1. CHARMM functional form

Bonded parameters Non-bonded parameters







2. Parameters defined for Nacl and NH4C1 (fortified itp, (genfl.pim)

| <u> </u> | Nacl :/ |
|---------------|--|
| \mathcal{O} | N Ur3 1 2-304440044702 |
| | NH1 C 1 1 2450000 01 2 0051500105 |
| | Ь. |
| n : | Nacl / |
| 9, | |
| 3 | $NH_{4}CI: H-N-H \longrightarrow \frac{HGP2}{HGP2} \stackrel{NG3P3}{NG3P3} \stackrel{HGP2}{HGP2} \stackrel{5}{\underbrace{1.09500000e+02}} \stackrel{(3.6819200e+02)}{\underbrace{3.6819200e+02}} \stackrel{(0.00000000e+00)}{\underbrace{0.00000000e+00}} \stackrel{(0.00000000e+00)}{\underbrace{0.00000000e+00}}$ |
| | 0 1/A 1/A |
| 6 . | Nacl: Na -> SOD 11 22.9898 (1.000) A (2.51367073323e-01) (1.962296e-01) |
| 1 | $\begin{array}{cccccccccccccccccccccccccccccccccccc$ |
| | γ σ; ε; |
| | $NH_{4}CI$ $N \longrightarrow \frac{NG3P3}{7} \frac{7}{14.007000} \frac{0.000}{0.000} A \frac{0.329632525712}{0.8368000} \frac{0.8368000}{0.8368000}$ |
| | HGP2 1 1.008000 0.000 A 0.040001352445 0.1924640 |
| | σ _i ε _i |
| | E_{ij} (Default) = $\sqrt{\ell_i \times \ell_j}$ R_{min}^{ij} (Default) = $\frac{R_{min,i} + R_{min,j}}{R_{min,i} + R_{min,j}}$ |
| | ~ |
| | $= \pm \left[(2^{\nu_0} \sigma_i) + (2^{\nu_0} \sigma_i) \right]$ |
| | · NBFIX overwrites defoult Eis and Rmin |
| | |
| | Na C CLA SOD 1 (3.32394311738e-01) (3.51037600000e-01) |
| | ø′ij €ij |
| | NH4C1: / |
| | In the set . |

3. Bonded parameters (0-3)

Step 1: Geometric data

- Fitting to gas-phase structures (Microwave, election diffraction) & crystal structures (X-vay)
- Adjust geometries manually

Step 2: Force constant heterocycles & simple functional groups

- Fitting to vibrational data (gas-phase infrared, Raman data/solution, cryptal data) for model systems
- Supplement with ab initio calculations (assignment of experimental vibrational frequencies to internal coordinates, obtain values for low-frequency torsional modes, determination of internal cular interaction contributions to vibrational spectra)

Step 3: optimisation

- Introduce Urey-Bradley terms for in-plane deformations and separating symmetric and asymmetric bond stretching modes
- Introduce improper dihedral terms to reproduce out of plane modes
- optimized at MP2/6-31G(d) level (frequencies and PED of vibrational spectrum, potential energy surface)

Step 4. Potential energy scans

- Important for backbone and side chain conformers to describe energy barriers and minimum-energy structures
- Use experimental gas-phase data and ab initio calculations to obtain energy surface
- Test the accuracy of potential function to reproduce structural distortions

4. Non-bonded parameters (10-1)

Step 1: Solute-water interaction)

- Calculate minimum Interaction energies and solvation structure for experimental thermodynamic parameters and molecular volumes with TIP3P water model
- Optimise partial atomic charges and interaction distance or angle at HF/6-31G(d) I cuel (compound-worth interaction) and dipole moment)

Step 2: Test

- Restorm condensed phase simulations to compare heats of vaporization and molecular volumes with experimental data
- Perform crystal simulations to compare heats of sublimation and unit cell parameters

5. Optimisation of non-bonded parameters (O,O) using osmotic pressure (NBFIX Parameters)

Step 2: Measurement

· Measure mean force on ions by 'membrane'

$$\langle F_{wan} \rangle = k \frac{1}{N} \sum_{i} \sum_{i} (|\mathcal{F}_{i} - z_{wan}|)$$

· Calculate osmotic pressure TI

$$\pi = \frac{\langle F_{wall} \rangle}{A}$$

k = force Constant (10 kcal/mol/A2)

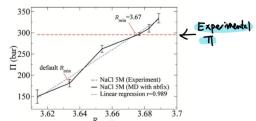
N = number of steps

i = index of ion

Z = Z-coordinate of ion

Step 3: Calibration of Rmin

· Sample II at different Rum and obtain best-fit line by linear regression



| Table 2. | Modified Ion-Ion LJ Paramet | ers |
|----------|-----------------------------|-----|

| | R_{\min}^{ij} Å | | | | |
|---------------------------------|-------------------|-------|--|--|--|
| ion pair | combination rule | NBFIX | | | |
| $Na^{+a} - CI^{-}$ | 3.633 | 3.676 | | | |
| $Na^{+b} - C1^{-}$ | 3.680 | 3.731 | | | |
| K ⁺ -Cl ⁻ | 4.033 | 4.081 | | | |

^a Parameterization of Na⁺ in 1994 from ref 2. ^b Reparameterizatio

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6. Optimisation using hydration free energy

A. Ion hydration free energies

· Real hydration free energy DG hyd: reversible work to move an ion from vacuum to interior of pure water phase at 298.15 K and 1 atm

Intrinsic bulk phose value =
$$\Delta Gelec + \Delta Gaisp + \Delta Grap$$
(electrostate) (attractive) (repulsive)

Two-stage

1. Change nentralisation

2. V.d.W removal /diapear

· Difference in hydration fractine ye relative to immediate neighbor in series
$$\Delta\Delta G_{nyd}$$
: based on Thermodynamiz Integration
$$V(\lambda) = (1-\lambda)^k V_0 + [1-(1-\lambda)^k] V_0 \qquad V_0, V_0 = U_0 + U_0 +$$

· Change in free energy for alchemical A>B mutation DGmut = DGnyd (B) - DGnyd (A) = DDGnyd (A>B)

| | ion | $\Delta G_{ m elec}$ (kcal/mol) | $\Delta G_{ m disp} \ m (kcal/mol)$ | $\Delta G_{\text{rep}} \ 	ext{(kcal/mol)}$ | $\Delta G_{ m hyd}^{ m intr}$ (kcal/mol) | $\Delta G_{ m hyd}^{ m real}^b \ m (kcal/mol)$ | $\Delta G_{ m hyd}^{ m expt}{}^c \ m (kcal/mol)$ | $\Delta \Delta G_{ m hyd}^{ m real}$ (kcal/mol) | $\Delta\Delta G_{ m hyd}^{ m exptc}$ (kcal/mol) | |
|---|-----------------|---------------------------------|--------------------------------------|--|--|---|---|---|---|------------|
| | F- | -124.1 | -1.5 | 5.0 | -120.6 | -107.2 | -99.1 to -121.6 | 29.1 | 28.0 to 30.6 | experiment |
| | CI- | -95.8 | -3.7 | 7.3 | -92.2 | -78.8 | -70.7 to -91.0 | 6.3 | 3.3 to 6.5 | Cryst mary |
| | Br^- | -89.1 | -4.9 | 8.0 | -86.0 | -72.6 | -64.9 to -84.6 | 8.7 | 7.7 to 11.1 | |
| | I- | -79.7 | -7.2 | 9.7 | -77.2 | -63.8 | -57.2 to -76.2 | | | |
| | Li ⁺ | -114.6 | -0.2 | 2.0 | -112.8 | -122.4 | -113.8 to -128.4 | 23.3 | 23.9 to 27.5 | |
| | Na ⁺ | -91.6 | -1.0 | 3.1 | -89.5 | -99.1 | -88.7 to -103.2 | 18.4 | 17.0 to 17.6 | |
| | K ⁺ | -73.7 | -1.9 | 4.5 | -71.1 | -80.7 | -71.2 to -86.0 | 6.6 | 5.1 to 5.6 | |
| 5 | Rb ⁺ | -67.2 | -2.7 | 5.4 | -64.5 | -74.1 | -66.0 to -80.6 | 6.5 | 5.5 to 7.7 | |
| | | | | | | | | | | |

B. Hydratin Free energy of alkali halides

· Total hydration free energy of neutral alkali halido, DGnyd(MX) = DGnyd (M1) + DGnyd (X-)

Table 4. Calculated (and Experimental) Hydration Free Energy of the Alkali Halides

| | • | | | | | | |
|-----------------|----------------------------------|-----------------|-----------------|-----------------|-----------------|--|--|
| | Hydration Free Energy (kcal/mol) | | | | | | |
| | Li ⁺ | Na ⁺ | K ⁺ | Rb⁺ | Cs ⁺ | | |
| F- | -229.6 (-229.0) | -206.3 (-203.8) | -187.9 (-186.6) | -181.3 (-181.2) | -174.8 (-173.8) | | |
| Cl- | -201.2 (-199.3) | -177.9 (-174.0) | -159.5 (-156.8) | -152.9 (-151.4) | -146.4 (-144.0) | | |
| Br^- | -195.0 (-192.9) | -171.7 (-167.6) | -153.3 (-150.4) | -146.7 (-145.0) | -140.2 (-137.6) | | |
| I- | -186.2 (-183.9) | -162.9(-158.7) | -144.5 (-141.5) | -137.9(-136.1) | -131.4(-128.7) | | |

^aExperimental hydration free energies (in kcal/mol) for LiX, NaX, KX, and RbX are from ref 65 and for CsX are from ref 63.

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→ △Gruyd = f(Runin, E) hyperruntace can be mapped from TI calculations

E is dependent on Runin for given hydration free energy

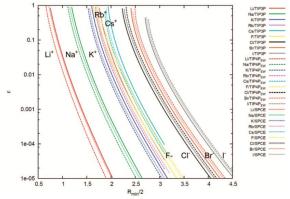


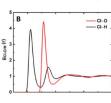
Figure 3. Correlations between R_{\min} and ε for a given free energy of hydration by using the Schmid values. Shown are the correlations in R_{\min} and ε from the $\Delta G_{\text{hydration}} = f(R_{\text{min}}, \varepsilon)$ hypersurface at a given value of the hydration free energies. The chosen values are those from Schmid and co-workers (see Table 10).117 Points on the same line have equivalent hydration free energies. The solid lines are for TIP3P water, the dashed lines are for TIP4P_{EW} water, and the dotted lines are for SPC/E water; each ion is represented by a different color. The units for the x and y axes are Angstroms and kcal/mol, respectively.

7. Optimisation using RDF

Radial distribution function
$$g(r) = \frac{p(r)}{p}$$

· Integration up to first minimum = coordination numbers (CNS)

$$CNs = \int_{0}^{r_{-min}} g(r) dr$$



| | Hydration Number | | | | | |
|-------------------|------------------|-----------------|---------------------|-----------------|--|--|
| | F- | CI- | Br ⁻ | I- | | |
| this work | 6.7 | 7.7 | 8.0 | 8.7 | | |
| experiment | 6.9^{a} | $5.3 - 7.3^{b}$ | $6.3 - 8.9^{c}$ | 6.7-9.1 | | |
| polarizable MM | $5.1-6.7^{e}$ | 6.0-8.4 | $6.6 - 9.0^{\circ}$ | 6.7-9.2 | | |
| QM | $4.9 - 5.0^{i}$ | $5.5 - 6.5^{j}$ | $5.6 - 6.5^{k}$ | $6.6 - 8.5^{l}$ | | |
| QM/MM | 5.7 ^m | 5.9-6.6" | - | 1-1 | | |
| nonpolarizable MM | 6.0-6.9° | $7.0 - 7.6^{p}$ | $7.2 - 7.7^{9}$ | 7.3-9.7" | | |

P = density until rman

| | | NBFI | X^b | |
|-----|----------------------------------|--------------------------------|-------------------------|--|
| ion | atom-type pair (MX) ^a | $\epsilon_{\rm MX}$ (kcal/mol) | R _{min,MX} (Å) | |
| F- | FLA-LIT | -0.032 | 3.2125 | |
| | FLA-SOD | -0.069 | 3.32575 | |
| | FLA-POT | -0.090 | 3.67875 | |
| | FLA-RUB | -0.100 | 3.8150 | |
| | FLA-CES | -0.120 | 4.015 | |
| Cl- | CLA-LIT | -0.046 | 3.5675 | |
| | CLA-SOD | -0.083875 | 3.7310 | |
| | CLA-POT | -0.114236 | 4.0810 | |
| | CLA-RUB | - | - | |
| | CLA-CES | -0.140 | 4.370 | |

- · Potential of mean Force W(r) = -kBT ln(g(r))
- · Radius of first hydration shell = First minimum

TABLE 13: Radii of the First Hydration Shell^a

| | this research | Jensen and S Jorgensen | Smith—Dang— Garrett | Beglov and Roux | Åqvist | Marcus ¹⁸ |
|-----------------|------------------|---------------------------|------------------------|--------------------|--------|----------------------|
| | | | TIP3P | | | |
| Li ⁺ | 1.96 | 2.04 | 1.97 | | 2.03 | 2.08 |
| Na ⁺ | 2.38 | 2.49 | 2.37 | 2.31 | 2.41 | 2.356 |
| K^{+} | 2.75 | 2.86 | 2.83 | 2.71 | 2.72 | 2.798 |
| Rb ⁺ | 2.92 | 3.00 | 2.93 | | 2.85 | 2.89 |
| Cs+ | 3.11 | 3.19 | 3.11 | | 3.05 | 3.139 |
| F- | 2.63 | 2.80 | 2.70 | | | 2.63 |
| Cl- | 3.13 | 3.29 | 3.24 | 3.12 | | 3.187 |
| Br- | 3.29 | 3.41 | | | | 3.373 |
| I- | 3.51 | 3.65 | 3.64 | | | 3.647 |
| rms | 0.07 | 0.09 | 0.05 | 0.07 | 0.06 | |
| | | | | | | |

8. Optimisation using crystal properties (LE, Lc)

- · LE: loss in the total lattice potential energy when crystal structure transform into gas phase, listed in CRC handbook
- · 10: length of the edge of the unit crystals / cation anion distances
- · Rmin is chosen to minimise the overall deviation with literature cation-anion distancy and LE _ at given AGInga

· Choose solutions that lead to stable crystal,

TABLE 4: Range of Acceptable Solutions at Different Ratios of Weights on Interionic Distance and LE on the Ion Radii Optimization $(W_{LE} = 1)^a$

| | $W_{\rm dis}=107$ | $W_{\rm dis} = 150$ | $W_{\rm dis}=200$ | $W_{\rm dis}=250$ | $W_{\rm dis}=30$ |
|-----------------|-------------------|---------------------|---------------------|-------------------|------------------|
| | | | R _{min} /2 | | |
| Li ⁺ | 0.886 | 0.986 | 1.079 | 1.078 | 1.078 |
| Na ⁺ | 1.325 | 1.361 | 1.379 | 1.384 | 1.387 |
| K^+ | 1.687 | 1.702 | 1.709 | 1.712 | 1.713 |
| Rb^+ | 1.803 | 1.811 | 1.815 | 1.817 | 1.818 |
| Cs^+ | 1.968 | 1.974 | 1.978 | 1.979 | 1.980 |
| F- | 2.377 | 2.346 | 2.259 | 2.180 | 2.144 |
| Cl- | 2.614 | 2.526 | 2.500 | 2.498 | 2.497 |
| Br- | 2.657 | 2.616 | 2.602 | 2.602 | 2.601 |
| I- | 2.876 | 2.862 | 2.856 | 2.855 | 2.855 |
| | | 1 | ms (Distance | (:) | |
| | 0.028 | 0.022 | 0.018 | 0.018 | 0.017 |
| | | | rms (LE) | | |
| | 3.28 | 3.97 | 4.49 | 4.62 | 4.68 |
| | | | | | |

^a By using eq 3, the radii of the ions (R_{min}) were optimized at various ratios of the respective weights on the inter-ionic distance $(W_{\rm dis})$ and LE $(W_{\rm LE})$. Displayed are the different $R_{\rm min}/2$ values optimized for the Schmid hydration free energy target values with TIP3P water. Acceptable solutions were those that led to stable crystals (as per Figure 5), maintained size consistency across the monovalent ion series, and had $Cs^+ < 2.5 \text{ Å}$ and $I^- < 3.5 \text{ Å}$. The units of the weights are kcal⁻¹mol (W_{dis}) and Å⁻¹ (W_{LE}) . The same data for the TIP4P_{FW} and SPC/E models are shown in the Supporting Information, Tables S4 and S5.

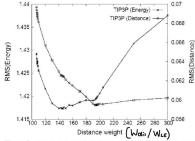


Figure 7. rms deviations of single water-ion binding energies and distances. The rms deviations are plotted as a function of the weight on interionic distance (Å-1) with a fixed weight on the LE (1 kcal-1mol) over the range of acceptable weight ratios (as per Table 4). The units are kcal/mol for the energy and Angstrom for the distance. TIP3P ions have the minimal rms in energy at a weight ratio of 146:1, whereas the minimal rms in distance occurs at 195:1. TIP4P_{FW} ions have the minimal rms deviation for both the energy and the distance at a weight ratio of 50.36:1. SPC/E is somewhat anomalous because the rms of the energy keeps increasing as the rms of the distance decreases. With the SPC/E model, because the minima are not colocalized, the weight ratio was taken at the middle point of both curves or at 27:1. Plots of the rms deviations for TIP4PEW and SPC/E are shown in the Supporting

TABLE 2: LE (kcal/mol) of Crystals of Alkaline Halide Salts as Obtained from the CRC Handbook, 162 Including both the Theoretical LEs Estimated from the Kapustinskii

| | | | | Theory | | |
|---|----|-------|-------|------------|-------|-------|
| | F | 246.2 | 217.5 | 193.1 | 185.0 | 177.8 |
| | CI | 199.3 | 183.8 | 167.5 | 162.5 | 157.0 |
| | Br | 188.3 | 175.0 | 160.4 | 155.6 | 151.1 |
| | 1 | 174.5 | 163.0 | 151.1 | 147.5 | 143.4 |
| | | | | Experiment | | |
| | F | 250.7 | 222.3 | 198.1 | 190.0 | 181.4 |
| | CI | 206.5 | 188.8 | 172.1 | 166.1 | 160.1 |
| - | Br | 196.0 | 180.2 | 165.2 | 159.7 | 154.6 |
| ^ | 1 | 182.6 | 168.5 | 155.4 | 151.1 | 146.5 |
| | | | | | | |

TABLE 3: LC (Angstroms) of Crystals of Alkaline Halide Salts (Top Half) and Interionic Distance (Angstroms) Calculated from the LC at Room Temperature (Bottom

| | Li | Na | K | Rb | Cs |
|----|-------|-------|----------|-------|-------|
| | | | LC | | |
| F | 4.027 | 4.634 | 5.347 | 5.652 | 6.014 |
| CI | 5.140 | 5.640 | 6.293 | 6.581 | 4.123 |
| Br | 5.501 | 5.977 | 6.600 | 6.889 | 4.295 |
| I | 6.023 | 6.473 | 7.066 | 7.342 | 4.568 |
| | | | Distance | | |
| F | 2.014 | 2.317 | 2.674 | 2.826 | 3.007 |
| CI | 2.570 | 2.820 | 3.147 | 3.291 | 3.571 |
| Br | 2.751 | 2.989 | 3.300 | 3.445 | 3.720 |
| I | 3.011 | 3.236 | 3.533 | 3.671 | 3.956 |

"The data were obtained from the first column of Table 1.2 from Sirdeshmukh et al 166

| R | ٩f | (| en | w |
|---|----|---|----|---|
| | | | | |

1. All- Atom Empirical Potential for Molecular Modeling and Dynamic Studies of Proteins

2. CHARMM General Force Field: A Force Field for Ding-Like Molecules Compatible with the CHARMM

All-Atom Additive Biological Force Fields

3. Simulations of Osmotic Pressure in Concentrated Aqueous Salt Solutions

4. Corrections in the CHARMM36 Parametization of Chloride Interactions with Proteins, Lipids, and Alkali Cations,

5. Determination ut Alkali and Halide Monovelent Ion Parameters for Use in Explicitly Solvated Biomolecular Simulation)

and Extension to other Halide Anion,