

Perform pure salt simulation (NH₄Cl)

1. Parameterisation methods
2. Measurements

Research on NH₄ conduction in ion channel

[a] Detailed Mechanism for AmtB Conducting NH₄ /NH₃: Molecular Dynamics Simulations

- Optimised charges by restrained ESP-fit method using ChelpG approach
 - N: -0.824; H: +0.456

[b] Ammonium Recruitment and Ammonia Transport by E. coli Ammonia Channel AmtB

- NH₄⁺ partial charges using OPLS charges
- NH₄⁺ bond and bond angle using CHARMM27 parameters, same as NH₃ moiety of Lysine

[c] Molecular Dynamics Simulations on the Escherichia coli Ammonia Channel Protein AmtB: Mechanism of Ammonia/Ammonium Transport

- Apply Mulliken charges at the HF/6-31G(d)
- LJ parameters same as amide groups

[d] Ammonium Transporters Achieve Charge Transfer by Fragmenting Their Substrate

- NH₄⁺ and surrounding water molecules and protein side chains are described by a polarizable force field based on the classical Drude oscillator, (62-65) and parametrized to reproduce both the free energy of hydration and the ion–protein interactions
- Pair-specific LJ parameters between the ions and atoms of the ligands are adjusted to reproduce the ab initio interaction energies
- Full geometry optimizations of the complexes between these ligands and the three cations Na⁺, K⁺, and NH₄⁺ are performed at the MP2(FC)/6-311++G(d,p) level using Gaussian 09 program

Research on NH₄ conduction in ion channel

	Method	Force field, water	Charges
Default	N from primary NH ₃ ⁺ , phosphatidylethanolamine H from polar H ⁺	CHARMM36, TIP3P	N: -0.33 H: +0.33
[a]	NH ₄ charges by restrained ESP-fit method using ChelpG approach	GROMOS87, SPC	N: -0.824 H: +0.456
[b]	NH ₄ ⁺ partial charges using OPLS charges, as OPLS and CHARMM partial charges of NH ₃ ⁺ in Lysine are nearly identical	CHARMM27, H atoms were added to crystal waters using PSFGEN in NAMD	N: -0.40 H: +0.35
[c]	N, H charges using Mulliken charges at the HF/6-31G(d)	CHARMM, TIP3P	Not specified
[d]	<ul style="list-style-type: none"> - NH₄⁺ and surrounding water molecules and protein side chains are described by a polarizable force field based on the classical Drude oscillator, and parametrised to reproduce both the free energy of hydration and the ion–protein interactions. - Pair-specific LJ parameters between the ions and atoms of the ligands are adjusted to reproduce the ab initio interaction energies. - Full geometry optimizations of the complexes between these ligands and the three cations Na⁺, K⁺, and NH₄⁺ are performed at the MP2(FC)/6-311++G(d,p) level using Gaussian 09 program. 	CHARMM27, TIP3P	/

Other NH₄ parameterisations

	Method	Force field, water	Charges
Default	N from primary NH ₃ ⁺ , phosphatidylethanolamine H from polar H ⁺	CHARMM36, TIP3P	N: -0.33 H: +0.33
Madrid [5]	N, H charges using OPLS-based model, scaled by 0.85	Madrid-2019, TIP4P/2005	N: -0.3400 H: +0.2975

RDF data (Na-O)

	No. of OH ₂ in first hydration shell	First peak	First minimum
Simulation [1]	5.702	2.36	3.18
Literature [2]	4.0-8.0	2.36	
MC in TIP4P [3]	6.2	2.50	
Madrid [6]	5.4	2.33	

RDF data (N-O)

	No. of OH ₂ in first hydration shell	First peak	First minimum
Simulation [1]	6.581	2.82	3.66
Literature [2]	8.1-10.0	2.6-3.05	
MC in TIP4P [3]	7.3	2.90	
MC in TIP3P [4]	7.0-7.1	2.63-2.70	
Madrid [5]	5.5	2.66	

RDF data (Cl-O)

	No. of OH ₂ in first hydration shell	First peak	First minimum
Simulation, NaCl [1]	7.911	3.16	3.84
Simulation, NH ₄ Cl [1]	7.227	3.16	3.80
Literature [2]	5.9-8.5	3.1-3.3	
MC in TIP4P [3]	7.6	3.25	
Madrid [6]	5.9	3.05	

Free energy calculations

	Absolute hydration energy of NH ₄	Absolute hydration energy of Na	Relative hydration energies between NH ₄ ⁺ and Na ⁺
Experiment [7]	-78.6		-21.7 kcal/mol
Free energy perturbation [4]	-79.55 (+ Born) -98.85		-28.87 kcal/mol
Empirical model [8]	-68.1	-87.2	-19.1 kcal/mol
MC simulation [3]	-73.1	-92.3	-19 kcal/mol

Osmotic coefficient at 1M/1m

	NH ₄ Cl	NaCl
Isopiestic vapour pressure method [9]	0.897	
MC simulations [10]		0.91-0.92
Experiment [11]		0.94
MD simulations [12]		0.93
Experiment [13]	0.927	
Hückel equation calculation [14]	0.902	
Experiment [15]	0.9671	

References

- [1] <https://github.com/Heiley-W/project/blob/main/RDF-analysis.ipynb>
- [2] Ionic radii in aqueous solutions <https://doi.org/10.1021/cr00090a003>
- [3] Halide, Ammonium, and Alkali Metal Ion Parameters for Modeling Aqueous Solutions <https://doi.org/10.1021/ct600252r>
- [4] Free Energy Calculations Involving NH_4^+ in Water <https://doi.org/10.1002/jcc.540120106>
- [5] Further extension of the Madrid-2019 force field: Parametrization of nitrate and ammonium ion <https://doi.org/10.1063/5.0177363>
- [6] A force field of Li^+ , Na^+ , K^+ , Mg^{2+} , Ca^{2+} , Cl^- , and in aqueous solution based on the TIP4P/2005 water model and scaled charges for the ions <https://doi.org/10.1063/1.5121392>
- [7] Ref 33 and 22 of [4] respectively
- [8] A simple empirical model describing the thermodynamics of hydration of ions of widely varying charges, sizes, and shapes [https://doi.org/10.1016/0301-4622\(94\)00051-4](https://doi.org/10.1016/0301-4622(94)00051-4)
- [9] The osmotic and activity coefficients of aqueous solutions of ammonium chloride and ammonium nitrate at 25° <https://doi.org/10.1039/TF9534900027>
- [10] Osmotic and activity coefficients from effective potentials for hydrated ions <https://doi.org/10.1103/PhysRevE.55.5689>
- [11] Ref 20 of [10]
- [12] Osmotic coefficients of atomistic NaCl (aq) force fields <https://doi.org/10.1063/1.2185105>
- [13] The Osmotic and Activity Coefficients of Some Salts Having Relatively Large Molar Volumes <https://doi.org/10.1021/je60071a020>
- [14] Mean Activity Coefficients and Osmotic Coefficients in Aqueous Solutions of Salts of Ammonium Ions with Univalent Anions at 25 °C <https://doi.org/10.1021/je300474k>
- [15] The Vapor Pressures and Activity Coefficients of Aqueous Solutions of Ammonium Chloride at 25° <https://doi.org/10.1021/ja01286a019>
- [a] Detailed Mechanism for AmtB Conducting $\text{NH}_4^+/\text{NH}_3$: 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>
- [c] Molecular Dynamics Simulations on the Escherichiacoli Ammonia Channel Protein AmtB: Mechanism of Ammonia/Ammonium Transport <https://doi.org/10.1021/ja0631549>
- [d] Ammonium Transporters Achieve Charge Transfer by Fragmenting Their Substrate <https://doi.org/10.1021/ja300129x>