Comprehensive Review of Molecular Dynamics Potentials

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Abstract

This paper provides a comprehensive comparative analysis of representative molecular dynamics force fields—CHARMM, AMBER, OPLS, ANI, AMOEBA, ReaxFF, and PCFF—focusing on their structural characteristics, evaluation criteria, and applications in chemistry. We discuss the strengths and weaknesses of each force field in terms of accuracy, transferability, computational efficiency, and application areas, and present practical guidelines to help researchers select the most suitable force field for their simulation objectives [1].

Terminology Definition

In this review, we use the term **force field** to refer to the complete set of mathematical functions, parameters, and rules that define the potential energy of a molecular system in molecular dynamics (MD) simulations. A force field typically includes all bonded and nonbonded interaction terms, parameter sets, and functional forms required to compute energies and forces for a given class of molecules. The term **potential function** (or potential energy function) refers specifically to the mathematical expressions within a force field that describe individual energy contributions, such as bond stretching, angle bending, torsion, van der Waals, and electrostatic interactions. In this context, 'force field' is the overarching framework, while 'potential function' denotes the specific energy terms used within that framework. Throughout this paper, we use 'force field' as the primary term for the overall methodology, and reserve 'potential function' for discussion of specific energy terms or mathematical forms [2].

1 Force Fields

1.1 CHARMM Force Field Potential Energy

The potential energy function of the CHARMM force field is [3]:

$$\mathrm{E}_{CHARMM} = \sum_{bonds} k_b(b-b_0)^2 + \sum_{angles} k_\theta(\theta-\theta_0)^2 + \sum_{Urey-Bradley} k_U(S-S_0)^2 + \sum_{dihedrals} k_\phi[1+\cos(n\phi-\delta)] + \sum_{impropers} k_\omega(\omega-\omega_0)^2 + \sum_{i<j}\left[\epsilon_{ij}\left(\left(\frac{R_{min,ij}}{r_{ij}}\right)^{12} - 2\left(\frac{R_{min,ij}}{r_{ij}}\right)^{6}\right) + \frac{q_i q_j}{\epsilon r_{ij}}\right]$$

In this equation, k_b, k_θ, k_U, k_ϕ, and k_ω represent the force constants for bonds, angles, Urey-Bradley 1,3 interactions, dihedrals, and improper torsions, respectively. The variables b and b_0 denote the bond length and its equilibrium value, while θ and θ_0 correspond to the bond angle and its equilibrium value. The Urey-Bradley term uses S and S_0 to describe the distance between 1,3 atoms and its equilibrium value. For dihedral angles, n is the periodicity and δ is the phase. The improper torsion angle and its equilibrium value are given by ω and ω_0. The Lennard-Jones parameters for each atom pair i, j are ϵ_{ij} and $R_{min,ij}$, and the electrostatic interactions are determined by the atomic charges q_i, q_j, the interatomic distance r_{ij}, and the dielectric constant ϵ. The inclusion of the Urey-Bradley term enhances the modeling of ring systems and vibrational spectra, while the NBFIX correction is applied to specific ion pairs, such as Lys$^+$–Cl$^-$ and Arg$^+$–Asp$^-$, to improve the accuracy of protein-ligand and membrane system simulations by correcting overestimated interactions.

1.2 AMBER Force Field Potential Energy

The potential energy function of the AMBER force field is [4]: $\mathrm{E}_{AMBER} = \sum_{bonds} k_b(b - b_0)^2 + \sum_{angles} k_\theta(\theta - \theta_0)^2 + \sum_{dihedrals} \frac{V_n}{2}[1 + \cos(n\phi - \gamma)] + \sum_{i<j} \left[\epsilon_{ij}\left(\left(\frac{R_{min,ij}}{r_{ij}}\right)^{12} - 2\left(\frac{R_{min,ij}}{r_{ij}}\right)^{6}\right) + \frac{q_i q_j}{\epsilon r_{ij}}\right]$ Here, k_b and k_θ are the force constants for bonds and angles, V_n is the barrier height for the dihedral term, n is the periodicity, and γ is the phase. ϵ_{ij} and $R_{min,ij}$ are the Lennard-Jones parameters, while q_i and q_j are atomic charges, r_{ij} is the interatomic distance, and ϵ is the dielectric constant. AMBER scales 1-4 electrostatic and Lennard-Jones terms (by 0.8333 and 0.5, respectively) for atoms separated by three bonds. RESP charges are derived from HF/6-31G* calculations to reproduce molecular electrostatic potentials. Here, bonds and angles are described by harmonic terms, torsions by periodic cosine functions, and nonbonded terms by Lennard-Jones 12-6 potentials and Coulomb terms. The core of AMBER is its sophisticated reparameterization strategy for the torsion term. The ϕ/ψ backbone dihedrals and side-chain χ angles are iteratively refined based on QM calculations and NMR experimental data, reproducing the relative stability of α-helices and β-sheets in a balanced manner. Another structural feature is the special treatment of 1–4 interactions. AMBER scales the electrostatic term by about 0.8333 and the Lennard-Jones term by half, adjusting repulsion and attraction, which is crucial for the formation and maintenance of protein secondary structures. Charge modeling uses RESP charges obtained from HF/6-31G* level electronic structure calculations, which maintains an additive point charge model while realistically reproducing structures and dynamics in protein and nucleic acid environments. The evolution of the AMBER series also demonstrates its originality. Starting from ff94 and ff99, updates such as ff99SB (recalibrated backbone parameters), ff99SB-ILDN (refined side-chain χ_1), ff14SB (revised backbone and side-chain parameters), and ff19SB (residue-specific backbone parameters) have dramatically improved the balance of protein secondary structures and the stability of long MD trajectories.

1.3 OPLS Force Field Potential Energy

The potential energy function of the OPLS force field is [5]: $\mathrm{E}_{OPLS} = \sum_{bonds} k_r(r - r_0)^2 + \sum_{angles} k_\theta(\theta - \theta_0)^2$
$+ \sum_{dihedrals} \left[\frac{V_1}{2}(1 + \cos\phi) + \frac{V_2}{2}(1 - \cos 2\phi) + \frac{V_3}{2}(1 + \cos 3\phi) + \frac{V_4}{2}(1 - \cos 4\phi)\right]$
$+ \sum_{i<j} 4\epsilon_{ij}\left[\left(\frac{\sigma_{ij}}{r_{ij}}\right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}}\right)^{6}\right] + \frac{q_i q_j}{\epsilon r_{ij}}$ In this equation, k_r and k_θ denote the force constants for bonds and angles, respectively. The terms V_1 through V_4 are Fourier coefficients that define the dihedral angle contributions. The parameters ϵ_{ij} and σ_{ij} represent the Lennard-Jones well depth and collision diameter for each atom pair, respectively. The variables q_i and q_j are the atomic charges, r_{ij} is the interatomic distance, and ϵ is the dielectric constant. OPLS scales 1-4 nonbonded terms by 0.5. Charges are derived from QM-based methods (e.g., CM1A, CM5) and may be locally corrected (LBCC). $+ \sum_{dihedrals} \frac{V_n}{2}[1 + \cos(n\phi - \gamma)] + \sum_{i<j} \left[\epsilon_{ij}\left(\left(\frac{R_{min,ij}}{r_{ij}}\right)^{12} - 2\left(\frac{R_{min,ij}}{r_{ij}}\right)^{6}\right) + \frac{q_i q_j}{\epsilon r_{ij}}\right]$ Where: Here, k_b and k_θ are the force constants for bonds and angles, V_n is the barrier height for the dihedral term, n is the periodicity, and γ is the phase. ϵ_{ij} and $R_{min,ij}$ are the Lennard-Jones parameters, while q_i and q_j are atomic charges, r_{ij} is the interatomic distance, and ϵ is the dielectric constant. AMBER scales 1-4 electrostatic and Lennard-Jones terms (by 0.8333 and 0.5, respectively) for atoms separated by three bonds. RESP charges are derived from HF/6-31G* calculations to reproduce molecular electrostatic potentials.

A distinctive feature of OPLS is the rule of scaling both electrostatic and Lennard-Jones 1–4 intramolecular nonbonded terms by 0.5. OPLS defines charges by scaling QM-based charges such as CM1A and CM5 (e.g., 1.14CM1A, 1.20CM5) or applying Local Bond Charge Correction (LBCC) for specific bond types. This approach provides more consistent accuracy for condensed-phase free energies and liquid properties, and is implemented in automated tools like LigParGen. The reparameterization of torsion terms is a key axis of OPLS development. OPLS-AA/M (2019) performed high-level QM scans (ωB97X-D/6-311++G(d,p)) for the α and γ dihedrals of the RNA backbone, and adjusted parameters using experimental NMR ^{3}J coupling data as benchmarks, along with sugar puckering and glycosidic torsion terms. This improved the unphysical conformer sampling issues seen in previous OPLS-AA and enhanced the stability of the A-form helix structure in RNA.

1.4 ANI force field Potential Energy

ANI (Accurate Neural Network Potentials for Organic Molecules) is a representative example of a machine learning-based force field (MLFF), bridging the gap between classical force fields and quantum mechanical methods for organic and small molecules [6].

The total energy in ANI is: $\mathrm{E}_{ANI} = \sum_{i=1}^{N} E_i(G_i)$ where E_i is the atomic energy predicted by a neural network from the atomic environment vector (AEV) G_i for atom i. The AEV encodes the local chemical environment (neighbor types, distances, angles). ANI uses a multilayer perceptron (MLP) to predict E_i from G_i, summing over all atoms to obtain the total energy. This approach enables large-scale MD simulations and free energy exploration with DFT-level accuracy for molecules up to 50 atoms, especially for C, H, O, N, S, and halogens.

1.5 AMOEBA force field Potential Energy

The AMOEBA (Atomic Multipole Optimized Energetics for Biomolecular Applications) force field is a polarizable force field that extends atom-centered charges to multipoles—monopole (q), dipole (μ), and quadrupole (Θ)—and includes explicit induced dipoles solved self-consistently [7].

The total potential energy of AMOEBA is: $\mathrm{E}_{AMOEBA} = E_{bond} + E_{angle} + E_{dihedral} + E_{vdW} + E_{elec,perm} + E_{pol}$ Where: The terms E_{bond}, E_{angle}, and $E_{dihedral}$ represent the standard bonded interactions in the AMOEBA force field. The van der Waals energy, E_{vdW}, is modeled using Halgren's buffered 14-7 function: $\mathrm{E}_{vdW} = \epsilon_{ij}\left[(1+\delta)\frac{R_{ij}^0}{R_{ij}+\delta R_{ij}^0}\right]^7 \left[(1+\gamma)\frac{R_{ij}^0}{R_{ij}+\gamma R_{ij}^0}\right]^7$ In this expression, δ and γ are buffering constants, R_{ij}^0 is the equilibrium distance, and ϵ_{ij} is the well depth. The term $E_{elec,perm}$ denotes the permanent electrostatic interaction between atomic multipoles, while E_{pol} accounts for the polarization energy arising from induced dipoles. The induced dipole moment μ_i for atom i is calculated as $\mu_i = \alpha_i\left(E_i^{ext} + \sum_{j\neq i} T_{ij}\mu_j\right)$, where α_i is the atomic polarizability and T_{ij} is the dipole interaction tensor. AMOEBA+ further introduces charge penetration corrections to improve the accuracy of short-range electrostatics. Long-range interactions are treated using multipole Particle Mesh Ewald (PME) or Ewald summation methods.

1.6 ReaxFF force field Potential Energy

ReaxFF (Reactive Force Field) is designed for reactive systems, allowing bond formation and breaking. The total energy is [8]: $\mathrm{E}_{ReaxFF} = E_{bond} + E_{over/under} + E_{angle} + E_{torsion} + E_{vdW} + E_{Coulomb} + E_{penalty}$ In this expression, E_{bond}, E_{angle}, and $E_{torsion}$ represent the standard bonded interactions, each weighted by the bond order. The term $E_{over/under}$ provides corrections for over- or under-coordination of atoms. The van der Waals interactions are described by E_{vdW}, which uses a shielded potential, while $E_{Coulomb}$ accounts for shielded Coulomb interactions with atomic charges determined by charge equilibration (QEq) or ACKS2 models. The $E_{penalty}$ term includes additional penalties to prevent unphysical configurations. In ReaxFF, bond order is decomposed into σ, π, and $\pi\pi$ components, each decaying exponentially with interatomic distance. The QEq method solves for atomic charges by electronegativity equalization, while ACKS2 provides improved polarization and field response. Importantly, all energy terms vanish as the bond order approaches zero, which enables dynamic changes in molecular topology during simulations.

1.7 PCFF Potential Energy

Polymer Consistent Force Field (PCFF) is designed for polymers and amorphous materials, expanded from CFF91. The total potential energy is [9]: $\mathrm{E}_{PCFF} = \sum_{bonds}(k_2(r-r_0)^2 + k_3(r-r_0)^3 + k_4(r-r_0)^4) + \sum_{angles}(k_2(\theta-\theta_0)^2 + k_3(\theta-\theta_0)^3 + k_4(\theta-\theta_0)^4)$ Where k_2, k_3, k_4 are force constants for quadratic, cubic, and quartic terms, respectively. This polynomial expansion allows for large deformations and nonlinear flexibility.

The torsion term is a Fourier series: $\mathrm{E}_{torsion} = \sum_{n=1}^{4} V_n[1+\cos(n\phi-\gamma_n)]$ where V_n are Fourier coefficients and γ_n are phase angles.

PCFF also includes cross terms (bond–angle, angle–torsion) for correlated deformations. Nonbonded terms use the Lennard-Jones 9–6 potential: $\mathrm{E}_{nonbonded} = \sum_{i<j}\left[\epsilon_{ij}\left(2\left(\frac{\sigma_{ij}}{r_{ij}}\right)^9 - 3\left(\frac{\sigma_{ij}}{r_{ij}}\right)^6\right) + \frac{q_i q_j}{\epsilon r_{ij}}\right]$ where σ_{ij} is the collision diameter (distance at which the potential is zero), ϵ_{ij} is the well depth. This form is suitable for volumetric and thermal properties of polymers.

Long-range electrostatic interactions are handled by Ewald summation. Although polarization effects are not explicitly included, macroscopic properties such as the bulk properties of amorphous polymers and glasses can be reproduced relatively stably. These features lead to several advantages: first, the polynomial-based internal coordinate terms provide numerical stability even for large structural deformations or long simulations; second, the introduction of cross terms allows for more precise modeling of deformation behaviors related to polymer flexibility; third, the use of Lennard-Jones 9–6 potentials is suitable for reproducing volumetric properties, thermal expansion coefficients, and compressibility of liquids and polymers.

2 Evaluation Criteria

Clear evaluation criteria are necessary to compare force fields in a balanced way. These criteria go beyond simple accuracy assessment and provide a framework for determining practical applicability and scientific validity, serving as the basis for analyzing the strengths and weaknesses of each force field [10].

2.1 Transferability

Transferability is an indicator of whether a force field (FF) can maintain consistent predictive performance in new environments beyond the chemical space for which it was parameterized. The degree of transferability is a key factor determining the generality and practical applicability of a force field, and is typically evaluated by three criteria. First, the coverage of parameter space reflects how many types of atoms, bonding patterns, functional groups, and charge states are included. Second, predictive reliability in out-of-distribution (OOD) environments shows whether the FF can produce stable results under conditions different from the training data. Third, agreement with experimental properties and high-level quantum mechanical (QM) calculations—such as free energy, density, and torsional barriers—serves as a direct means of verifying transferability. These criteria are essential for defining the practical scope of a model, beyond mere accuracy.

2.2 Long-Range Interactions

Long-range interactions are factors that determine the structural and thermodynamic accuracy of MD simulations, playing a decisive role especially in polar environments or interfacial phenomena. Evaluation is mainly performed in three dimensions. First, the method of handling interactions, including electrostatic and polarization terms, is key—whether fixed charges, induced dipoles, or multipole expansions are used. Second, the use of techniques such as Ewald summation, Particle Mesh Ewald (PME), and Thole damping is examined to see if long-range terms are physically implemented. Third, the reproducibility of macroscopic properties such as dielectric constant, liquid density, and interfacial energy quantitatively demonstrates the accuracy of long-range modeling. Precise treatment of long-range interactions is critical for the reliability of FFs in practical applications such as ion solvation, protein–ligand binding, and electrode–electrolyte interface reactions.

2.3 Numerical Stability

Numerical stability is a criterion for evaluating the computational robustness of a force field, directly related to the ability to perform long simulations and maintain physical consistency. The first indicator is energy drift, which checks how well the total energy is maintained in the NVE ensemble. The second is the maintenance of long-term trajectories, with RMSD, structural integrity, and the persistence of local interaction networks as key metrics. The third is the convergence of iterative numerical processes, including stable convergence of induced dipoles or charge equilibration, and the possibility of unphysical phenomena (e.g., charge runaway). Numerical stability is not just a matter of algorithmic performance, but a decisive criterion for determining whether the predicted dynamics are physically valid.

2.4 Interpretability and Uncertainty Quantification

Interpretability refers to how directly the parameters of a force field are connected to physical and chemical concepts, serving as a criterion for evaluating model transparency and the ability to analyze failure causes. The clearer the physical meaning of the parameters, the easier it is to trace the operating principles and limitations of the model. Uncertainty quantification (UQ) is the process of numerically expressing the reliability of FF predictions, with representative techniques including Bayesian inference, ensemble modeling, and active learning. These techniques help detect instability in OOD environments and provide predictive confidence. Thus, interpretability and UQ are essential evaluation axes that go beyond simple performance metrics, enabling researchers to use results based on scientific evidence.

3 Application

Recently, molecular dynamics (MD) simulation has become a core tool in computational chemistry applications, with explosive use in three fields in particular: battery materials, drug development, and catalysis research [11]. According to Web of Science analysis, since 2020, MD-based research in these three fields accounts for more than 35

3.1 Battery Research

In battery research, MD simulation is essential for understanding the structure of electrode–electrolyte interfaces, electrolyte stability, and ion conduction mechanisms. ReaxFF and PCFF are each well-suited for battery applications due to their unique strengths [12]. ReaxFF is currently the most widely used reactive force field in battery research. Several reviews emphasize that ReaxFF can directly model chemical reactions at the electrode–electrolyte interface, electrolyte decomposition, and solid electrolyte interphase (SEI/CEI) formation at the atomic level [21]. For example, ReaxFF is essential in studies tracking dendrite growth on lithium metal anodes or analyzing polysulfide conversion reactions in sulfur cathodes. The core of ReaxFF is its definition of bond order as a continuous function of interatomic distance, dynamically handling bond formation and breaking, and naturally reflecting charge transfer during reactions through charge equilibration models such as QEq and ACKS2. Thanks to this structure, ReaxFF exhibits high transferability and provides stable predictions for new electrolyte compositions or electrode materials. Its computational efficiency—hundreds to thousands of times faster than AIMD—enables simulations of tens of nanoseconds, making it widely used for evaluating interface stability and electrolyte additive effects [18]. Recently, parameter optimization based on active learning and uncertainty quantification techniques have further enhanced the reliability and interpretability of battery research using ReaxFF. In contrast, while PCFF cannot model reactivity, it is frequently mentioned for its ability to reliably predict the structural and thermodynamic properties of polymer and organic electrolytes. PCFF uses a comprehensive potential function that includes cross-terms, not just simple harmonic terms, allowing precise modeling of bonds, angles, torsions, and van der Waals interactions, resulting in excellent structural stability and numerical robustness. For example, reports show that the density and viscosity of glyme-based electrolytes calculated with PCFF match experimental values well, indicating high transferability [12]. PCFF also effectively handles long-range interactions, making it suitable for reproducing the macroscopic properties of polymer electrolytes, electrode binders, and composites. Such cases support PCFF as a reliable general-purpose force field for electrolyte composition design and electrode stabilization studies [12,13].

3.2 Drug Development

In drug development, MD simulation is a key tool for predicting the binding modes, stability, solubility, and interactions of candidate molecules with target proteins. The choice of force field directly affects the reliability and transferability of computational results, with CHARMM, AMBER, and AMOEBA being the most widely adopted systems [13]. CHARMM was developed from the outset with a focus on proteins and nucleic acids, and was later expanded to include lipids and small molecules. This versatility makes it strong for modeling drug target environments such as protein–ligand complexes and protein–membrane protein interactions. For example, GPCRs are clinically important drug targets, and CHARMM is widely used for analyzing drug binding modes by accurately reproducing membrane lipid environments **?**. The inclusion of correction terms such as NBFIX also improves the accuracy of binding affinity calculations by mitigating the overestimation of charged ligand–protein interactions. AMBER is advantageous for capturing subtle structural changes in drug–target interactions, as it has been precisely refined for protein backbone and side-chain dihedral angles based on QM data and NMR experiments [7,15]. For example, in studies of target proteins sensitive to active site structural changes, such as kinase inhibitors, the latest AMBER series (ff14SB, ff19SB) provides stable and reliable results for free energy calculations and drug ranking evaluations [15]. Ligand parameters using the RESP charge model also show high compatibility in real protein environments and are standard in virtual screening and optimization stages [7,15]. AMOEBA goes beyond the limitations of traditional fixed-charge force fields by explicitly incorporating multipole and induced polarization effects [10,16,17]. In drug research, where polar ligands, metal ions, or hydrogen bond networks are important, AMOEBA provides improved accuracy over conventional FFs. In fact, AMOEBA-based simulations have shown meaningful results in protein–ligand binding free energy calculations and studies of ion transport protein mechanisms [16,17]. Its ability to accurately reproduce solvation free energies and interfacial properties of water and ions also makes it effective for predicting drug delivery pathways and in vivo behavior [10,16].

3.3 Catalysis Research

In catalysis research, the key is to model complex reaction pathways and the behavior of active sites at the atomic level, and ANI, AMOEBA, and ReaxFF are used based on their respective strengths [14]. ANI, as a machine learning-based force field, has high transferability and is suitable for exploring new catalyst candidates. For example, studies predicting ligand exchange reaction pathways in single-atom metal catalysts have reported that ANI maintains DFT-level accuracy while greatly improving computational efficiency [18]. These results show that ANI can be a useful tool in catalyst screening. AMOEBA is particularly effective in biocatalyst systems where charge distribution and long-range interactions are important, as it explicitly considers multipoles and induced polarization. In studies of metalloenzyme catalysts, AMOEBA has been shown to accurately model the electrostatic interactions between active site metal ions and substrates, helping to explain transition state stabilization mechanisms [16,17]. ReaxFF is widely used in reactive catalyst research because it can dynamically handle bond formation and breaking. Studies have reported direct modeling of oxidation–reduction reactions on metal oxide surfaces, hydrocarbon cracking, and coking phenomena on catalyst surfaces at the atomic level [19,18]. Its efficiency—hundreds of times greater than AIMD—makes it suitable for reproducing complex multi-step catalytic reactions on long time scales.

4 Conclusion

In this review, we summarized the structural characteristics and strengths and weaknesses of representative molecular dynamics force fields—CHARMM, AMBER, OPLS, ANI, AMOEBA, ReaxFF, and PCFF—and considered their applicability in major application areas such as batteries, drug development, and catalysis research. Traditional force fields excel at stable modeling of biomolecules and organic molecules, polarizable force fields offer precision in long-range interactions, and reactive force fields have unique advantages in reflecting bond formation and breaking. Machine learning-based force fields also present new possibilities in terms of transferability and computational efficiency, and their future applications are highly anticipated. The future development of force fields will be directed toward achieving a balance between accuracy, transferability, and computational efficiency, which is expected to make a key contribution to solving various scientific and engineering problems such as battery material innovation, acceleration of drug development, and next-generation catalyst design.The summarized chart can be seen at the end of this paper.
tabularx

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Table 1: Comparison of Representative Molecular Dynamics Force Fields

Force Field	**Potential Function**	**Strengths**	**Weaknesses**	**Transferability**	**Long-Range Interaction**
CHARMM	Harmonic bonds/ angles, Urey-Bradley, cosine dihedrals, Lennard-Jones 12-6, Coulomb	Versatile, well-validated for proteins/ nucleic acids	Parameterization complex, limited reactivity	High (biomolecules, membranes)	Ewald sum, NBFIX corrections
AMBER	Harmonic bonds/ angles, cosine dihedrals, Lennard-Jones 12-6, Coulomb	Accurate for proteins/nucleic acids, refined torsions	Limited to biomolecules, fixed charges	High (proteins, DNA/ RNA)	Ewald sum, 1-4 scaling
OPLS	Harmonic bonds/ angles, Fourier dihedrals, Lennard-Jones 12-6, Coulomb	Good for organics, liquids, drugs	Limited polarization, fixed charges	High (organics, drugs)	Ewald sum, 1-4 scaling
ANI	Neural network atomic energy sum	DFT-level accuracy, fast, transferable	Limited elements, not reactive	High (for covered elements)	No explicit long-range, can combine
AMOEBA	Harmonic bonds/ angles, multipole electrostatics, induced dipoles, buffered 14-7 vdW	Explicit polarization, accurate for water/ions	Expensive, parameterization difficult	High (biomolecules, ions)	Multipole PME/ Ewald
ReaxFF	Bond order-dependent, shielded Coulomb/ vdW, dynamic topology	Reactive, bond breaking/ formation, many elements	Complex parameterization, less interpretable	High (many elements/reactions)	Shielded Coulomb, QEq/ ACKS2
PCFF	Polynomial bonds/ angles, Fourier dihedrals, Lennard-Jones 9-6, Coulomb, cross terms	Good for polymers, stable for large deformations	Not reactive, no explicit polarization	Moderate (polymers, organics)	Ewald sum, no polarization