discussed through the blog: nmrlipids.blogspot.fi. Everyone is invited to join the discussion and make contributions through the blog. The manuscript will be eventually submitted to an appropriate scientific journal. Everyone who has contributed to the work through the blog will be offered coauthorship. For more details see: nmrlipids.blogspot.fi.

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SUPPLEMENTARY INFORMATION

Appendix A: Effect of ion model and polarization

It has been suggested that the missing electronic polarizability can be compensated by scaling the ion charge in simulations [85]. To test if this would improve the Na^+ ion binding behaviour, we ran simulations with Berger-DPPC-97, BergerOPLS-DPPC-06 and Slipids with scaled Na^+ and Cl^- ions. For Berger-DPPC-97 and BergerOPLS-DPPC-06 models the ion charge in systems listed in Table I was simply scaled with 0.7 and the related files are available at [96–99]. For simulations with Slipids the ion model by Kohagen et al. was used [89] and the related files are available at [100]. The simulation parameters were identical to those employed in the simulation of POPC with 130 mM NaCl (see Methods). The order parameter changes and Na^+ binding affinity are decreased by the charge scaling but yet overestimated respect to the experiments as seen from Figs. 5 and 6. Thus the overestimated binding affinity cannot be fixed by only scaling charges.

We also tested the effect of charge scaling in the case of CaCl_2 with CHARMM36 model. The ion model by Kohagen et al. [?] was used and the related files are available at [?]. Figures 5 and 7 show that the scaling does not improve the CaCl_2 binding behaviour respect to the experiments. The same scaled model with Slipid in the main text also overestimated the CaCl_2 effect. However, the effect of scaling cannot be analyzed in this case since Slipid simulation was not run with non-scaled CaCl_2 model.

Appendix B: Density distributions with different CaCl_2 concentrations

The density distributions with all simulated CaCl_2 concentrations are shown in Fig. 7.

Appendix C: methods

1. Simulated systems

All simulations are ran with a standard setup for planar lipid bilayer in zero tension with periodic boundary conditions with Gromacs software package (version numbers 4.5-X-5.0.X).

2. Analysis

The order parameters were calculated from simulation trajectories directly applying the equation $S_{\text{CH}} = \langle \frac{3}{2} \cos^2 \theta - \frac{1}{2} \rangle$, where θ is the angle between a given C–H bond and the bilayer normal and average is taken over all lipids and time frames. For united atom models, the positions of hydrogen atoms were calculated for each molecule in each frame *a posteriori* by using the *protonate* tool in Gromacs 4.0.2 [101]. For statistical

error estimate order parameter for each lipid molecule was separately calculated and the error of the mean over these values was used as done also in the previous work [35]. The statistical error in the order parameter was estimated by calculating the average value separately for each lipid molecule, and then the average and standard error of the mean over the ensemble of lipids (as done also in previous work [35]). All the scripts used in analysis and the resulting data are available in the GitHub repository [102]

3. Simulation details

a. Berger

POPC The simulation without ions is the same as in [103] and the files are available at [37]. The starting structures for simulations with ions is made by replacing water molecules with appropriate amount of ions. The Berger force field was used for the POPC [104], with the dihedral potential next to the double bond taken from [105]. The ion parameters from ffgmx [38] were used. Timestep of 2 fs was used with leap-frog integrator. Covalent bond lengths were constrained with LINCS algorithm [106, 107]. Coordinates were written every 10 ps. PME [108, 109] with real space cut-off 1.0 nm was used for electrostatics. Plain cut-off was used for the Lennard-Jones interactions with a 1.0 nm cut-off. The neighbour list was updated every 5th step with cut-off 1.0 nm. Temperature was coupled separately for lipids, water and ions to 298 K with the velocity-rescale method [110] with coupling constant 0.1 ps^{-1} . Pressure was semi-isotropically coupled to the atmospheric pressure with the Parrinello-Rahman barostat [111].

DPPC The simulation without ions is the same as in [35] and the files are available at [42]. The initial configuration contains 72 DPPC lipids and 2880 SPC water molecules. The standard Berger DPPC force field was used [104] (simulations indicated as Berger-DPPC-97 in Table I). The electrostatics were handled with PME [108, 109], with real-space Coulomb cut-off set at 1.0 nm. Lennard-Jones potentials were cut off 1.0 nm. The neighborlist for all non-bonded interactions was updated every 10 steps. Temperature was set to 323K with the velocity-rescale method [110] using a coupling constant of 0.1 ps^{-1} . Semi-isotropic pressure coupling at 1 ATM was handled with the Parrinello-Rahman barostat [111] with 1 ps coupling constant. The time step was 4 fs, and coordinates were written every 10 ps. The total simulation time was 120 ns (without pre-equilibration) and last 60 ns was used in the order parameter analysis.

For simulations with added salt, the appropriate number of SPC water molecules were randomly replaced with ions. Ions were described by the ffgmx parameters [38]. In simulations with scaled charges, charge-scaling was applied by scaling the ion charges by a factor 0.7. Conditions in the ion simulations were as with the pure DPPC described above. The duration of the simulations was 120 ns (without pre-equilibration) and last 60 ns was used in the order parameter analysis.

All the simulation files for pure DPPC simulations can be

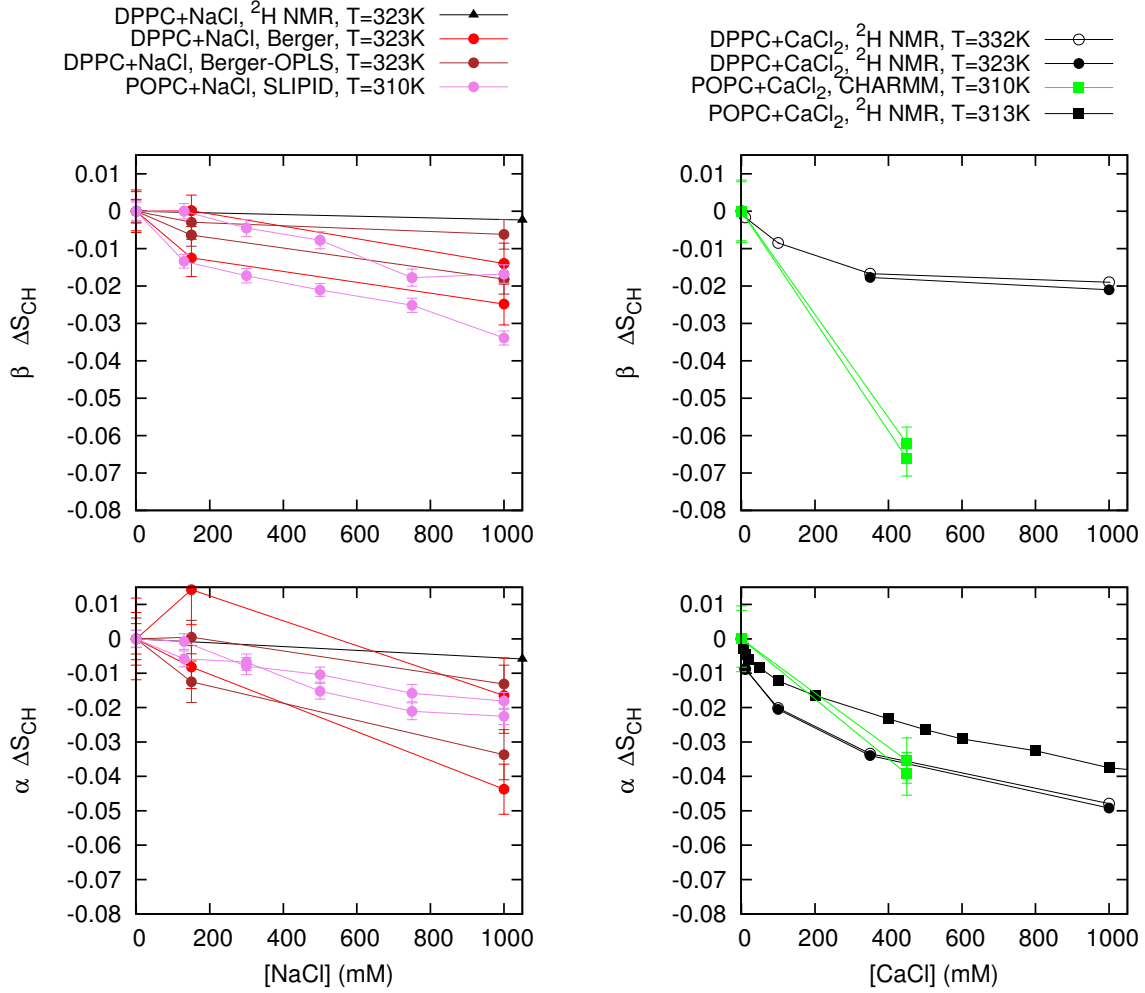


FIG. 5: Order parameter changes in simulations using ion models with scaled charge.

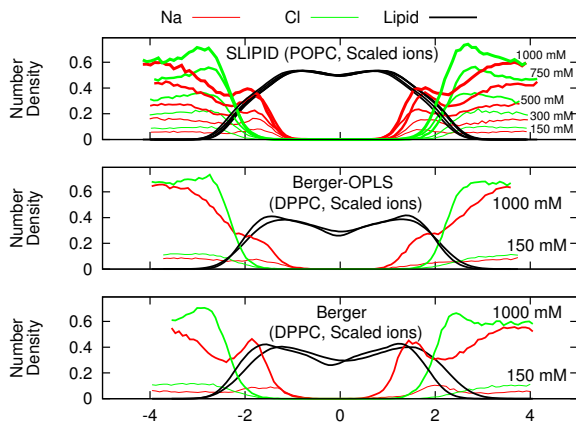


FIG. 6: Atom number density profiles along membrane normal coordinate z for lipids, Na^+ and Cl^- ions from simulations using ion models with scaled charges. The lipid densities are scaled with 100 (unit atom) or 200 (all atom model) to make them visible with the used y-axis scale.

found at [42] and for the simulations with ions at [43, 44] and with scaled ions at [96, 97].

b. BergerOPLS

For simulations without ions, the initial configuration contains 72 DPPC lipids and 2880 SPC water molecules. For simulations with added salt, the appropriate amount of SPC water molecules were randomly replaced with ions. The number of ions is reported in Table I. For the lipids, we used the same version of Berger force field as in previous simulations, described in [104]; for the ions, we used the qvist parameters [47] (commonly used within the OPLS-AA force field). Issues related to the compatibility between Berger and OPLS-AA force fields are described in ref. [45]. A set of simulations was carried out using reduced electrostatic charges on the ions; in this case, a charge of 0.7 e was used on the ions, as described in refs. [85, 89]. Except for the ion force field, all simulation parameters (for non-bonded interactions, integration time

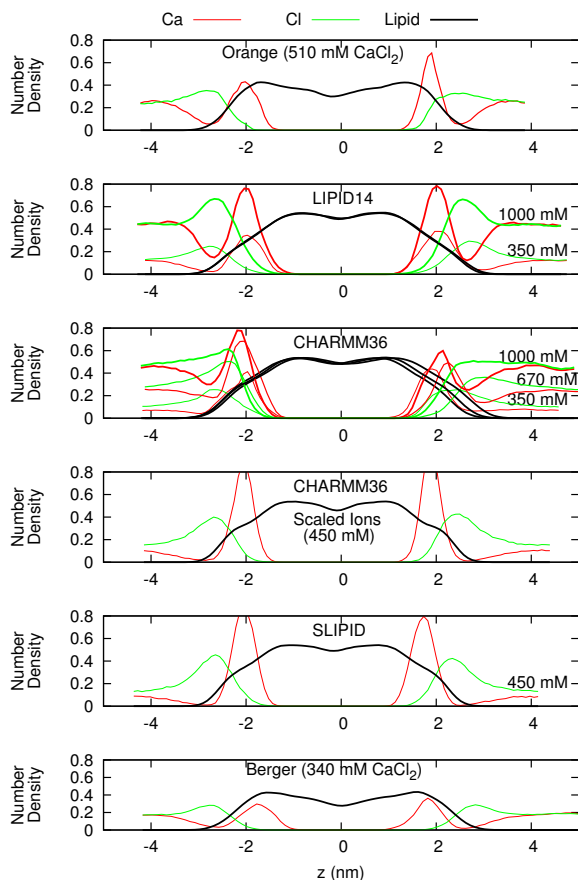


FIG. 7: Number density profiles for lipids, Ca^{2+} and Cl^- ions from simulations with different force fields and different CaCl_2 concentrations. The lipid densities are scaled with 100 (united atom) or 200 (all atom model) to make them visible with the used y-axis scale. Figure discussed in https://github.com/NMRLipids/lipid_ionINTERACTION/issues/4.

step, thermostat, etc.) were identical to the parameters used in the Berger DPPC simulations described above.

All simulation files can be found at [46] for pure DPPC simulations, at [48, 49] for simulations with ions, and at [98, 99] for simulations with ions with scaled charges.

c. CHARMM36

POPC with NaCl The simulation without ions is taken directly from [35, 51]. The starting structures for simulations with NaCl were made by replacing randomly located water molecules of the structure of pure POPC simulation with appropriate amount of ions. The force field for lipid were the same as in [35, 51]. The ion parameters with NBFIX by Venable et al. [52] were used. Simulations were ran with Gromacs 4.5.5 software [112]. Timestep of 2 fs was used with leap-frog integrator. Covalent bonds with hydrogens were constrained with LINCS algorithm [106, 107]. Coordinates were written every 5 ps. PME with real space cut-off 1.4 nm was used

for electrostatics. Lennard-Jones interactions were switched to zero between 0.8 nm and 1.2 nm. The neighbour list was updated every 5th step with cut-off 1.4 nm. Temperature was coupled separately for lipids and solution to 303 K with the velocity-rescale method [110] with coupling constant 0.2 ps. Pressure was semi-isotropically coupled to the atmospheric pressure with the Berendsen method [113].

POPC with CaCl_2 The starting structures with varying amounts of CaCl_2 ions were constructed using the CHARMM-GUI Membrane Builder (<http://www.charmm-gui.org/>) online tool [114]. All runs were performed with Gromacs 5.0.3 software package [115] and CHARMM36 additive force field parameters for lipids [50] and ions were obtained from CHARMM-GUI input files. Standard CHARMM-GUI mdp options were used. Particularly, h-bond lengths were constrained with LINCS [106, 107]. The temperatures of the lipids and the solvent were separately coupled to the Nose-Hoover [116, 117] thermostat with a target temperature of 303 K and a relaxation time constant of 1.0 ps. Semi-isotropic pressure coupling to 1 bar was obtained with the Parrinello-Rahman barostat [111] with a time constant of 5 ps. Equations of motion were integrated with the Verlet algorithm [118] using a timestep of 2 fs. Long-range electrostatic interactions were calculated using the PME [108, 109] method with a fourth order smoothing spline. A real space cut-off of 1.2 nm was employed with grid spacing of 0.12 nm in the reciprocal space. Lennard-Jones interactions were smoothly switched to zero between 1.0 nm and 1.2 nm. Verlet cutoff-scheme [118] were used with the long-range neighbor list updated every 20 steps. Coordinates were written every 10 ps. After energy minimization and an equilibration run of 0.5 ns, 200ns simulations were ran and the last 100ns of each simulation was employed for the analysis.

d. MacRog

The simulation parameters are identical to those employed in our earlier study [35] for the full hydration and dehydration simulations. The initial structures with varying amounts of NaCl were constructed from an extensively hydrated bilayer by replacing water molecules with ions using the Gromacs tool genion [119]. Even at the highest considered salt concentration, the amount of water molecules per lipid after this replacement process was still greater than 50.

e. Orange

3.Jukka Maatta and Luca Monticelli, please deliver as much details as you can. I think these simulations were actually carried out by Samuli, no?

f. Slipids

DPPC The simulation without ions from [35], available at [68] was used. For the simulations with ions, the start-

ing DPPC lipid bilayer, which was built with the online CHARMM-GUI [114] (<http://www.charmm-gui.org/>), contained 600 lipids, 30 water molecules/lipid, Na^+ and Cl^- ions (150 mM NaCl). The TIP3P water model was used to solvate the system and ion parameters by Roux [69, 70] were used. the GROMACS software package version 4.5.5 [112] and the Stockholm lipids (Slipids) force field parameters for phospholipids were used. After energy minimization and a short equilibration run of 50 ps (time step 1 fs), 100 ns production runs were performed using a time step of 2 fs with leapfrog integrator. All covalent bonds were constrained with the LINCS [106, 107] algorithm. Coordinates were written every 100 ps. PME [108, 109] with real space cut-off at 1.0 nm was used for Coulomb interactions. Lennard-Jones interactions were switched to zero between 1.0 nm and 1.4 nm. The neighbour lists were updated every 10^{th} step with a cut-off of 1.6 nm. Temperature was coupled separately for upper and bottom leaflets of the lipid bilayer, and for water to one of the temperatures reported above with the Nosé-Hoover thermostat [116, 117] using a time constant of 0.5 ps. Pressure was semi-isotropically coupled to the atmospheric pressure with the Parrinello-Rahman [111] barostat using a time constant of 10 ps.

POPC The simulation without ions from [35], available at [72] was used. Additionally, a POPC bilayer consisting of 200 lipids, hydrated with 45 water molecules per lipid, was simulated in the presence of 130 mM NaCl. **4.Details from the simulation with CaCl** The Slipids model [67, 71] was employed for lipids, the tip3p model [120] for water, and the ion parameters by Smith and Dang [73] for NaCl. The system was first equilibrated for 5 ns with a time step of 1 fs after which a 100 ns production run was performed using a time step of 2 fs. Trajectories were written every 100 ps. The system was kept in a tensionless state at 1 bar using a semi-isotropical Parrinello-Rahman barostat [111] with a time constant of 1 ps. The temperature was maintained at 310 K with the velocity rescaling thermostat [110]. The time constant was set to 0.5 ps for both lipids and solvent (water and ions) which were coupled separately. Non-bonded interactions were calculated within a neighbor list with a radius of 1 nm and an update interval of 10 steps. The Lennard-Jones interactions were cut-off at 1 nm, whereas PME [108, 109] was employed for long-range electrostatics. Dispersion correction was applied to both energy and pressure. All bonds were constrained with the LINCS [106, 107]. algorithm.

g. Lipid14

The starting structures with varying amounts of ions were constructed using the CHARMM-GUI Membrane Builder (<http://www.charmm-gui.org/>) online tool [114]. The GROMACS compatible force field parameters generated in [35] and available at [121] were used. The TIP3P water model [120] was used to solvate the system and Åqvist [47] parameters were used for ions. All runs were performed with Gromacs 5.0.3 software package [115] and LIPID14 force field parameters for POPC [75].

H-bond lengths were constrained with LINCS [106, 107]. The temperatures of the lipids and the solvent were separately coupled to the Nose-Hoover [116, 117] thermostat with a target temperature of 298.15 K and a relaxation time constant of 0.1 ps. Semi-isotropical pressure coupling to 1 bar was obtained with the Parrinello-Rahman barostat [111] with a time constant of 2 ps. Equations of motion were integrated with the Verlet algorithm [118] using a timestep of 2 fs. Long-range electrostatic interactions were calculated using the PME [108, 109] method with a fourth order smoothing spline. A real space cut-off of 1.0 nm was employed with grid spacing of 0.12 nm in the reciprocal space. Lennard-Jones potentials were cut-off at 1 nm, with a dispersion correction applied to both energy and pressure. Verlet cutoff-scheme [118] were used with the long-range neighbor list updated every 20 steps. Coordinates were written every 10 ps.

After energy minimization and an equilibration run of 5 ns, 200ns production runs were performed and analysed. In case of the CaCl2 systems only the last 100ns of each simulation was employed for the analysis.

h. Ulmsneiders

The starting structures with varying amounts of ions were constructed using the CHARMM-GUI Membrane Builder (<http://www.charmm-gui.org/>) online tool [114]. The force field parameters were obtained from Lipidbook [122]. The TIP3P water model [120] was used to solvate the system. Additionally, the simulations of ion-free bilayer were repeated with both Verlet and Group cutoff-schemes [82]. There was no significant difference in headgroup or glycerol backbone order parameters between these cutoff-schemes. All runs were performed with Gromacs 5.0.3 software package [115]. The glycerol backbone order parameters without ions were not the same as reported in the previous study [35]. The origin of discrepancy was located to the different initial structures which was taken from CHARMM-GUI in this work and from Lipidbook in the previous work. Since the order parameters with the initial structure from CHARMM-GUI are closer to the experimental values, the results indicate that the structure available from Lipidbook is stuck to a state with incorrect glycerol backbone structure, for more discussion see https://github.com/NMRLipids/lipid_ionINTERACTION/issues/8.

All-bond lengths were constrained with LINCS [106, 107]. The temperatures of the lipids and the solvent were separately coupled to the Nose-Hoover [116, 117] thermostat with a target temperature of 298.15 K and a relaxation time constant of 0.1 ps. Semi-isotropical pressure coupling to 1 bar was obtained with the Parrinello-Rahman barostat [111] with a time constant of 2 ps. Equations of motion were integrated with the Verlet algorithm [118] using a timestep of 2 fs. Long-range electrostatic interactions were calculated using the PME [108, 109] method with a fourth order smoothing spline. A real space cut-off of 1.0 nm was employed with grid spacing of 0.12 nm in the reciprocal space. Lennard-Jones potentials were cut-off at 1 nm, with a dispersion correction ap-

plied to both energy and pressure. Verlet cutoff-scheme [118] were used with the long-range neighbor list updated every 20 steps. Coordinates were written every 10 ps. After energy minimization and an equilibration run of 5 ns, 200ns simulations were ran and the last 100ns of each simulation was employed for the analysis.

Jukka Määttä

Vasily S. Oganessian

O. H. Samuli Ollila co-designed the project with MSM and managed the work. Ran and analyzed several simulations. Wrote the manuscript.

Joona Tynkkynen

Appendix D: Author Contributions

Andrea Catte

Mykhailo Grych

Matti Javanainen provided data with several lipid and ion models. Discussed the project actively with OHSO. Supervised the work of JT.

Markus S. Miettinen

Luca Monticelli

TODO

	P.
1. There is something wrong in these stoichiometry numbers.	5
2. The P-N vector tilting analysis should be considered	6
3. Jukka Maatta and Luca Monticelli, please deliver as much details as you can.	9
4. Details from the simulation with CaCl	10

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