Accurate and Transferable Reactive Molecular Dynamics Models from Constrained Density Functional Theory

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KEYWORDS. Molecular Dynamics, Density Functional Theory, Proton Transfer, pK\textsubscript{a} Calculation, Free Energy Sampling

ABSTRACT Chemical reactions constitute the central feature of many liquid, material, and biomolecular processes. Conventional molecular dynamics (MD) is inadequate for simulating chemical reactions given the fixed bonding topology of most force fields, while modeling chemical reactions using ab initio molecular dynamics is limited to shorter time and length scales given its high computational cost. As such, the multiscale reactive molecular dynamics method provides one promising alternative for simulating complex chemical systems at atomistic detail on a reactive potential energy surface. However, the parameterization of such models is a key barrier to their applicability and success. In this work, we present reactive MD models derived from constrained density functional theory that are both accurate and transferable. We illustrate the features of these models for proton dissociation reactions of amino acids in both aqueous and protein environments. Specifically, we present models for ionizable glutamate and lysine that predict accurate absolute pK\textsubscript{a} values in water, as well as their significantly shifted pK\textsubscript{a} in staphylococcal nuclease (SNase) without any modification of the models. As one outcome of the new methodology, the simulations show that the deprotonation of ionizable residues in SNase can be closely coupled with sidechain rotations, which is a concept likely generalizable to many other proteins. Furthermore, the present approach is not limited to only pKa prediction, but can enable the fully atomistic simulation of many other reactive systems along with a determination of the key aspects of the reaction mechanisms.
INTRODUCTION

Molecular dynamics (MD) can be a powerful computational tool for studying the kinetics and thermodynamics of liquid, material, and biomolecular systems and other associated processes. Conventional MD (referred to herein as classical MD) usually requires a pre-defined bonding topology of the systems being simulated. Since this topology remains fixed during the course of the simulation, conventional MD is strictly speaking only suited for simulating physical processes without chemical reactions. In contrast, the *ab initio* molecular dynamics (AIMD) approach\(^1\) represents a natural choice for simulating reactive processes because it solves the electronic Schrödinger equation on-the-fly and does not rely on a fixed bonding structure of the system. We also note, on the other hand, that chemical reactions can be intrinsically multiscale, i.e., they can be coupled with multiple collective and corporative motions that span spatial and temporal scales of several orders of magnitude. Given the multiscale nature of reactions, an efficient MD simulation model is needed to sample the required space and time scales in order to obtain statistically meaningful results. However, AIMD calculations can be prohibitively expensive and therefore often limited to sub-nanosecond timescales for a system consisting of hundreds of electrons. In addition, the accuracy of AIMD is highly correlated with the adopted electronic structure method underlying the implementation of the AIMD algorithm. A popular approach is the generalized gradient approximation (GGA) within the framework of electronic density functional theory (DFT), which often overestimates charge transfer and partial covalency.\(^2\) Using significantly more computational expensive hybrid functionals has been found to be necessary for achieving quantitative accuracy, e.g., in the description of somewhat simple and non-reactive systems such as liquid water.\(^3\)

An alternative approach is the multiscale reactive molecular dynamics (MS-RMD) method,\(^4-7\) which can be up to three-orders of magnitude more computationally efficient compared to AIMD.
MS-RMD enables microsecond sampling of complex systems, making it effective for accurately modeling condensed phase chemical reactions for which the varying bonding topologies can be defined, with sufficient sampling of the coupled, but relatively slow, processes. MS-RMD was previously formulated as a force-matching (FM) algorithm,\textsuperscript{5-7} in which the models were parametrized to best reproduce the atomic forces of \textit{ab initio} calculations in a least-squares sense. The FM-based MS-RMD model was shown to successfully reproduce the benchmark results of the reference \textit{ab initio} model in both aqueous\textsuperscript{5} and biomolecular environments,\textsuperscript{7} as well as to explain and reproduce experimental thermodynamic and kinetic data.\textsuperscript{8-12} These models were parameterized in a case-by-case basis, whereby training \textit{ab initio} calculations were conducted each time the MS-RMD model was applied to a new chemical environment.

In the condensed phase, the MS-RMD approach describes the system as a linear combination of as many as 20-30 diabatic states, each of which corresponds to a resonance form of the system with a different bonding topology. Conventional DFT was adopted as the reference \textit{ab initio} method; however, due to the lack of diabatic state information, only the ground electronic state was fit in the MS-RMD FM scheme. To better address this issue, \textit{ab initio} diabatic methods have been employed in this work to facilitate a more systematic and new parametrization approach for the RMD models at the diabatic state level. Furthermore, this newer diabatic matching (DM) approach can be regarded as a generalization of our original FM method that focuses only on the ground electronic state. The quantum diabatic method chosen here is constrained DFT (CDFT)\textsuperscript{13} that is flexible in dealing with various atomic charge prescriptions such as Mulliken,\textsuperscript{14} Hirshfeld,\textsuperscript{15} and Becke,\textsuperscript{16} but we note that other diabatic methods such as the multistate DFT (MS-DFT)\textsuperscript{17,18} could also be employed.
As an important category of chemical reactions, proton transport (PT) via Grotthuss proton shuttling\textsuperscript{19} along confined water and titration of protonable residues in biomolecular systems, represents a key step in many protein functional cycles.\textsuperscript{20-30} Employing an efficient and accurate computational approach that explicitly models this PT process is crucial for understanding the full working mechanisms associated with these enzymes, channels, and transporters.

As detailed in this work, the deprotonation events of ionizable amino acids in both water and in the protein staphylococcal nuclease (SNase) were examined using the new DM method. Importantly, the computational efficiency of MS-RMD allows for the computation of the full free energy profile for the coupled proton dissociation process with local conformational changes in SNase. We show that our model can predict the pK\textsubscript{a} of the very different glutamate (Glu; E) and lysine (Lys; K) amino acids in both aqueous solution and solvated SNase, in good agreement with experimental results and without any need to reparametrize the model. Due to this system transferability, we anticipate that the new DM MS-RMD models will be more widely applied to other biomolecular systems to study PT and its coupled phenomenon, notably hydration change, global protein conformational change, as well as ligand transport. Moreover, since neither MS-RMD nor CDFT is limited to PT reactions, our approach could significantly advance the systematic development of accurate and transferrable reactive MD models to simulate other chemical reactions with much greater computational efficiency.

METHODS

MS-RMD Methodology. The MS-RMD framework can be regarded as a linear combination of force fields of conventional molecular mechanics (MM). The latter approach assumes a fixed bonding topology that cannot be changed during the MD simulation. As such, MM lacks the ability
to describe chemical reactions. However, the MS-RMD approach considers multiple resonance states, including the reactant state and the product state of the reaction. In the context of proton solvation and transport, each diabatic state is associated with a different localized protonated species, e.g., a solvated neutral Glu as state $|1\rangle$ in Figure 1A, or the contact ion pair formed by a charged Glu and hydronium as state $|2\rangle$. The diabatic states are resolved by proposing hypothetical PT reactions. For instance, state $|2\rangle$ is resolved as the product state of $|1\rangle$ after a proton transfer from the protonated Glu, and state $|3\rangle$ originates from a proton transfer from state $|2\rangle$. The aforementioned search process is essentially a depth-first search that follows the hydrogen bond networks, and a maximum search depth of 3, i.e. up to three solvation shells of the excess proton is shown to be sufficient when modeling most PT reactions while limiting the number of states in a computationally feasible range. The Hamiltonian of the system is then expressed in the following diabatic state representation:

$$H_{RMD} = \sum_{ij} |i\rangle h_{ij} \langle j|$$

The diagonal term $h_{ii}$ is usually taken to be the energy function described by a suitable MM force field, based on the assumption that the classical force field accurately depicts a diabatic state given a well-defined bonding topology. The off-diagonal element, $h_{ij}$, describes the coupling between two states $|i\rangle$ and $|j\rangle$ and is modeled by a physically inspired ansatz in a MM form. (These terms are more fully defined in the following section on Force Field.) The ground state of the reactive system can be obtained through solving the following eigenvalue problem “on the fly” as a function of nuclear configuration, such that

$$H_{RMD} \mathbf{c} = E \mathbf{c}$$
The eigenvector $\mathbf{c} = \{c_i\}$ with the lowest eigen energy is the diabatic representation of the ground state (which depends on the instantaneous configuration of the nuclear coordinates), and that also corresponds to the relative weights of the diabatic state contributions to the adiabatic ground state description of the system. The latter relation may be better understood by noting that the ground state energy can also be expressed as the $c_i$ weighted diabatic energies

$$E = \sum_{ij} c_i c_j h_{ij}$$

The atomic forces, as the energy gradient, are $c_i$ weighted diabatic forces according to the Hellmann-Feynman theorem:

$$\mathbf{F} = \sum_{ij} c_i c_j \mathbf{F}_{ij}$$

where $\mathbf{F}_{ij}$ is the diabatic force defined as $-\nabla h_{ij}$. Furthermore, the $\mathbf{c}$ vector provides a convenient way to track the effective position of the excess proton, which is the so-called center of excess charge (CEC),

$$\mathbf{r}_{\text{CEC}} = \sum_i c_i^2 \mathbf{r}_{i}^{\text{COC}}$$

The $\mathbf{r}_{i}^{\text{COC}}$ is the center of charge of the protonated moiety in state $|i\rangle$. The CEC defined in such a way can be regarded as a $c_i^2$ weighted average of the excess protonic charge defect position. (Due to bond breaking and forming during the PT process, the identity of $\text{H}^+$ is not associated with any specific proton in the system.) Thus, the CEC is needed to indicate the position of $\text{H}^+$ and to further define continuous reaction coordinates (RCs) for enhanced free energy sampling simulations of PT reactions, which is discussed later in greater detail in the Simulation Details section.
Figure 1. Illustration of MS-RMD states for (A) Glu in water and (B) Lys in water. The protonated moiety in each diabatic state is circled in blue. Note that typically 20-30 coupled bonding topology states are included in the condensed-phase calculations, but only four states are shown here for clarity.

**Force Field (FF).** The FF functional forms used in MS-RMD are provided in this section, while the detailed training method and procedure of the models will be provided in the later discussion of parametrization of MS-RMD using CDFT.

The diagonal $h_{ii}$ terms are described by the standard CHARMM36 FF\textsuperscript{32} with several adaptations clarified below. The original harmonic O-H bond in a protonated Glu carboxylic group as well as the N-H bond in the Lys ammine group are replaced by a Morse bond to better describe the proton disassociation curve:
where $r$ represents the bond length, $D, \alpha, r_0$ are bond parameters, taken from ref\textsuperscript{6} for Glu. The bond parameters for Lys were optimized to match an energy scan of the bond disassociation, in which the proton was scanned with respect to nitrogen within a distance range of 0.9 Å to 1.9 Å with 0.1 Å intervals. The reference energies were computed with the functional/basis-set combination $\omega$B97X\textsuperscript{33}/TZV2P in CP2K\textsuperscript{34} coupled with Libxc.\textsuperscript{35} In any diabatic state wherein a protonated Glu or Lys was found, such as state $|1\rangle$ shown in Figure 1, a trainable energy offset $V_{\text{d} \text{const}}$ was added to the total energy of the system to bridge zero points of the classical MM potential energy surfaces (PESs), that were originally parametrized for nonreactive protonated and deprotonated forms of the amino acids.

The hydronium FF parameters including bonds, angles, and Lennard-Jones (LJ) were obtained from ref\textsuperscript{36}. Additionally, additive repulsions between hydronium and Glu carboxyl/Lys amine were employed to correct the over-attraction between point charges present in the MM FFs, as given in the following equations:

$$U_{\text{OX}}^{\text{rep}} = B \exp \left( -b(r_{\text{OX}} - d_{\text{OX}}^0) \right) \cdot \sum_{j=1}^{3} \exp \left( -b' q_{\text{H},jX}^2 \right)$$

and

$$U_{\text{HX}}^{\text{rep}} = C \exp \left( -c(r_{\text{HX}} - d_{\text{HX}}^0) \right)$$

The $r_{\text{OX}}$ represents the distance between hydronium oxygen and Glu carboxylic oxygen/Lys amine nitrogen, and $r_{\text{HX}}$ represents the associated distance with the hydronium hydrogen. The vector $q_{\text{H},jX}$ is the proton-sharing vector defined as follows:
\[ q_{HjX} = r_{OHj} - \frac{1}{2} r_{OX} \]

where the atoms O and X follow the same definition as above, while \( H_j \) represents one of the three hydrogens of the hydronium structure. The \( B, b, b', C, c \) are tunable parameters, while \( d_{OX}^0 = 2.4 \) Å and \( d_{HX}^0 = 1.0 \) Å were fixed and do not need fitting since they can be absorbed into the prefactors \( B \) and \( C \).

As part of the MM FF, some of the nonbonded LJ interactions were tuned as well to better describe proton-transfer reactions. While the standard 12-6 LJ functional form was used as shown here:

\[ U_{LJ} = 4\epsilon \left[ \sigma \left( \frac{r}{\sigma} \right)^{12} - \left( \frac{r}{\sigma} \right)^6 \right] \]

the LJ parameters \( \sigma \) and \( \epsilon \) for interactions between the carboxyl/ammine and water/hydronium were adjusted. To be specific, the modified interactions were between eight atom pairs: (1) protonated Glu carboxyl oxygen (OEP) and water oxygen (Ow), (2) Glu carboxyl proton (HEP) and Ow, (3) deprotonated Glu carboxyl oxygen (OE) and hydronium oxygen (OH), (4) OE and hydronium proton (HH), (5) protonated Lys ammine nitrogen (NKP) and Ow, (6) protonated Lys ammine proton (HKP) and Ow, (7) deprotonated Lys ammine nitrogen (NK) and OH, and (8) NK and HH.

The off-diagonal energy term of \( h_{ij} \) between amino acid and water proposed in ref\(^6\) was used here as well:

\[ h_{ij} = c_1 \exp(-c_2(r_{HX} - c_3)^2) \]

The atom X represents the carboxyl oxygen or the ammine nitrogen, and the atom H represents the shared proton between Glu/Lys with water. The \( c_1, c_2, \) and \( c_3 \) were treated as trainable parameters.
**CDFT Theory.** CDFT has been well documented in the literature.\textsuperscript{13} As the name indicates, CDFT is essentially DFT with constraints:

\[
E^{\text{CDFT}} = \min_{\rho} \max_{\lambda} \left( E[\rho] + \lambda \left( \int \text{d}r \ w(r)\rho(r) - N \right) \right)
\]

which is a minimization problem with the constraint on the electronic density. The \( E[\rho] \) here is the density functional, and \( \lambda \) is the Lagrange multiplier. A constraint is defined by a weighting function \( w(r) \) and the target value \( N \):

\[
\int \text{d}r \ w(r)\rho(r) \equiv N
\]

In this work, the total Becke atomic charges on molecules were constrained and the associated weighting function adopted the following form:

\[
w(r) = \sum_{I} w_{I}^{\text{Becke}}(r)
\]

The Becke population function \( w_{I}^{\text{Becke}}(r) \) is a smooth indicator function which becomes unity when close to atom \( I \) and decays to zero when more distant. The constraint target number \( N \) was computed from the “promolecule” density \( \bar{\rho}(r) \):

\[
N = \int \text{d}r \ w(r)\bar{\rho}(r) = \int \text{d}r \ w(r)(\rho_{A}(r) + \rho_{B}(r))
\]

where \( \rho_{A} \) and \( \rho_{B} \) were the ground-state electronic density of the fragments A (identified as the protonated species) and B (identified as the remainder). Accordingly, the summation provided in eq 14 runs over all atoms in fragment A. As a result, eq 12 with the constraint in eq 13, seeks the diabatic state whose electronic structure mimics a direct superposition of a pure fragment A plus a pure fragment B.
Considering a system featuring one Glu/Lys sharing a proton with one water, two diabatic states can be defined: a protonated Glu/Lys plus a neutral water (denoted as $|1\rangle$), and a deprotonated Glu/Lys plus a hydronium (denoted as $|2\rangle$). To compute state $|1\rangle$ in CDFT, fragment A was defined as the Glu/Lys and fragment B was the water. In state $|2\rangle$, fragment A was the hydronium and fragment B was the negatively charged Glu/Lys. After obtaining the diabatic energies and wavefunctions, the ground state of the system can be expressed in the diabatic representation from a configuration interaction (CI) calculation:

$$H^{\text{CDFT}} c = E S c$$

where the CDFT Hamiltonian is composed of the CDFT diabatic energies and the couplings between diabatic states:

$$H^{\text{CDFT}} = \begin{pmatrix} E_1 & \langle \Psi_1 | \hat{H} | \Psi_2 \rangle \\ \langle \Psi_2 | \hat{H} | \Psi_1 \rangle & E_2 \end{pmatrix}$$

and the matrix $S$ describes the overlap between diabatic states:

$$S = \begin{pmatrix} 1 & \langle \Psi_1 | \Psi_2 \rangle \\ \langle \Psi_2 | \Psi_1 \rangle & 1 \end{pmatrix}$$

**Parametrization of MS-RMD Using CDFT.** The original FM-based MS-RMD parametrization was designed to minimize the force residual between ground-state MS-RMD forces and the ground-state *ab initio* forces $F$, such that

$$\chi^2 = \left( |F^{\text{RMD}} - F^{\text{QM}}|^2 \right)$$

where the bracket indicates some sort of ensemble average. The MS-RMD atomic forces $F^{\text{RMD}}$ are computed from the Hellmann-Feynman theorem (eq 4) and depend on the FF parameters noted
in the Force Field section. We note from eq 4 that the ground-state forces depend on the contributions from both ground-state wavefunction \( c \) and the diabatic forces \( F_{ij} \). The parametrization based solely on the ground-state force residual (eq 19) is likely to overfit due to the error cancellation in \( c \) and \( F_{ij} \). The rationale of our new approach is to separate the ground state wavefunction \( c \) and diabatic forces in the training procedure. Accordingly, two residuals, defined utilizing the diabatic information computed by CDFT, should be minimized with respect to MS-RMD parameters:

\[
\chi_c^2 = \left| c^{\text{RMD}} - c^{\text{CDFT}} \right|^2
\]

and

\[
\chi_F^2 = \sum_{ij} \left| F_{ij}^{\text{RMD}} - F_{ij}^{\text{CDFT}} \right|^2
\]

where the CDFT diabatic forces are defined as \( F_{ij}^{\text{CDFT}} = -\nabla H_{ij}^{\text{CDFT}} \). The residual eq 21 differs from eq 19 since the diabatic forces \( (F_{ij}) \) are compared individually instead of the comparison of the total ground-state force which is the \( c_i^2 \) weighted \( F_{ij} \) according to the Hellman-Feynman theorem.

We note that, as an eigenvector, the ground state wavefunction \( c^{\text{RMD}} \) and \( c^{\text{CDFT}} \) are determined by the diabatic energies in \( H^{\text{RMD}} \) and \( H^{\text{CDFT}} \), respectively. Thus, minimizing \( \chi_c^2 \) can be regarded as an implicit energy matching process. In this sense, the DM approach systematically matches the energy and force through minimization of \( \chi_c^2 \) and \( \chi_F^2 \), sequentially. This technique can be beneficial since it is reported that including both energy and forces in the loss function results in a more reliable machine-learned FF.\(^{37}\)

The multistate empirical valence bond (MS-EVB) version 3.2 model\(^{36}\) has been successful in describing the solvation and transport of an excess proton in pure water. Therefore, our
parametrization of MS-RMD kept the hydronium-water PT model unchanged, focusing instead on diagonal and off-diagonal terms that correspond to the proton transfer between Glu/Lys and its first solvation shell proton-acceptor water. The training set was generated by placing one water at $r_{oo}$ (distance between water oxygen and carboxyl oxygen of Glu) or $r_{on}$ (distance between water oxygen and amine nitrogen of Lys), ranging from 2.2 Å to 2.8 Å with a 0.1 Å spacing, and for each $r_{oo}$ or $r_{on}$, the shared proton was placed at nine equally spaced positions with $r_{oh}$ ranging from 1.0 Å to $r_{oo} - 1.0$ Å for Glu and $r_{nh}$ ranging from 1.0 Å to $r_{on} - 1.0$ Å for Lys. The CDFT calculations were based on these configurations at a DFT/basis-set level of BLYP/TZV2P or $\omega$B97X/TZV2P, followed by a CDFT-CI calculation performed using the DFT Kohn-Sham surrogates for the diabatic state wavefunctions. To reduce computational cost and achieve better convergence, the $\omega$B97X-level CDFT was carried out with Glu/Lys sidechains only. (We note that calculations that included backbones at the BLYP level showed no difference in $c$ from the sidechain-only ones.) All CDFT calculations were performed using the CP2K package.

Optimizing MS-RMD parameters was carried out using an in-house Python script to minimize the residual in eq 20 via the Nelder-Mead method$^{38}$ initiated from the previous MS-RMD model parameters$^6$ followed by a refinement by the Broyden–Fletcher–Goldfarb–Shanno (BFGS) method; all parameters thus obtained are summarized in Table 1. Due to the non-orthogonality of CDFT diabatic states, the $c^{CDFT}$ vector does not normalize to unity. However, since only the relatively stability of $|1\rangle$ and $|2\rangle$ matters in the fitting, we were able to achieve good agreement between $c^{RMD}$ and normalized $c^{CDFT}$ (see Figure S1) via directly minimizing eq 20. Note that the models obtained from minimizing eq 20 exhibited good accuracy and transferability even prior to applying further improvements using force residual eq 21, which is detailed in the Results and Discussion section below.
Simulation Details. The Glu/Lys in water simulations were conducted with one protonated solute solvated in 241 water for Glu and in 237 water for Lys in a cubic box with a side length of 20 Å. Temperature was controlled by a Nose-Hoover chain at 300 K, and a timestep of 1 fs was used to integrate the system. To enhance the sampling of proton disassociation from Glu/Lys, well-tempered metadynamics (WT-MTD) was performed. The RC for Glu driven in WT-MTD was defined as the distance between the excess proton CEC and the closer Glu carboxyl oxygen, implemented as

\[ \xi_{CEC}^{Glu} = -\frac{1}{\kappa} \log\left[ \exp\left( -\kappa (r_1 - \bar{r}) \right) + \exp\left( -\kappa (r_2 - \bar{r}) \right) \right] + \bar{r} \]

where \( \kappa = 40 \text{ Å}^{-1} \), \( r_1 \) and \( r_2 \) denote the CEC separation from the two carboxyl oxygen atoms, and \( \bar{r} = (r_1 + r_2)/2 \). The RC, \( \xi_{CEC}^{Lys} \) for Lys was the distance between CEC and amine nitrogen. The initial Gaussian height for WT-MTD was 0.8 kcal/mol, and the bias factor was set to 12. The Gaussians were deposited every 1 ps with a fixed width of 0.1 Å. To restrain the sampling in regions of interest, a harmonic potential soft wall with a 25 kcal/mol Å\(^{-2} \) force constant was added on the RC \( \xi_{CEC} \) if its value exceeded 8 Å. The WT-MTD was run for ~20 ns for both Glu and Lys, and the potential of mean force (PMF) was obtained by summing the deposited Gaussians. The error bar of the PMF was estimated by partitioning the full trajectory into 8 blocks and calculating the standard deviation of PMFs computed from the last 5 blocks.

The pK\(_a\) of Glu/Lys was computed from their PMFs via

\[ pK_a = \log\left( c_0 \int_0^{\dagger} 4\pi \xi_{CEC}^2 e^{-\beta(F(\xi_{CEC}) - F(\infty))} d\xi_{CEC} \right) \]

where \( c_0 = 1/1660 \text{ Å}^{-3} \) is the standard state concentration (1 M) expressed in number density, \( F(\xi_{CEC}) \) is the PMF, and \( F(\infty) \) is the value when \( \xi_{CEC} \) is sufficiently large and \( F(\xi_{CEC}) \) reaches a plateau. The integral was evaluated up to the dividing surface (denoted by \( \dagger \) ) between protonated
and deprotonated Glu/Lys. However, the integral value did not change if the integral went further because the free energy passing the dividing surface was sufficiently high for weak acids and the exponential integrand at further distances vanishes. Note that the $F(\xi_{\text{CEC}})$ used in $pK_a$ calculation (shown in Figure 2) differs from the PMF directly summed from Gaussians (denoted as $F'(\xi_{\text{CEC}})$) via the relation

$$4\pi \xi_{\text{CEC}}^2 e^{-\beta F(\xi_{\text{CEC}})} = e^{-\beta F'(\xi_{\text{CEC}})}$$

In essence, eq 24 converts the probability density for the system to visit $[\xi_{\text{CEC}}, \xi_{\text{CEC}} + d\xi_{\text{CEC}}]$ into the probability density of visiting the infinitesimal spherical shell $4\pi \xi_{\text{CEC}}^2 d\xi_{\text{CEC}}$. The resulting $F(\xi_{\text{CEC}})$ thus becomes a plateau with a sufficiently large $\xi_{\text{CEC}}$, in contrast to the behavior of $F'(\xi_{\text{CEC}})$ that reflects the increasing probability density in $[\xi_{\text{CEC}}, \xi_{\text{CEC}} + d\xi_{\text{CEC}}]$ due to the larger accessible volume of the $4\pi \xi_{\text{CEC}}^2 d\xi_{\text{CEC}}$ spherical shell.

Our simulations of SNase consisted of one SNase protein (PDB id: 1U9R) solvated in a cubic water box of 70 Å on a side with 0.15 M of sodium chloride added. A buried residue V66 was mutated into Glu/Lys to form the V66E and V66K mutants. For both the protonated and deprotonated E66/V66 mutants, classical MD equilibrations were conducted in the constant NPT ensemble at 298 K under 1 atm for 200 ns. The temperature and pressure were controlled by a Nose-Hoover chain and by the Parrinello-Rahman barostat, respectively. All the bonds involving hydrogens were constrained using the LINCS algorithm and a timestep of 2 fs was used to propagate the system. All classical equilibrations were carried out in the GROMACS MD package.

The SNase MS-RMD simulations, initiated from classical equilibrations, were conducted in NVT ensemble at 298 K using a timestep of 1 fs. The RC for proton disassociation from E66/K66 was defined as the same as the $\xi_{\text{CEC}}$ for Glu/Lys in water. A second RC $d_{\text{SC}}$ was defined as follows.
\[ d_{SC} = \mathbf{v}_{SC} \cdot \mathbf{n}_{prot} \]

to characterize the sidechain rotation of E66/K66, given that protonated/deprotonated forms of E66/K66 were found to display distinct sidechain orientations during classical equilibrations (Figure 3). In eq 25, \( \mathbf{v}_{SC} \) represents the vector pointing from E66/K66 \( \alpha \)-carbon to the geometric center of carboxylic group (COO) of E66 or the amine nitrogen of K66, and \( \mathbf{n}_{prot} \) is a vector defined to reflect the protein overall orientation:

\[ \mathbf{n}_{prot} = \frac{\mathbf{r}_{C2} - \mathbf{r}_{C1}}{|\mathbf{r}_{C2} - \mathbf{r}_{C1}|} \tag{26} \]

where \( \mathbf{r}_{C1} \) is the center of backbone atoms of residues 15-19 and 61-65, and \( \mathbf{r}_{C2} \) is the center of backbone of residues 90-94 (illustrated in Figure S2 of the Supporting Information). To restrain the lateral diffusion of the hydrated proton when completely dissociated from E66/K66, a harmonic potential soft wall \( u_{res} \) was added on a collective variable \( r_{\perp} \) defined as the length of the orthogonal part of \( \mathbf{v}_{CEC} \) with respect to \( \mathbf{n}_{prot} \):

\[ r_{\perp} = |\mathbf{v}_{CEC} - (\mathbf{v}_{CEC} \cdot \mathbf{n}_{prot})\mathbf{n}_{prot}| \tag{27} \]

where \( \mathbf{v}_{CEC} \) is the vector pointing from E66 COO center or K66 nitrogen to the CEC. The force constant of the wall was 10 kcal/mol/Å², and the restraining potential was switched on when \( r_{\perp} \geq 7 \) Å. To enhance the sampling of both \( \xi_{CEC} \) and \( d_{SC} \), two-dimensional umbrella sampling (2D-US) on the two RCs was performed. Each US window was run for \( \sim 1 \) ns and the total simulation time was \( \sim 1 \) μs for both V66E and V66K. The weighted histogram analysis method (WHAM)⁴⁶ was used to combine the 2D-US data and compute the PMF, \( F(\xi_{CEC}, d_{SC}) \), from which the one-dimensional (1D) PMF (Figure 3E) for proton dissociation was obtained by integrating out the \( d_{SC} \) degree of freedom (DOF). Specifically,

\[ F(\xi_{CEC}) = -\beta^{-1} \ln \left( \int e^{-\beta F(\xi_{CEC}, d_{SC})} d_{SC} \right) \tag{28} \]
Then, following the derivation in ref \(^47\), the pK\(_a\) of E66/K66 was given by

\[
pK_a = \log \left( c_0 S_u \int_0^\xi e^{-\beta (F(\xi_{CEC}) - F(+\infty))} d\xi_{CEC} \right)
\]

where the meaning of \(c_0\) and the integral range were the same as eq 23, and the \(S_u = \int_0^\infty 2\pi r_\perp e^{-\beta u_{res}(r_\perp)} dr_\perp\) corrects for the introduced radial restraint on CEC. The errors reported for PMFs and pK\(_a\) were obtained from partitioning the trajectories of all US windows into 6 equally sized blocks and calculating the standard deviation using the final 4 blocks. All MS-RMD simulations were performed using the LAMMPS MD package\(^48\) coupled with RAPTOR\(^4\) for reactions and PLUMED 2\(^49\) for the free energy sampling.
**RESULTS AND DISCUSSION**

**Benchmark of Reactive Models in Water.** The MS-RMD parameters obtained using the DM approach with ωB97X CDFT data are provided in Table 1, and model parameters determined from the BLYP data are given in Table S1. The resulting MS-RMD Glu/Lys models were benchmarked in water by computing the PMF of their ionization (Figure 2).
The potential of mean force (PMF) contains arguably the most valuable information about the system as it provides the full free energy profile as a function of the reaction progress (monitored by the RC value). At \( \xi_{\text{CEC}} \approx 0.5 \, \text{Å} \), a narrow and deep free energy well was observed in both the Glu and Lys PMFs. The molecular configurations corresponding to the well are protonated Glu/Lys (Figure 2 insets), and this well in the PMF reveals the weak acid nature of both Glu and Lys. The steep wall at \( \xi_{\text{CEC}} < 0.5 \, \text{Å} \) is caused by the large energy penalty of compressing O-H/N-H bond of Glu/Lys. The smooth uphill increase in the region of \( 0.5 \, \text{Å} < \xi_{\text{CEC}} < 1.4 \, \text{Å} \) arises from the energy barrier of proton disassociation from Glu/Lys to its first solvation shell water. The free energy was observed to reach a peak at around 1.4 Å, the point at which the proton is shared by Glu/Lys and the water, forming a Glu/Lys-replaced Zundel (H\(_5\)O\(_2^+\)) configuration (Figure 2 insets). The second free energy well was noted at \( \xi_{\text{CEC}} \approx 2.3 \, \text{Å} \) when the excess proton is found within the first solvation shell water. The resulting H\(_3\)O\(^+\) and negatively charged Glu closely interact with each other to form a contact ion pair (CIP) (Figure 2A inset). The favorable Coulombic interaction yields a deeper potential well for Glu compared to that of Lys. In the latter case, a CIP cannot be formed between a neutral deprotonated Lys and H\(_3\)O\(^+\), but the system is stabilized by forming an Eigen cation (H\(_3\)O\(^+\) (H\(_2\)O)\(_3\)) with one water substituted by the Lys (Figure 2B inset).

It is seen that a second free energy potential well at around 2.3 Å is shallower within the \( \omega \)B97X model in comparison with that of the BLYP model, which is consistent with the expectation that the GGA functional BLYP over-stabilizes the CIP due to its overestimation of charge transfer compared with the hybrid functional \( \omega \)B97X. After moving beyond that well, the value of the free energy increases within the range of \( 2.3 \, \text{Å} < \xi_{\text{CEC}} < 4 \, \text{Å} \), which corresponds to proton dissociation from the first shell water. Although the excess proton mostly resides on a
second shell water when $\xi_{\text{CEC}} \approx 4$ Å (Figure 2 insets), this layer of water is sufficiently diffusive to become indistinguishable from bulk water, given that both PMFs reach a plateau after this point.

Table 1. Optimized MS-RMD Model Parameters Using $\omega$B97X CDFT Data.

|        | Glu       | Lys       | Glu       | Lys       |
|--------|-----------|-----------|-----------|-----------|
| $B$    | 3.94793   | 1.01096   | -153.284  | -67.0979  |
| $b$    | 1.41638   | 1.41969   | 0.23117   | 0.0175896 |
| $b'$   | 1.08444   | 1.07948   | 1.39561   | 1.68765   |
| $C$    | 3.8605    | 0.989666  | 0.72595   | 0.0107436 |
| $c$    | 1.14669   | 1.14233   | 1.29196   | 1.77364   |
| $c_1$  | -25.0422  | -25.015   | 0.125249  | 0.115627  |
| $c_2$  | 2.99968   | 3.02538   | 3.00742   | 3.20591   |
| $c_3$  | 1.40533   | 1.37087   | 0.162054  | 0.162548  |
| $D$    | 143.003   | 157.014   | 3.07772   | 3.23758   |
| $\alpha$ | 1.8       | 1.70825   |           |           |
| $r_0$  | 0.975     | 1.02389   |           |           |

The units of the listed parameters use kcal/mol as the energy unit and Å as the length unit. The Glu Morse bond parameters were taken from ref6.

For a direct comparison with the experimental results, we calculated the $pK_a$ of Glu and Lys in water from the PMF using eq 23. The resulting data are summarized in Table 2. We found that the $\omega$B97X models accurately predicted the $pK_a$ values for both Glu and Lys. By contrast, our results based on the BLYP models were rather less accurate, but still within ~1 pH unit of error. It is important to note that these MS-RMD models were not fit in the aqueous phase; rather, we fit
the parameters from gas phase CDFT calculations and transferred that model to the bulk water environment.

Table 2. MS-RMD Predicted and Experimental pKₐ values of Glu and Lys.

|        | In Water | In SNase V66 Mutants |
|--------|----------|----------------------|
| Glu    |          |                      |
|        | Simulation (ωB97X) | 4.1±0.2 | 9.8±0.3<sup>a</sup> |
|        | Simulation (BLYP)  | 3.4±0.4 |                      |
|        | Experiment       | 4.15<sup>b</sup> | 9.00-9.10<sup>c</sup> (8.73-9.28<sup>d</sup>) |
| Lys    |          |                      |
|        | Simulation (ωB97X) | 10.7±0.2 | 5.8±0.3<sup>a</sup> |
|        | Simulation (BLYP)  | 10.0±0.1 |                      |
|        | Experiment       | 10.67<sup>b</sup> | 5.61-6.05<sup>e</sup> (6.25-6.45<sup>f</sup>) |

<sup>a</sup> The PDB structure (1U9R) used in the simulation was the PHS form of SNase (engineered with three substitutions: P117G, H124A, and S128L). Note that the missing 45-50 loop in the solved structure was not modeled in our simulations, and thus the simulated system more resembles the Δ+PHS form (additional G50F, V51N and 44-49 deletion from PHS).

<sup>b</sup> Taken from ref<sup>50</sup>.

<sup>c</sup> pKₐ in Δ+PHS by potentiometry taken from ref<sup>51</sup>.

<sup>d</sup> pKₐ in PHS from chemical denaturation taken from ref<sup>51</sup>.

<sup>e</sup> pKₐ in Δ+PHS from chemical denaturation taken from ref<sup>52</sup>.

<sup>f</sup> pKₐ in PHS by potentiometry take from ref<sup>53</sup>.

This success of the DM-based MS-RMD models encouraged us to apply them to the more complicated aqueous protein system, SNase, without reparameterization and in a directly transferable manner. Given that the ω B97X models showed better agreement with the experimental pKₐ in water than the BLYP models, the latter models were not implemented in the subsequent SNase simulations.
Figure 3. The coupling between proton dissociation and sidechain orientation in SNase. (A) Classical equilibrated configurations of V66E mutants when E66 is deprotonated (green) and protonated (gray). (B) The potential of mean force in kcal/mol of E66 ionization and its sidechain rotation. The minimum free energy path is shown as a black curve. The PMF statistical error can be found in Figure S3A of the Supporting Information. (C) Classical equilibrated configurations of V66K mutants when K66 is deprotonated (green) and protonated (gray). (D) The PMF of K66 ionization and its sidechain rotation. The minimum free energy path is shown in black. The PMF error can be found in Figure S3B of the Supporting Information. (E) Comparison of ionization PMFs of Glu (red) and Lys (blue) in water (dashed) and in SNase (solid; computed via eq 29).

**Benchmark of Reactive Models in SNase.** SNase is a well-known protein model system for studying titration $pK_a$ values of internal ionizable groups, including many different mutants.$^{51-53}$ Several SNase mutants have been generated by focusing on one of the buried hydrophobic residues, V66, and substituting it with Asp, Glu and Lys. The $pK_a$ of the mutated residue has been measured experimentally and large $pK_a$ shifts were observed in favor of the neutral forms of the residues.$^{51-53}$ Therefore, the SNase mutants provide an ideal and well-characterized protein environment for benchmarking our reactive MD models against experimental observations.

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Classical equilibration simulations of the V66E and V66K mutants were performed for both protonated and deprotonated forms of E66 and K66. For the neutral form of E66 (deprotonated) and K66 (protonated), the residue adopted a buried conformation, while a charged E66/K66 was found to be exposed to water through the rotation of its sidechain to stabilize its charge in the more highly polarizable medium (Figure 3A & Figure 3C). This observation is consistent with the experimental pKₐ shifts for Glu and Lys toward stabilizing a neutral form.

Considering the distinct conformations that are dependent on the protonation state, a RC, $d_{SC}$, reflecting sidechain orientation was defined as noted earlier and explicitly sampled along with the proton dissociation RC, $\xi_{CEC}$, which describes proton disassociation in the reactive 2D-US (see Simulation Details for details). The next section provides a detailed discussion of these informative 2D PMF findings (Figure 3B & Figure 3D) calculated by 2D-US, but we first discuss the pKₐ values of E66 and K66 as calculated from the PMFs (Figure 3E). According to Table 2, the calculated pKₐ values were found to be in very good agreement with those of their experimentally determined counterparts, again with no reparameterization of the DM MS-RMD model beyond that done in the gas phase. We found the agreement with the experimental results was closer for the Lys model, which shows an excellent match. The Lys and Glu models were parametrized following the same procedure, except that the Morse bond of Lys was fit to a gas-phase energy scan, while Glu was taken from our previous work,⁶ where the bond parameters were chosen to fit the original CHARMM harmonic bond potential. The better performance of our Lys model suggests that the current Glu model may be readily improved by a bond energy scan followed by a reparameterization. Notably, we used the exactly same MS-RMD parameters of Glu/Lys in water when simulating SNase, and even still the MS-RMD models demonstrated high accuracy and transferability in predicting the acidic and basic residue pKₐ values in these distinct environments.
**Proton Transport and Conformation Coupling in SNase.** As discussed in the prior section, we compared the predicted $pK_a$ values with the experimental values. It is worth noting that a reactive MD model is not only useful for calculating reaction equilibrium constants, but it can also predict reaction rates when combined with appropriate kinetic theory and modeling, such as activated rate theory\(^{54}\) or a more complex Markov state model\(^{55}\). More importantly, atomistic details obtained from reactive MD simulations enable a detailed exploration of the reaction mechanisms, as well as the identification of crucial factors and interactions affecting the mechanism. In terms of SNase, an important question arises regarding how the proton transport is coupled with the protein conformations. As discussed earlier, the classical equilibrium data indicate that the sidechain orientation of E66/K66 depends on its protonation state. However, in the absence of knowledge of the explicit reaction pathways, classical simulations can only determine the metastable basin states. In contrast, reactive MD can reveal whether the sidechain rotation facilitates the protonation/deprotonation process or is instead a result of the amino acid conformation responding to a protonation state change. Interestingly, the answer is likely neither alone according to our 2D PMF results (Figure 3B and Figure 3D). The most probable reaction pathway (or, equivalently, the minimum free energy path; MFEP) shows that the protonation dissociation and the sidechain rotation are not two independent processes that happen in a stepwise manner. Instead, these two processes are highly and reciprocally coupled, which can be verified by the ramped slope of the MFEP connecting the two end points of the charged, exposed E66/K66 state and the neutral buried state. It is worth noting that the coupling between $\xi_{CEC}$ and $d_{SC}$ in the V66E mutant is the highest in the range $\xi_{CEC} < 4 \text{ Å}$, while the MFEP passing $\xi_{CEC} = 4 \text{ Å}$ has a flatter shape. The strong coupling in the proton dissociation/association region is attributed to the solvation penalty of both
a buried charged Glu and the hydrated excess proton. In contrast, the V66K mutant exhibits a weaker coupling in the proton dissociation phase because the charged Lys adopts a water-exposed position that provides the solvation environment for the dissociated excess proton. Due to the ramped slope of the MFEP, if the PT degree of freedom $\xi_{\text{CEC}}$ is driven by some external force such as a proton gradient, and if this driving is a quasistatic process, then the movement of $\xi_{\text{CEC}}$ will result in a response of the movement in $d_{\text{SC}}$ along the curvy MFEP (and vice-versa). Importantly, in addition to the sidechain orientation observed in this study, we found in our previous work that this type of coupling typically occurs between PT and water hydration in confined hydrophobic spaces of proteins and other materials.8, 10, 12, 30, 56 This outcome may also be the case for PT and ligand transport in some proton-driven transporters; indeed, if this is the case then it is understandable why the excess proton and the ligand can exhibit a coupled driving force for the transport.

**CONCLUSIONS**

As a generalization to the previous FM MS-RMD approach, we have presented here a DM framework to systematically parameterize reactive MD models from CDFT. We used the proton dissociation reactions of Glu and Lys as our case studies and found the DM-based models can reproduce the experimental absolute $pK_a$ of the acid and the basic amino acid in water. We also confirmed that the same reactive MD models were able to accurately capture the large $pK_a$ shifts introduced by the apolar SNase protein environment. In addition, the efficiency of the reactive MD enabled us to compute the joint free energy surface of the excess proton CEC coordinate, along with the sidechain orientation of E66/K66, from which we discovered that PT is coupled to this local conformational change. As such, the two processes can be considered as mutually
cooperative, in contrast to being a sequential process whereby the protonation state change occurs either before or after a conformational change. Since the results indicate that our models are transferable, we believe they can likely be readily applied to other biomolecular and biomaterial systems. Moreover, the noted efficiency of these MS-RMD models can facilitate the discovery of other protein motions and degrees of freedom coupled to the PT process, such as hydration, global conformational change, and ligand transport. Finally, we anticipate that the DM MS-RMD approach can provide a potentially powerful tool for developing accurate and transferrable reactive MD models for other chemical reactions in the future.

ASSOCIATED CONTENT

Supporting Information. The Supporting Information is available free of charge. An additional table of the optimized MS-RMD model parameters using BLYP CDFT data, additional figures showing the fitted MS-RMD model wavefunction $c$, illustrating the reactive coordinate definitions in SNase, and showing the statistical errors in PMFs of SNase.

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Author Contributions

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

ACKNOWLEDGMENTS
This research was supported in part by the National Institute of General Medical Sciences (NIGMS) of the U.S. National Institutes of Health (NIH) through grant R01 GM053148 and in part by the U.S. Department of Energy (DOE), Office of Basic Energy Sciences, Separation Science Program of the Division of Chemical Sciences, Geosciences, and Biosciences under Award Number DE-SC0018648. Computational resources were provided by the Research Computing Center (RCC) at the University of Chicago. The authors appreciate insightful discussions with Dr. Xinyou Ma.
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Minimize $\chi^2 = \left| c^{\text{MS-RMD}} - c^{\text{CDPT}} \right|^2$