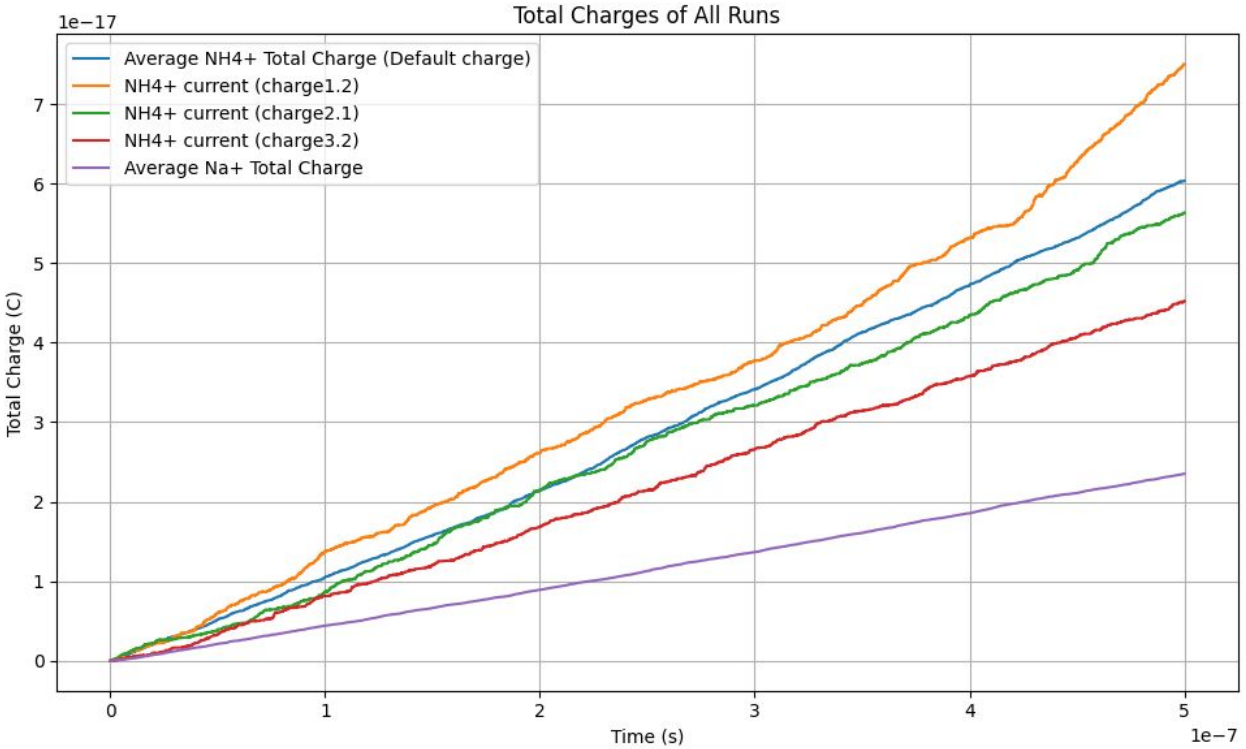
Van der Waals’ parameters for NH4

Different NH4+ vdW parameters (Ion channel simulations)

	Charge (e)	Source	vdW parameters
charge0	N: -0.33 H: +0.33	Original CHARMM parameters	σ = 0.3296 ε = 0.8368
Charge1	N: -0.40 H: +0.35	NH4+ partial charges using OPLS charges, as OPLS and CHARMM partial charges of NH3+ in Lysine are nearly identical [b]	σ = 0.3296 ε = 0.8368
Charge2	N: -0.625490 H: +0.406372	Partial charges were derived using electrostatic potential fitting. Energy constants were taken from the CHARMM, version 22, forcefield for primary amines.[h]	Not given (Its parameters were obtained using the Extensible Computational Chemistry Environment (ECCE)49 after performing quantum mech-anics calculations using NWChem.50,51 The ammonium ion was built in ECCE and geometrically optimized at the RHF level of theory with the 6-31111G(3df,3pd)basis set, with Pople(3df,3pd) as a polarization function,and with Pople-style as a diffusion function)
Charge3	N: -0.824 H: +0.456	NH4 charges by restrained ESP-fit method using ChelpG approach [a]	Not given (The GROMOS87 force field (19) was applied to the protein, and the parameters for the lipid were those used in previous MD studies of lipid bilayers (20–23). The charges of NH3 and NH+4 were obtained by a restrained ESP-fit method using the ChelpG approach)

(Reference: Channel conductance for different charge distributions)



← N: -0.40; H: +0.35

← Default
← N: -0.63; H: +0.41

← N: -0.82; H: +0.46

← Na+

Different NH4+ vdW parameters (General)

	Molecule	Charge	σ for N (Å)	ε for N (kJ/mol)
Default CHARMM	Phosphatidylethanolamine NH3+ / CH3NH3+	-0.33	3.296	0.8368
OPLS [II]	NH4+	-0.4	3.250 A	0.71128
OPLS [II]	CH3NH3+	-0.3	3.250 A	0.71128
Madrid [III]	NH4+	-0.34	3.15 A	0.711

Different N atom types in CHARMM

NG1T1 7 14.007000 0.000 A 0.318941741094 0.7531200 ; N for cyano group

NG2D1 7 14.007000 0.000 A 0.329632525712 0.8368000 ; N for neutral imine/Schiff's base (C=N-R, acyclic amidine, gunaidine)

NG2O1 7 14.007000 0.000 A 0.329632525712 0.8368000 ; NITB, nitrobenzene

NG2P1 7 14.007000 0.000 A 0.329632525712 0.8368000 ; N for protonated imine/Schiff's base (C=N(+)H-R, acyclic amidinium, guanidinium)

NG2R43 7 14.007000 0.000 A 0.329632525712 0.8368000 ; amide in 4-memebered ring (planar), AZDO, lsk

NG2R50 7 14.007000 0.000 A 0.329632525712 0.8368000 ; double bound neutral 5-mem planar ring, purine N7

NG2R51 7 14.007000 0.000 A 0.329632525712 0.8368000 ; single bound neutral 5-mem planar (all atom types sp2) ring, his, trp pyrrole (fused)

NG2R52 7 14.007000 0.000 A 0.329632525712 0.8368000 ; protonated schiff base, amidinium, guanidinium in 5-membered ring, HIS, 2HPP, kevo

NG2R53 7 14.007000 0.000 A 0.329632525712 0.8368000 ; amide in 5-memebered NON-SP2 ring (slightly pyramidized), 2PDO, kevo

NG2R57 7 14.007000 0.000 A 0.329632525712 0.8368000 ; 5-mem ring, bipyrroles

NG2R60 7 14.007000 0.000 A 0.336759715457 0.2510400 ; double bound neutral 6-mem planar ring, pyr1, pyzn

NG2R61 7 14.007000 0.000 A 0.329632525712 0.8368000 ; single bound neutral 6-mem planar ring imino nitrogen; glycosyl linkage

NG2R62 7 14.007000 0.000 A 0.367050271874 0.2092000 ; double bound 6-mem planar ring with heteroatoms in o or m, pyrd, pyrm

NG2R67 7 14.007000 0.000 A 0.329632525712 0.8368000 ; 6-mem planar ring substituted with 6-mem planar ring (N-phenyl pyridinones etc.)

NG2RC0 7 14.007000 0.000 A 0.329632525712 0.8368000 ; 6/5-mem ring bridging N, indolizine, INDZ, kevo

NG2S0 7 14.007000 0.000 A 0.329632525712 0.8368000 ; N,N-disubstituted amide, proline N (CO=NRR')

NG2S1 7 14.007000 0.000 A 0.329632525712 0.8368000 ; peptide nitrogen (CO=NHR)

NG2S2 7 14.007000 0.000 A 0.329632525712 0.8368000 ; terminal amide nitrogen (CO=NH2)

NG2S3 7 14.007000 0.000 A 0.329632525712 0.8368000 ; external amine ring nitrogen (planar/aniline), phosphoramidate

NG301 7 14.007000 0.000 A 0.356359487256 0.1464400 ; neutral trimethylamine nitrogen

NG311 7 14.007000 0.000 A 0.356359487256 0.1882800 ; neutral dimethylamine nitrogen

NG321 7 14.007000 0.000 A 0.354577689820 0.2510400 ; neutral methylamine nitrogen

NG331 7 14.007000 0.000 A 0.352795892384 0.2928800 ; neutral ammonia nitrogen

NG3C51 7 14.007000 0.000 A 0.329632525712 0.8368000 ; secondary sp3 amine in 5-membered ring

NG3N1 7 14.007000 0.000 A 0.365268474438 0.2510400 ; N in hydrazine, HDZN

NG3P0 7 14.007000 0.000 A 0.329632525712 0.8368000 ; quarternary N+, choline

NG3P1 7 14.007000 0.000 A 0.329632525712 0.8368000 ; tertiary NH+ (PIP)

NG3P2 7 14.007000 0.000 A 0.329632525712 0.8368000 ; secondary NH2+ (proline)

NG3P3 7 14.007000 0.000 A 0.329632525712 0.8368000 ; primary NH3+, phosphatidylethanolamine

→ N Parameters are the same for charged molecules

Different σ/R_{min,Na} and its effect on osmotic pressure [IV]

	σ for Na (Å)	ε for Na (kJ/mol)
Matched with absolute hydration free energy [IV]	2.8214	-0.196
[V]	2.7275	-0.1962296

Table 1. Ion LJ Parameters

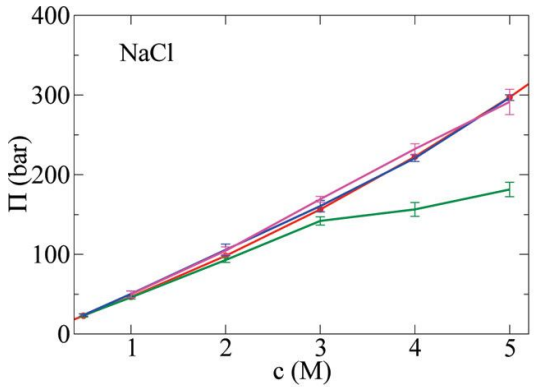
ion	$\frac{1}{2}R^i_{min}$ (Å)	E^i_{min} (kcal/mol)
Na^{+a}	1.36375	−0.0469
Na^{+b}	1.41075	−0.0469
K^+	1.76375	−0.0870
Cl^-	2.27000	−0.1500

[a] Parameterization of Na^+ in 1994 from ref 2. [b] Reparameterization of Na^+ in 2008 from ref 39.

Table 2. Modified Ion−Ion LJ Parameters

	R^{ij}_{min} Å	
ion pair	combination rule	NBFIX
$Na^{+a} - Cl^-$	3.633	3.676
$Na^{+b} - Cl^-$	3.680	3.731
$K^+ - Cl^-$	4.033	4.081

[a] Parameterization of Na^+ in 1994 from ref 2. [b] Reparameterization of Na^+ in 2008 from ref 39.



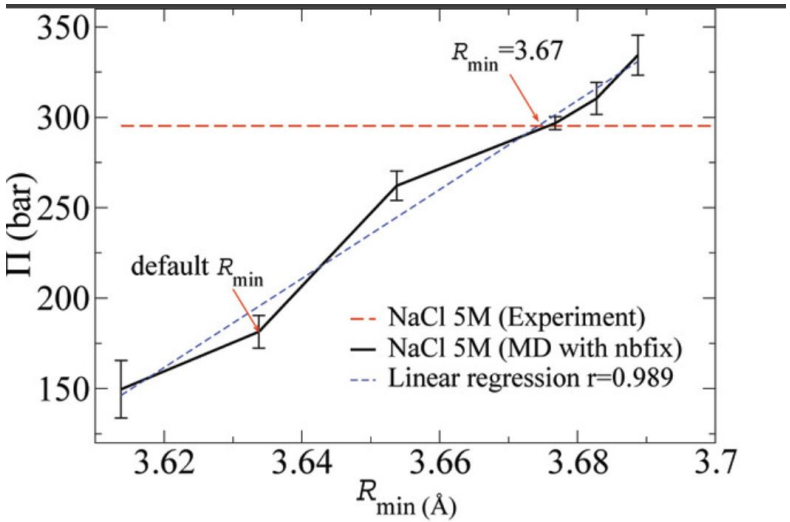
Effect of NBFIX on osmotic pressure at different concentrations

Red: Experiment
Green: No NBFIX
Blue: NBFIX on model a
Magenta: NBFIX on model b

Deviation at high concentrations is due to excess of ion pairing

Using osmotic pressure to find the optimal R_{min, ion-ion} [IV]

1. Use NBFIX to alter R_min^ij between Na-Cl at 5M NaCl
2. Use linear regression to find R_min to produce experimental pressure
3. Result: 3.676 A, 0.043 A larger than default 3.633 A from combination rule



Reference

[I] Combined ab initio/empirical approach for optimization of Lennard-Jones parameters for polar-neutral compounds https://doi.org/10.1002/jcc.1166

[II] Monte Carlo simulations of the hydration of ammonium and carboxylate ions https://pubs.acs.org/doi/10.1021/j100401a037

[III] Further extension of the Madrid-2019 force field: Parametrization of nitrate and ammonium ions https://doi.org/10.1063/5.0177363

[IV] Control of Ion Selectivity in LeuT: Two Na+ Binding Sites with Two Different Mechanisms https://doi.org/10.1016/j.jmb.2008.01.015

[V] Dmitrii Beglov, Benoît Roux; Finite representation of an infinite bulk system: Solvent boundary potential for computer simulations. J. Chem. Phys. 15 June 1994; 100 (12): 9050–9063. https://doi.org/10.1063/1.466711

[VI] Yun Luo, Benoît Roux; Simulation of Osmotic Pressure in Concentrated Aqueous Salt Solutions https://doi.org/10.1021/jz900079w

[a] Detailed Mechanism for AmtB Conducting NH4+/NH3: Molecular Dynamics Simulations https://doi.org/10.1529/biophysj.106.090191

[b] Ammonium Recruitment and Ammonia Transport by E. coli Ammonia Channel AmtB https://doi.org/10.1529/biophysj.106.089714

[h] Free-energy profiles for ions in the influenza M2-TMD channel https://doi.org/10.1002/prot.22376