

Accurately Predicting CO₂ Reactive Absorption Properties in Aqueous Alkanolamine Solutions by Molecular Simulation Requiring No Solvent Experimental Data

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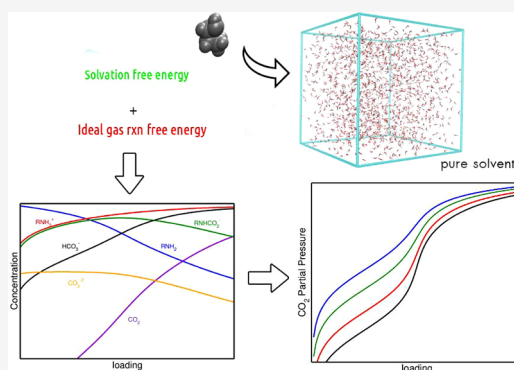


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ABSTRACT: We present a general atomistic simulation framework for efficient reactive equilibrium calculations in dilute solutions, and its application to CO₂ reactive absorption in aqueous alkanolamine solutions. No experimental data of any kind are required for the solvents, and no empirical adjustments are required for its implementation. This hybrid methodology calculates reaction equilibrium constants by combining high-level quantum chemical calculations of ideal-gas standard reaction Gibbs energies (ΔG^0) with conventional solvation free energy calculations obtained from classical force field methodology. For these quantities we use explicit solvent molecular dynamics simulations with the General AMBER Force Field (GAFF). The resulting equilibrium constants are then coupled with a macroscopic Henry Law based ideal solution model to calculate the solution speciation and the CO₂ partial pressure, P_{CO_2} . We show results for seven primary amines: monoethanolamine (MEA), 2-amino-2-methylpropanol (AMP), 1-amino-2-propanol (1-AP), 2-amino-2-methyl-1,3-propanediol (AMPD), 2-aminopropane-1,3-diol (SAPD), 2-(2-aminoethoxy)ethanol or diglycolamine (2-AEE or DGA, respectively), and 2-amino-1-propanol (2-AP). Experimental speciation and P_{CO_2} data for some of these are available, with which we validate our methodology. We predict new results for others in cases when such data are unavailable, and provide explanations for the experimental inability to detect carbamate solution species in relevant cases. Our results for the pK value of the carbamate reversion reaction are within the chemical accuracy limit of 218.546/ T units (corresponding to 1 kcal·mol⁻¹ in the corresponding free energy change) in comparison with experimental results when such data exist, which at 298.15 K corresponds to 0.73 pK units. The precision of our pK predictions is comparable to that which can be obtained from conventional experimental methodologies for these quantities. Our results suggest that the presented molecular simulation methodology may provide a robust and cost-efficient tool for solvent screening in the design of post-combustion CO₂ capture processes.



1. INTRODUCTION

Increasing atmospheric concentrations of CO₂ and other greenhouse gases and their consequent environmental effects have prompted a large body of research probing the CO₂ capturing properties of adsorbing materials and absorbing chemical solvents. Carbon capture and storage (CCS) is considered to be one of the most viable short-term options for reducing global carbon emissions.^{1,2} Chemical absorption using aqueous alkanolamine solutions currently being used in industry are considered one of the most mature options for large-scale CO₂ capture.³ However, the capture process suffers from several drawbacks, including high solvent regeneration energy costs, as a result of both parasitic energy losses, due to the high latent heat of the water cosolvent, and formation of the thermally stable carbamates, which also result in poor cyclic capacity.⁴ In order to circumvent these problems, various alternative solvents, such as nonaqueous solvents,⁵ lipophilic amines,⁶ and phase changing compounds⁷ have been recently considered. Unravelling the

effects of different functional groups in the amine structures on their behavior is crucial for the design of improved alkanolamine-based CO₂ solvents. For example, heavily hindered alkanolamines have been shown to reversibly absorb CO₂ in an equimolar ratio and CO₂ can be completely desorbed at relatively low regeneration temperatures.⁸

The CO₂ capturing properties of the absorbent are a consequence of the kinetic and chemical reaction equilibrium properties resulting from the CO₂ dissolution, and the equilibrium composition of CO₂ in the solvent is an important tool for solvent screening. In the case of primary and secondary

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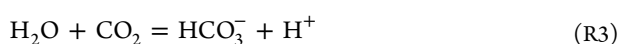
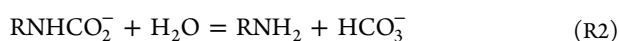
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amines, CO₂ is absorbed primarily in the solution in the form of the carbamate (RNHCO₂⁻), bicarbonate (HCO₃⁻), and carbonate (CO₃⁻²) species, in coexistence with the neutral (RNH₂) and protonated (RNH₃⁺) amine species, water and its ionization products, and free CO₂.

The set of linearly independent chemical equations used to model chemical reaction equilibrium is governed only by the requirement that their number is $R = N - \text{rank}(\mathbf{A})$, where N is the number of species and \mathbf{A} is the species formula matrix.⁹ The actual set of reactions used need not be related to any postulated or actual reaction mechanics, and may be motivated by computational convenience. The following stoichiometry provides a convenient thermodynamic basis for describing the reaction equilibria of the indicated species in the case of primary and secondary amines.



Tertiary amines do not form carbamates, and for these reactions R1 and R2 can be replaced by their sum



The equilibrium constants (or equivalently, the pK values) for reactions R3–R5 as functions of temperature are experimentally well-known. Their experimental determination for reactions R1 and R2 requires experimental data for each postulated solvent. Furthermore, the equilibrium constants can only be determined indirectly from such data, by fitting to the parameters of an empirically based chemical potential model.

pK values have been determined in this way by fitting to potentiometric titration measurements for the carbamate reversion reaction R2,¹⁰ and for the amine protonation reaction,^{10–16} which is the linear combination R1 + R2 – R3.



pK values have also been obtained by fitting thermodynamic models to experimental spectroscopically obtained speciation data of CO₂-loaded solutions.^{17–21} In such experimental studies, the presence of the fast proton-exchanging species (*i.e.*, the CO₃⁻²/HCO₃⁻ or (RNH₃⁺/RNH₂) pairs) complicates the data analysis, and usually only the total concentration of the carbonate/bicarbonate pair is available and can be used in the parameter fitting. Finally, parameters of chemical potential models and/or equations of state have been fitted to reaction models of CO₂ solubility data.²² In other cases, the reactions have been approximated by pseudo-reaction physical association models incorporated in the SAFT^{23–26} or the CPA^{27,28} approaches.

Experimental screening of the vast number of potential solvent candidates is prohibitively expensive and time-consuming, and more predictive and less costly computational tools offer a promising alternative and complementary approach. The ability to accurately predict the equilibrium speciation and the associated CO₂ partial pressure for CO₂-loaded solutions of

candidate solvents is one of the most important requirements, which is very challenging due to the complex chemical reaction and phase equilibria involved.

Three general approaches have been used toward this goal: combined Electronic Structure (ES) dielectric continuum solvent (DCS) models, *ab initio* Molecular dynamics (MD) methods, and classical force-field (CFF) methodologies. The first group includes methods based on the Conductor-like Screening Model for Realistic Solvents (COSMO-RS)^{29,30} and Solvation Models based on Density (SMD).³¹ These have been used to study reaction mechanisms and the relative stability of the carbamate product species.^{32–35} Alternative DCS methods such as the SMDx family of Cramer et al.,³¹ usually trained on hydration free energy data of neutral molecules at 298.15 K, may be potentially applied to such systems; however, their extension to ionic species and to higher temperatures has not been fully tested. Whereas the deficiencies of the continuum solvation models can be partially overcome by incorporating explicit solvent molecules in the first solvation shell,³⁶ their application to flexible molecules is not straightforward.³⁷

In the second group, Nakai et al.^{38–40} used density-functional tight-binding MD simulations to study reaction mechanisms in CO₂ chemical absorption and regeneration processes in aqueous amine solutions. While such approaches do not require *a priori* knowledge of the identities of the product species, they require detailed geometric criteria to dynamically evaluate their chemical identity and population at each step of the MD simulation. Moreover, such *ab initio* methods have only been carried out for relatively small system sizes and scale poorly with the system size, making them highly inefficient for the high throughput CO₂ solvent screening task. Other *ab initio* approaches based on first-principles calculations have also been developed and used for speciation predictions in reactive systems,⁴¹ and they share the same disadvantages.

CFF methodologies have been employed by the groups of Vlugt et al.,⁴² Maginn et al.,⁴³ and our group.^{44,45} Balaji et al.⁴² used the Reaction Ensemble (REMC) algorithm^{46,47} (see also Johnson et al.⁴⁸) in conjunction separately obtained ideal-gas electronic structure (ES) free energy calculations and fractional insertion of molecular species, in a preliminary study of reaction equilibria in the MEA–CO₂–H₂O system. Although the REMC algorithm was incorrectly implemented (by omitting the atomization energies in the ideal-gas ES calculations⁴⁴), it was fortuitously able to reasonably predict the most abundant species (but not those present in minor concentrations) in the system at low to moderate CO₂ loadings. Mullen et al.⁴³ applied the REMC algorithm in conjunction with an enhanced Monte Carlo sampling approach for CO₂ absorption in a reactive ionic liquid. MC-based approaches for complex systems such as those involved in CO₂ reactive absorption generally suffer from the computational disadvantage in the case of even moderately complex molecules of requiring special system-specific sampling moves; they also require very long computation times and/or large system sizes to deal with the concentrations of species present in small amounts. These drawbacks make the REMC approach inefficient for their use in solvent screening.

Based on a recently developed reaction equilibrium algorithm requiring only straightforward conventional CFF-based MD free energy calculations, coupled with ES ideal-gas ES free energy calculations,⁴⁹ we recently implemented⁴⁴ a general and computationally efficient reaction equilibrium algorithm to predict speciation concentrations (including for species present

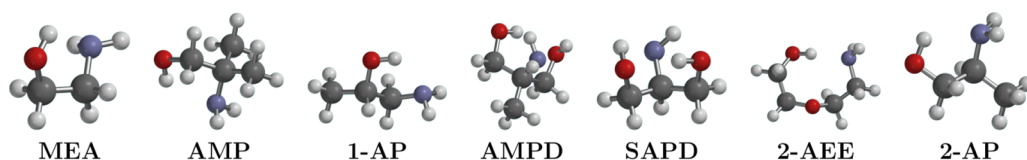


Figure 1. Molecular structures of the studied alkanolamines.

in very small concentrations) and P_{CO_2} in a preliminary study in the case of the benchmark CO_2 –MEA– H_2O system.

The goal of this paper is to improve this CFF-based methodology and to illustrate its application to the accurate prediction of CO_2 reactive absorption speciation and P_{CO_2} data as functions of loading, temperature, and solvent composition, for aqueous MEA and for six additional primary alkanolamine systems, whose molecular structures are shown in Figure 1. Where experimental data are available, we compare our predictions with experimentally obtained P_{CO_2} and solution speciation data in the literature. For situations in which experimental data are unavailable, our calculations provide predictions that await experimental verification.

2. MOLECULAR-BASED THERMODYNAMIC METHODOLOGY

A major challenge in implementing reaction equilibrium calculations from molecular simulations is the expression of the macroscopic thermodynamic models involved in terms of molecular simulation quantities. These little known relationships are briefly described in this section.

The equilibrium composition of a closed chemically reacting system at specified (T, P) can be obtained by minimizing its Gibbs free energy subject to the conservation of mass and electroneutrality constraints, and implemented by calculating the solution of the R equations

$$\Delta G_j(T, P; \mathbf{x}) \equiv \sum_{i=1}^{N_i} \nu_{ij} \mu_i(T, P; \mathbf{x}) = 0; \quad j = 1, 2, \dots, R \quad (1)$$

where ν_{ij} is the stoichiometric coefficient of species i in reaction j and \mathbf{x} represents the system composition vector. The reaction equilibrium composition can be readily accomplished by a wide range of numerical algorithms⁹ and chemical potential models, and we employ here a Henry Law based model. The chemical potentials (for both solutes and solvent) in this model are expressed as

$$\begin{aligned} \mu_i(T, P; \mathbf{m}) &= \mu_i^\dagger(T; P) + RT \ln \left(\frac{m_i}{m^0} \right) \\ &+ RT \ln \gamma_i(T, P; \mathbf{m}); \quad i = 1, 2, \dots, N_{\text{solv}} \end{aligned} \quad (2)$$

where T is the absolute temperature, P is the pressure, R is the universal gas constant, m_i is the molality of species i , γ_i is its Henry Law activity coefficient, and \mathbf{m} is the vector of species molalities. $m^0 = 1 \text{ mol} \cdot \text{kg}^{-1}$ solvent.

We have previously shown⁵⁰ that the standard chemical potential $\mu_i^\dagger(T; P)$ of solute species i can be calculated in terms of molecular simulation quantities by

$$\begin{aligned} \mu_i^\dagger(T, P) &= \mu_i^0(T; P^0) + RT \ln \left(\frac{RT M_{\text{solv}} m^0 \rho_{\text{solv}}^*(T, P)}{1000 P^0} \right) \\ &+ \mu_i^{\text{res}, \text{NVT}; \infty}[T, \rho_{\text{solv}}^*(T, P)] \end{aligned} \quad (3)$$

where $P^0 = 1 \text{ bar}$ is the standard state pressure and $\mu_i^0(T; P^0)$ is the ideal gas chemical potential of species i , which can be calculated from the partition function of its ideal-gas molecule under the harmonic oscillator rigid rotor approximation,^{51,52} $\rho_{\text{solv}}^*(T, P)$ is the density of the pure solvent (water in our case), M_{solv} is its molecular weight, and $m^0 = 1 \text{ mol} \cdot \text{kg}^{-1}$ solvent. For a solute, $\mu_i^{\text{res}, \text{NVT}; \infty}[T, \rho_{\text{solv}}^*(T, P)]$ is its residual chemical potential at infinite dilution in the solvent (also referred to as its intrinsic hydration free energy, $\Delta G_{\text{hyd}}(T, P)$), and the same quantity for the solvent is its self-solvation free energy; both are calculated by conventional MD simulations in the NVT ensemble.

In the following, we restrict attention to the ideal solution approximation, $\gamma_i = 1$ (expressions for the nonideal case are given in our previous paper⁴⁴). The solvent chemical potential is obtained from the Gibbs–Duhem equation as⁴⁴

$$\begin{aligned} \mu_{\text{solv}}(T, P; \mathbf{m}) &= \mu_{\text{solv}}^\dagger(T; P) + RT \ln \left(\frac{1000}{M_{\text{solv}} m^0} \right) \\ &- RT \left(\frac{1 - x_{\text{solv}}}{x_{\text{solv}}} \right) \end{aligned} \quad (4)$$

We remark that, for reactions in which the solvent (here water) participates, the solvent chemical potential is typically approximated in experimental studies by its Raoult Law form

$$\mu_{\text{solv}}(T, P; \mathbf{m}) = \mu_{\text{solv}}^*(T, P) + RT \ln(x_{\text{solv}}) \quad (5)$$

where $\mu_{\text{solv}}^*(T, P)$ is the pure solvent chemical potential and x_{solv} is its mole fraction. Substitution of eqs 2–4 in eq 1 yields the final working equations:

$$\begin{aligned} \frac{\Delta \tilde{G}_j(T, P)}{RT} + \sum_{i=1}^{N_{\text{solv}}} \nu_{ij} \ln \left(\frac{m_i}{m^0} \right) \\ + \nu_{\text{solv}, j} \left(\frac{x_{\text{solv}} - 1}{x_{\text{solv}}} \right) = 0; \quad j = 1, 2, \dots, R \end{aligned} \quad (6)$$

where $\nu_{\text{solv}, j}$ is the stoichiometric coefficient of the solvent in reaction j , and

$$\Delta \tilde{G}_j(T, P) = \Delta G_j^0(T; P^0) + \Delta G_j^{\text{res}, \text{NVT}; \infty}(T, P) \quad (7)$$

$$\begin{aligned} + RT \bar{V}_j \ln \left(\frac{RT M_{\text{solv}} m^0 \rho_{\text{solv}}^*(T, P)}{1000 P^0} \right) + \nu_{\text{solv}, j} RT \ln \left(\frac{1000}{M_{\text{solv}} m^0} \right) \end{aligned} \quad (8)$$

where

$$\Delta G_j^0(T; P^0) = \sum_{i=1}^{N_i} \nu_{ij} \mu_i^0(T; P^0) \quad (9)$$

$$\Delta G_j^{\text{res}, \text{NVT}; \infty}(T, P) = \sum_{i=1}^{N_i} \nu_{ij} \mu_i^{\text{res}, \text{NVT}; \infty}(T; P) \quad (10)$$

$$\bar{\nu}_j = \sum_{i=1}^{N_i} \nu_{ij} \quad (11)$$

$\Delta \tilde{G}_j(T, P)$ is commonly expressed in terms of the equilibrium constant K_j via

$$\text{p}K_j(T, P) \equiv -\log_{10} K_j = \frac{\Delta \tilde{G}_j(T, P)}{RT \ln(10)} \quad (12)$$

We remark that the third term in eq 8 can be separated into a temperature-dependent term (often referred to as the “standard state correction”) and a density term, which is often mistakenly neglected in pK calculations (see Noroozi and Smith⁴⁵).

3. SIMULATION DETAILS

3.1. Ideal-Gas Reaction Free Energies. In order to find the most stable conformer of the molecular/ionic species, an extensive gas phase conformational search was first performed for the geometries of the protonated, carbamate, and neutral forms of each amine using the Merck Molecular Mechanics Force Field (MMFF94) implemented in the Spartan v.18 Software package.⁵³ For each species, for each of the 10 lowest energy conformers obtained from this search we performed further geometry optimizations to find the lowest free energy conformers arising from five different high-level composite quantum chemical (QM) methods: G4, G3, G3B3, CBS-QB3, and CBS-APNO in Gaussian16.⁵⁴ We ensured that, for each QM method, the conformer converged to a stable minimum of the potential energy surface with positive real vibrational frequencies. We then used the conformer with the lowest free energy/chemical potential for the subsequent ideal-gas reaction free energy calculations for each of the five QM methods. The combination of the results of these five methods is described in the Results and Discussion section.

3.2. Force Field Development and Hydration Free Energy Calculations. For the amine's neutral (RNH_2), protonated (RNH_3^+), and carbamate (RNHCO_2^-) forms, and for the bicarbonate ion (HCO_3^-), the Lennard–Jones (LJ) and intramolecular bonded (bond stretching, angle bending, and dihedral torsion) potential parameters of the force fields were modeled in a consistent manner using the General Amber Force Field⁵⁵ parameters within its default functional form by using the Antechamber package in AMBER tools,⁵⁶ which employs an algorithm to assign the parameters based on the atom types. Carbon dioxide (CO_2) was modeled using the TraPPE potential of Pottorf,⁵⁷ and to be consistent with GAFF parametrization the solvent (water) was modeled with the TIP3P Force Field.

To calculate the partial charges, high-level QM methods are generally preferred to refine the geometry of the lowest-energy solute conformer as described in the previous section. However, to be consistent with the ideal-gas geometry of the force fields in the hydration free energy calculations, we used the lowest free energy conformer at the G4 level of the previous section as representative of the solute gas-phase geometry to calculate its electrostatic potential energy grid at the GAFF default HF/6-

31G* level using the Merz–Kollman scheme in Gaussian16. We also examined the effects of determining the partial charges from several different QM electron density determination methodologies (B3LYP/6-311++G(d,p), MP2/aug-cc pVTZ, and MP2/aug-cc pVTZ+PCM) on the resulting hydration free energies and the equilibrium constants, which is discussed in Section 4.3.

Finally, we used the two-step Restrained Electrostatic Surface Potential (RESP) fitting method⁵⁸ within the Antechamber software package to assign the partial charges. The Gromacs-formatted topologies were then generated using the acpype (version 2019) python interface.⁵⁹

MD simulations of the hydration free energies in eq 11 were performed using a single solute molecule solvated in a periodic box of 1500 water molecules using the Gromacs (version 2016.3) program,⁶⁰ with initial configurations generated using the packmol software package.⁶¹ A steepest-descent minimization was then performed to remove any bad contacts, followed by a short (100 ps) NVT equilibration run followed by a 12 ns NPT simulation with the first 2 ns discarded to determine the system density. Free energy simulations to decouple the solute molecule from its solvent environment were then initiated from the equilibrated configurations in an NVT ensemble, with the box size corresponding to the calculated density.

The equations of motion were integrated using the Gromacs stochastic Langevin scheme, with a friction constant of 1.0 ps^{-1} . The pressure was maintained using a Parrinello–Rahman pressure coupling constant of 2.0 ps. The Lennard–Jones short-range interactions were smoothly switched off between 12 and 12.5 Å, and the electrostatic interactions were computed using the particle mesh Ewald (PME) method with a 12 Å real-space cutoff, 1.0 Å grid spacing, sixth-order spline interpolation, and accuracy of 10^{-6} . The free energy of decoupling the solute molecule from its solvent environment was calculated using the Gromacs Bennett Acceptance Ratio (BAR) method (gmx bar). We employed six equally spaced λ values and linear decoupling for the electrostatic interaction, followed by 20 equally spaced λ values with $\Delta\lambda = 0.05$ to decouple the LJ interactions using the standard GROMACS soft-core potential function originally proposed by Beutler et al.,⁶² with parameters (in GROMACS notation) $sc\text{-}\alpha = 0.5$, $sc\text{-}\text{power} = 1$ and $sc\text{-}\sigma = 0.3$. For each alchemical window, we used a 12.5 ns simulation with the first 2.5 ns discarded for equilibration.

4. RESULTS AND DISCUSSION

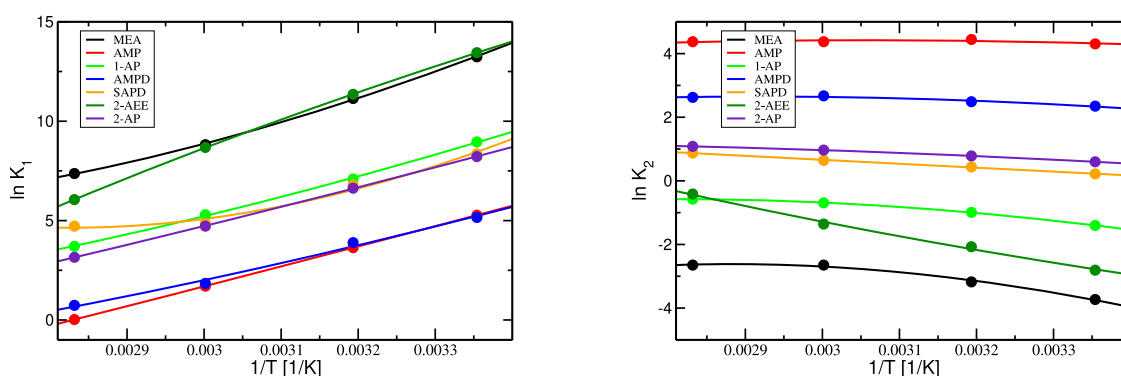
4.1. Ideal–Gas Standard Reaction Free Energies.

Tables S1 and S2 of the Supporting Information show our calculated ideal-gas standard reaction free energies $\Delta G_j^0(T; P^0)$ of eq 9 for reactions R1 and R2 at the four temperatures (298.15 K, 313.15 K, 333.15 K, 353.15 K) for the set of seven amines considered, using five different composite QM methods.

As noted by Somer et al.,⁶³ improved predictions can arise from the use of combinations of several high level methods, since methods such as G4 tend to overestimate and methods such as CBS-QB3 tend to underestimate the reaction free energy. The variations in the different methods also enable us to infer the uncertainty rooted in the different chemical species of the same class of molecules. For example, in our previous work,⁴⁵ we found that for the amine species, the ideal gas free energies vary significantly among the QM methods, depending on the size and flexibility of the molecules involved. Based on the Table S1 results, for most species the Gaussian-n theories (G4, G3,

Table 1. Predicted pK Values for reactions R1 and R2 from This Work at the Indicated Temperatures and $P = 1$ bar

T (K)	MEA	AMP	1-AP	AMPD	SAPD	2-AEE	2-AP
Reaction R1							
298.15	−5.75 _{0.56}	−2.29 _{0.58}	−3.89 _{0.66}	−2.24 _{0.52}	−3.63 _{0.62}	−5.84 _{0.50}	−3.57 _{0.49}
313.15	−4.84 _{0.54}	−1.58 _{0.55}	−3.08 _{0.63}	−1.69 _{0.51}	−2.95 _{0.59}	−4.93 _{0.49}	−2.88 _{0.46}
333.15	−3.83 _{0.49}	−0.74 _{0.52}	−2.30 _{0.60}	−0.80 _{0.50}	−2.11 _{0.55}	−3.77 _{0.48}	−2.05 _{0.44}
353.15	−3.20 _{0.50}	−0.01 _{0.49}	−1.61 _{0.58}	−0.32 _{0.49}	−2.05 _{0.51}	−2.63 _{0.48}	−1.37 _{0.41}
Reaction R2							
298.15	1.62 _{0.42}	−1.87 _{0.50}	0.61 _{0.40}	−1.02 _{0.60}	−0.09 _{0.53}	1.22 _{0.66}	−0.26 _{0.48}
313.15	1.38 _{0.40}	−1.93 _{0.49}	0.43 _{0.39}	−1.08 _{0.59}	−0.19 _{0.51}	0.90 _{0.65}	−0.34 _{0.47}
333.15	1.15 _{0.39}	−1.90 _{0.47}	0.30 _{0.37}	−1.16 _{0.57}	−0.28 _{0.49}	0.59 _{0.63}	−0.42 _{0.45}
353.15	1.15 _{0.38}	−1.90 _{0.46}	0.25 _{0.36}	−1.14 _{0.55}	−0.38 _{0.48}	0.18 _{0.62}	−0.47 _{0.44}

**Figure 2.** Temperature dependence of the equilibrium constants for reactions R1 and R2 for the seven amines studied.

G3B3) tend to predict higher $\Delta G_j^0(T; P^0)$ values than those of the complete basis set (CBS-QB3, CBS-APNO) approaches. We note that the R2 values generally indicate slightly smaller standard deviations than those of R1, except for the species containing multiple hydroxyl groups (SAPD, AMPD, 2-AEE). For these species reaction R2 shows significant scatter among the QM methods.

For speciation calculations involving reactions R1 and R2, we used the average $\Delta G_j^0(T; P^0)$ values from the five methods in Tables S1 and S2. Tables S8–S12 show the raw Gaussian16⁶⁰ output for each species from which they were calculated. Their standard deviations are about 3 kJ·mol^{−1}, which we take as a surrogate measure of the uncertainty in the $\Delta G_j^0(T; P^0)$ values. This value is well within a “chemical precision standard” of 1 kcal·mol^{−1}.

4.2. Equilibrium Constants pK_1 and pK_2 . Table 1 summarizes our pK_1 and pK_2 results for the seven alkanolamines studied at the indicated temperatures and $P = 1$ bar. The underlying data used for their calculation are given in the Supporting Information as follows. Table S4 shows the simulated $\mu_{\text{res},\text{NVT};\infty}(T, P)$ values for the neutral (RNH_2), protonated (RNH_3^+), and carbamate (RNHCO_2^-) forms of the seven alkanolamines at the four temperatures of this study. Table S5 shows $\mu_{\text{res},\text{NVT};\infty}(T, P)$ values for HCO_3^- , for CO_2 using the Trappe FF,⁵⁷ and for H_2O using the TIP3P FF. The $\Delta \tilde{G}_j(T, P)$ and $pK_j(T, P)$ values for reactions R1 and R2 used in the reaction equilibrium calculations listed in Tables S6 and S7.

The indicated uncertainties are one standard deviation, which are seen to be within a “chemical precision standard” of 1 kcal·

mol^{−1} for $\Delta \tilde{G}_j(T, P)$ in eq 8. This translates to a precision in pK units of

$$\Delta pK = \frac{4184}{2.303RT} = \frac{218.546}{T} \quad (13)$$

which at 298.15 K is 0.73 pK units.

The dependence of the equilibrium constants on temperature is shown in Figure 2, using regressions to the expression

$$pK = a + b/T + c \ln(T) \quad (14)$$

The values of the parameters (a, b, c) are given in Table S3 of the SI. Interestingly, the right panel of Figure 2 shows that, in comparison with the carbamate forming amines (MEA, 1-AP, 2-AEE), the pK_2 values for the sterically hindered amines (AMP, AMPD, SAPD, 2-AP) show a weaker temperature dependence.

4.3. Effects of Different Partial Charge Methods on the pK Values. As described in Section 3, for the pK calculations and the resulting equilibrium compositions we used the default HF/6-31G* partial charges based on each molecule’s G4 optimized geometry, from which the electrostatic surface grid and the RESP atomic partial charges were obtained. Numerous studies^{64,65} have addressed the effects on the $\mu_{\text{res},\text{NVT};\infty}$ values of different QM approaches used to obtain the FF partial charges. To examine this effect for our systems, we considered representative $\mu_{\text{res},\text{NVT};\infty}$ values for MEA and for AMP at $T = 298.15$ K based on RESP partial charge assignment arising from several different QM methodologies: the default GAFF HF/6-31G* results from Table S3, B3LYP/6-311++G(d,p), MP2/aug-cc-pVTZ in the gas phase, and a MP2/aug-cc-pVTZ calculation in the presence of polarizable continuum solvent (MP2/aug-cc-pVTZ+PCM, with a dielectric constant of 78.39). These are shown in Table 2.

Table 2. Comparison of GAFF Predicted Intrinsic Hydration Free Energies, $\mu^{\text{res,NVT};\infty}$ (in $\text{kJ}\cdot\text{mol}^{-1}$) of the Protonated, Neutral, And Carbamate Forms of MEA and AMP at $T = 298.15$ K Using Different Sets of Partial Charges in Conjunction with RESP

Species	MP2/aug-cc-pVTZ+PCM	HF/6-31G*	B3LYP/6-311++G(d,p)	MP2/aug-cc-pVTZ
monoethanolamine (MEA)				
RNH_2	-32.89 _{0.05}	-30.23 _{0.14}	-26.94 _{0.19}	-23.30 _{0.07}
RNH_3^+	-243.87 _{0.09}	-239.43 _{0.10}	-235.95 _{0.1}	-234.71 _{0.13}
RNHCOO^-	-400.63 _{0.08}	-366.79 _{0.19}	-365.63 _{0.15}	-358.62 _{0.27}
2-amino-2-methylpropanol (AMP)				
RNH_2	-38.53 _{0.03}	-34.35 _{0.13}	-31.68 _{0.16}	-27.50 _{0.07}
RNH_3^+	-228.33 _{0.06}	-222.50 _{0.11}	-216.22 _{0.13}	-215.57 _{0.12}
RNHCOO^-	-393.84 _{0.06}	-352.33 _{0.10}	-349.64 _{0.12}	-342.94 _{0.04}

The results show relatively small ($3\text{--}8 \text{ kJ}\cdot\text{mol}^{-1}$) differences from our default HF/6-31G* calculations in the cases of B3LYP/6-311++G(d,p) and MP2/aug-cc-pVTZ). However, when the polarizable continuum model (PCM) is included in the calculation of the electron density (MP2-aug-cc-pVTZ+PCM), the hydration free energy of the carbamate anion (RNHCO_2^-) becomes considerably more negative (by $30\text{--}40 \text{ kJ}\cdot\text{mol}^{-1}$) compared to the unpolarized charge density (mp2-aug-cc-pVTZ) result. In contrast, the charges derived from the polarized electronic density causes the hydration free energy of the protonated amines (RNH_3^+) becomes more negative by only $5\text{--}6 \text{ kJ}\cdot\text{mol}^{-1}$. Partial charges obtained from the RESP methodology already tend to over polarize anions in the absence of PCM,⁶⁶ and our results show that this becomes excessive in its presence.

Representative pK values at 298.15 K for reactions R1 and R2 calculated from eqs 8–12 using columns 3–5 of Table 2 and the data of Tables S1, S2, and S4 are shown in Table 3. Whereas the

Table 3. Comparison of the Predicted pK Values of Reactions R1 and R2 for the MEA and AMP Systems at $T = 298.15$ K Using Different Sets of Partial Charges from Table 2, the ΔG^0 Values in Table S1 and S2, and the $\mu^{\text{res,NVT};\infty}$ Values for H_2O , CO_2 , and HCO_3^- in Table S4

Reaction	HF/6-31G*	B3LYP/6-311++G(d,p)	MP2/aug-cc-pVTZ
monoethanolamine (MEA)			
R1	-5.75 _{0.56}	-6.09 _{0.56}	-5.92 _{0.56}
R2	1.62 _{0.42}	2.00 _{0.41}	1.41 _{0.41}
2-amino-2-methylpropanol (AMP)			
R1	-2.29 _{0.58}	-1.64 _{0.58}	-1.81 _{0.58}
R2	-1.87 _{0.50}	-1.85 _{0.50}	-1.31 _{0.50}

$\mu^{\text{res,NVT};\infty}$ vary substantially across the QM levels in Table 2, the pK values in Table 3 are not overly sensitive to the different partial charge methodologies. However, we note that our comparisons were obtained using GAFF Lennard–Jones force-field parameters, which are optimized to the HF/6-31G* partial charges. A more complete comparison of the effects of the different theories/levels on the hydration free energies would require re-optimization with respect to experiment of the Lennard–Jones force-field parameters for each theory/level. Since the partial charges tend to be the major contribution to the hydration free energy values, we do not expect such a reoptimization to produce a large effect. In any event, such a study is beyond the scope of this work, and would also contradict its purely predictive approach.

4.4. Carbamate Stability Constant, K_2 . In this section we discuss our results for the equilibrium constant K_2 of the

carbamate reversion reaction R2 (the inverse of the carbamate formation reaction equilibrium constant), in comparison with those obtained from experiment at the representative temperature 298.15 K when such data are available.

In our approach, we directly predict $K_2(T, P)$ from simulation quantities using eq 12. $K_2(T, P)$ cannot be directly measured experimentally, but must be obtained indirectly using

$$\ln K_2(T, P) = \sum_{i=1}^{N_i} \nu_{i2} [\ln m_i^* + \ln \gamma_i(T, P; \mathbf{m}^*)] \quad (15)$$

where the molalities and activity coefficients refer to an experimentally measured equilibrium composition, \mathbf{m}^* , and ν_{i2} is the reaction stoichiometric coefficient of species i in reaction R2. One approach is by means of extrapolation to zero ionic strength of the experimentally measured species activity coefficients of eq 15, and another is by fitting the measured equilibrium data to the parameters of a thermodynamic model for the chemical potentials.

Our predicted p K_2 values at the representative temperature $T = 298.15$ K are shown in Table 4, where they are compared with experimental results from the literature. The major source of uncertainty in our pK calculations is that of the ideal-gas ΔG_2^0 term in eq 9. For the experimental values, the sources of uncertainty/error in p K_2 are the uncertainties in any model used

Table 4. Comparison with Literature Data of Calculated p K_2 for the Carbamate Reversion Reaction R2 at $T = 298.15$ K (unless Indicated Otherwise) and $P = 1$ bar

Amine	This work, Table 2	Literature
monoethanolamine (MEA)	1.62 _{0.42}	1.71(291.15 K), ⁶⁷ 1.25, ⁶⁸ 1.31, ⁶⁹ 1.86 ⁷⁰ 1.81, ⁷¹ 1.46, ⁷² 1.60, ⁷³ 1.76 _{0.02} ¹⁸
2-amino-2-methyl-1-propanol (AMP)	-1.87 _{0.50}	-2.15, ⁷⁴ -1.66, ⁷⁴ <-0.70(303 K), ¹⁷ <-1, ⁷⁵ -1.0 ₆
1-amino-2-propanol (1-AP)	0.61 _{0.40}	1.70 _{0.2} ⁷⁷
2-amino-2-methyl-1,3-propanediol (AMPD)	-1.02 _{0.60}	sterically hindered
2-(2-aminoethoxy) ethanol (2-AEE)	1.22 _{0.66}	1.75 ⁷⁸
serinol(2-aminopropane-1,3-diol) (SAPD)	-0.09 _{0.53}	no carbamate detected ⁷⁷
2-amino-1-propanol (2-AP)	-0.26 _{0.48}	0.6 _{0.1} , ⁷⁷ 0.98 ¹⁸

^aCalculated from the mole-fraction-based apparent equilibrium constant of 0.47 from Ciftja et al.⁷⁹

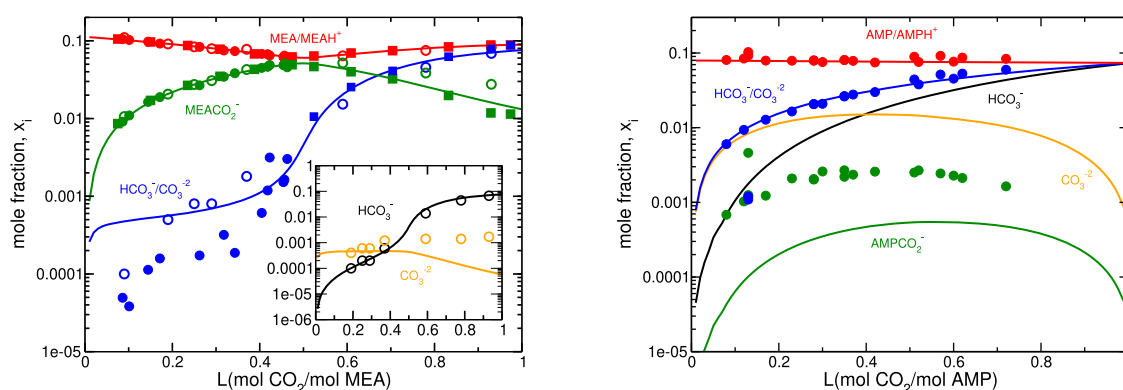


Figure 3. Speciation predictions (curves) for 30 wt % aqueous MEA and AMP solutions of CO_2 at $T = 298.15$ K and $P = 1$ bar, and their comparison with experimental data. For MEA/ MEA^+ , all experimental data points are indistinguishable and fall on the predicted curve. For MEA carbamate, open green circles are data of Jakobsen et al.,⁹⁰ filled green circles are data of Hilliard⁹¹ and filled green squares are data of Böttlinger et al.⁷¹). For the MEA $\text{HCO}_3^-/\text{CO}_3^{2-}$ data, open blue data points refer to the separately measured and subsequently combined data of Jakobsen et al.⁹⁰ (the separate concentrations are shown in the inset); filled data points refer to measurements of the combination only (filled blue circles of Hilliard⁹¹ and filled blue squares of Böttlinger et al.⁷¹). The data of Jakobsen et al.⁹⁰ and of Böttlinger et al.⁷¹ are at 293.15 K, and the data of Hilliard are at 300.15 K. Experimental data for AMP are from Ciftja et al.⁷⁴ at 298.15 K.

for the activity coefficients and the uncertainties in the experimental composition measurements. The latter is likely the greater contributor, since both the neutral and the protonated amine pair are present as is the case for the bicarbonate/carbonate pair, and it is very difficult to experimentally distinguish the individual species concentrations from NMR data.

We have already noted that our $\text{p}K$ uncertainties are within a “chemical precision standard” of 0.73 $\text{p}K$ units at 298.15 K. We remark that the precisions of experimental studies are often not provided in their publications (but we highlight the careful experimental work of the Tremaine group,²⁰ which recently studied $\text{p}K_2$ values from 283.2–313.2 K for 2-methylpiperidine using NMR spectroscopy and reported precisions of 0.35–1.50 $\text{p}K$ units).

$\text{p}K_2(T, P)$ for MEA has been the subject of numerous experimental studies,^{17,18,69,73,77} using the indicated approaches or variants thereof. For MEA at 298.15 K, our predictive methodology gives $\text{p}K_2 = 1.62 \pm 0.42$. The spread of the literature $\text{p}K$ values (1.25–1.86) is partly due to differences in the activity coefficient models used by the authors and, likely more importantly, to the difficulty in the measurement of the concentrations of the proton exchanging species. The precision of our prediction is seen to be similar to that of the experimentally measured values. (See also Section 6.)

There are fewer experimental $\text{p}K_2$ results for the other alkanolamines. Several groups^{20,74–76,78,79} have reported an “apparent equilibrium constant” for $\text{p}K_2$ for a range of solvents based on the approximations that the activity of water is unity and that the activity coefficients for RNHCO_2^- and HCO_3^- are equal and hence cancel in the activity coefficient ratio at all concentrations. The latter behavior (referred to herein as the iso-Coulombic approximation, ICA) is based on the fact that the cancellation holds exactly in the Debye–Hückel activity coefficient model for the iso-Coulombic reaction R2 at all concentrations. $\text{p}K_2$ obtained from the ICA is referred to as an “apparent equilibrium constant”. We can see mild supporting evidence for the ICA from the $\mu_{\text{res},\text{NVT};\infty}$ values for RNHCO_2^- and HCO_3^- in Tables S3 and S4 of the Supporting Information, where it is seen that they are of the same sign and similar magnitude. We also found (not shown) that simulations show

that this behavior continues to hold as the solution concentrations increase.

Our predicted AMP value is $\text{p}K_2 = -1.87 \pm 0.50$. McCann et al.¹⁷ studied the AMP system using ^1H NMR. They did not detect carbamate, but they noted that $\text{p}K_2 < -0.70$ at 303 K. Other authors reported apparent equilibrium constants based on the ICA. Sartori and Savage⁷⁵ reported $\text{p}K_2 < -1.0$ at 313 K in their ^{13}C NMR study. Ciftja et al.⁷⁹ obtained a value of $\text{p}K_2 = -2.15$ and later⁷⁴ a value of $\text{p}K_2 = -1.66$, based on ^{13}C NMR measurements. Yamada et al.⁷⁶ reported $\text{p}K_2 \approx -1.0$ for AMP from ^{13}C NMR studies. The negative AMP $\text{p}K_2$ value compared to that of MEA indicates that AMP carbamate formation is thermodynamically less favored, a consequence of the steric effect of the two methyl groups ($-\text{CH}_3$) on the α carbon connected to the amine nitrogen atom.

The addition of a $-\text{CH}_3$ group to the β carbon of MEA gives 1-AP. For this molecule, we predict a carbamate formation constant of $\text{p}K_2 = 0.61 \pm 0.40$, which is smaller than that of MEA. This indicates a small steric effect, arising from the $-\text{CH}_3$ group being further away from the amino group. The experimental study of Conway et al.⁷⁷ also noted significant carbamate formation in the 1-AP solution, and they reported $\text{p}K_2 = 1.7$.

We did not find any experimental carbamate/bicarbonate concentration data for AMPD. Similarly to AMP, it is a sterically hindered amine and we predict $\text{p}K_2 = -1.02 \pm 0.60$.

For 2-AEE, we predict $\text{p}K_2 = 1.21 \pm 0.66$ at 298.15 K; this system was experimentally studied by Al-Juaied et al.⁷⁸ using ^{13}C NMR, who reported an apparent $\text{p}K_2 = 1.75$ for 17.7 M 2-AEE at relatively low CO_2 loading at 300 K. (See the iso-Coulombic discussion above.)

While Conway et al.⁷⁷ did not observe carbamate formation in SAPD, Bougie et al.⁸⁰ suggested carbamate formation in SAPD similar to that of unhindered amines based on the trend of the solubility data. For SAPD, we predict a value of $\text{p}K_2 = -0.09 \pm 0.53$ at 298.15 K, indicating that it is a mildly carbamate-forming amine.

Removing one of the $-\text{CH}_3$ groups from the α carbon of AMP gives 2-AP. For 2-AP, the predicted $\text{p}K_2$ value increases to $\text{p}K_2 = -0.26 \pm 0.48$, which lies between that of MEA and AMP. Fernandes et al.¹⁸ reported a value of $\text{p}K_2 = 0.98$ at 298.15 K for

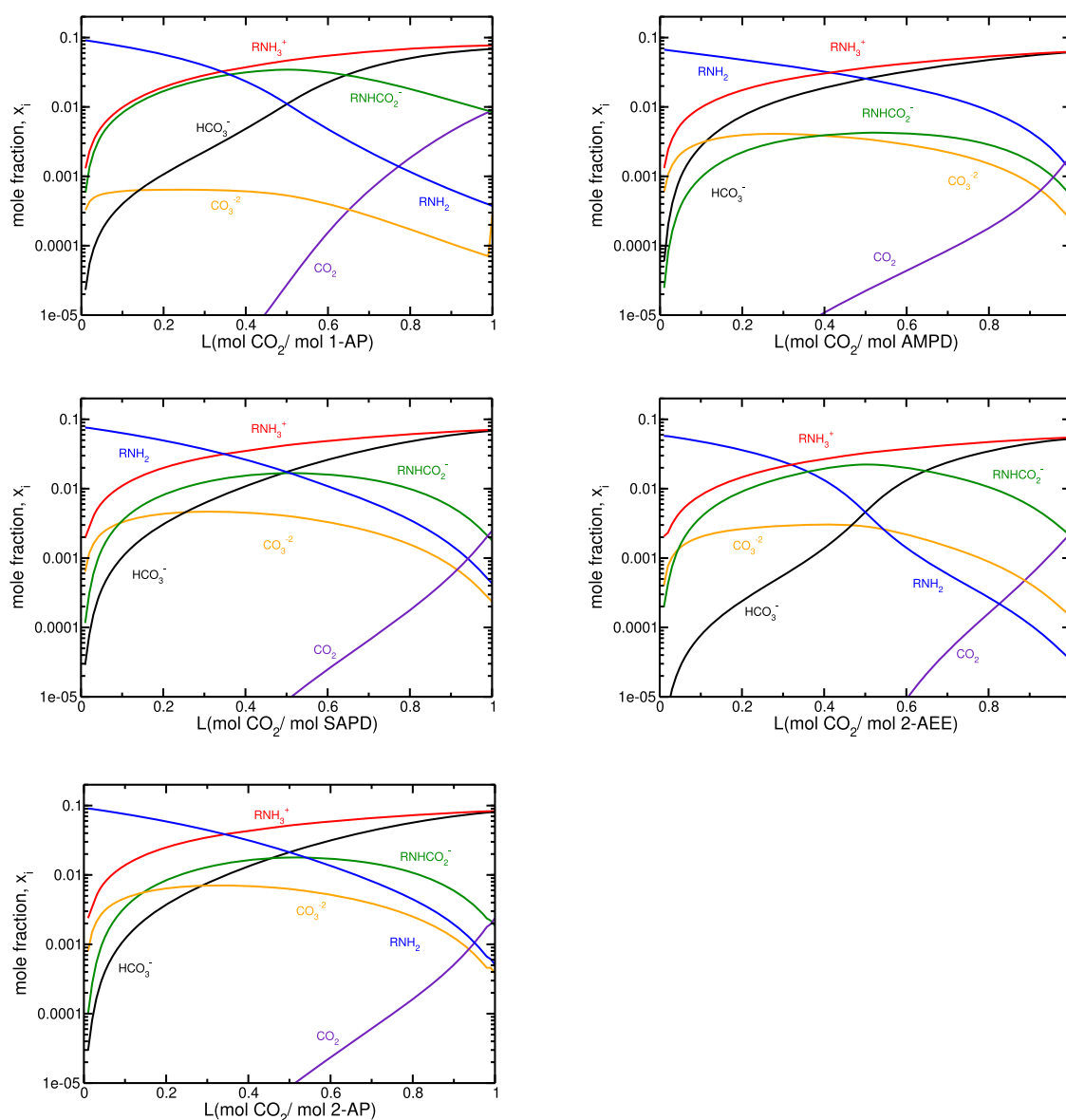


Figure 4. Speciation predictions (curves) for reactive absorption of CO_2 in 30 wt % amine aqueous solutions at $T = 298.15 \text{ K}$ and $P = 1 \text{ bar}$. No experimental data exists for comparison.

2-AP from their NMR study. In a more recent study by the same group,⁷⁷ they obtained $\text{p}K_2 = 0.6 \pm 0.1$, which agrees with our predicted value within their mutual uncertainties.

Figures 3 and 4 of Section 4.6 show the decreasing carbamate concentrations for the solvents as their $\text{p}K_2$ value decreases. For AMP, the alkanolamine with the lowest $\text{p}K_2$ value, evidence of the experimental difficulty of observing carbamate is indicated in Figure 3, where it is seen that its carbamate mole fraction becomes less than 10^{-4} at low and at high CO_2 loadings.

In general, comparison with the (often limited) experimental data shows that the molecular models employed here are able to capture, qualitatively and to a reasonable quantitative accuracy, the observed trend in the steric effects on carbamate formation for the common primary amines used in the PCC process studied herein.

4.5. Consistency Tests for the Amine Protonation Constants. For a wide range of amines, experimental data are available for the amine protonation reaction $\text{p}K_8$ of reaction R8.⁸⁹ Furthermore, the equilibrium constants for reactions

R3–R5 are well studied, based on the CO_2 – H_2O equilibria for a wide range of temperatures.⁸¹ Since reaction R8 is the sum $\text{R1} + \text{R2} - \text{R3}$, this allows the prediction of any one of the equilibrium constants from those of the others. In particular, this approach allows the prediction of amine protonation $\text{p}K_8$ values from molecular simulation that are independent of knowledge of the intrinsic hydration free energy of the proton, precise values of which remain unknown despite extensive experimental and theoretical efforts.

In Table 5, we show predictions of $\text{p}K_8$ from our simulation results for the equilibrium constants of reactions R1 and R2 in conjunction with the experimental data of Edwards et al.⁸¹ for the bicarbonate reaction R3. It is seen that the $\text{p}K_8$ values predicted in this way are generally within 1 pK unit of the experimental values. Since we have previously seen that our $\text{p}K_2$ values agree well with the corresponding experimental values and the only species not appearing in both R1 and R2 is the protonated amine species, RNH_3^+ , we conjecture that an

Table 5. Prediction of the Amine Protonation Constant pK_8 Independently of Knowledge of the Proton (H^+) Hydration Free Energy at 298.15 K Using $pK_8 = pK_1 + pK_2 - pK_3$, in Conjunction with Our Results for pK_1 and pK_2 in Table 1 and the Well-Established Experimental Value $pK_3 = 6.30$ ⁸¹ for the Bicarbonate Reaction R3

amine	$-pK_8$ (this work)	$-pK_8$ (expt)
MEA	10.42 _{0.50}	9.51, ⁸² 9.44, ⁸³ 9.50, ⁸⁴ 9.51 _{0.01} ⁸⁵ 9.59 _{0.19} , ⁸⁶ 9.50, ⁸⁷ 9.44 _{0.01} ⁸⁸
AMP	10.45 _{0.52}	9.67 _{0.01} ¹⁸
1-AP	9.57 _{0.56}	9.50
AMPD	9.63 _{0.44}	8.84 _{0.01} ¹⁸
SAPD	10.07 _{0.55}	8.55
2-AEE	10.97 _{0.48}	9.42
2-AP	10.13 _{0.52}	9.52 _{0.01} , ¹⁸ 9.40

improved treatment of this species would lead to better agreement with the experimental pK_8 values.

4.6. Speciation. Our species concentrations were calculated using the Henry Law based chemical potential model of eq 2, using our pK_1 and pK_2 values in conjunction with the well-known experimental pK data for reactions R3–R5.⁸¹ We first calculated compositions using the ideal solution form of the model ($\ln \gamma_i = 0$) and then performed preliminary calculations

using the methodology of Smith and Qi⁴⁹ for extending the model to the nonideal case. We found that the equilibrium compositions resulting from the first iteration of this approach changed by very small amounts from those of the ideal solution, and our results presented here are those of the ideal solution form of the model.

Whereas there exists extensive CO_2 solubility data as a function of its partial pressure for a wide range of amines, only a few NMR-based studies have studied speciation data in the solvent.^{71,74,90,91} For the amines considered in this work, we only found NMR measurements for MEA and for AMP, which are shown in Figure 3 along with our predictions.

For MEA (left panel of Figure 3), our results are in excellent agreement with the experimental results at CO_2 loadings of 0.4 and greater, where the mole fractions are greater than about 0.005. There is significant scatter in the experimental data at low loadings for the HCO_3^-/CO_2^{-2} pair, reflecting the experimental difficulty of accurately measuring such low concentrations. As already noted in Section 4.4, these difficulties can lead to significant scatter in the experimentally determined pK_2 value if such data are used for its estimation.

Jakobsen et al.⁹⁰ fitted a thermodynamic model to their NMR data to separate the HCO_3^-/CO_2^{-2} and considered low CO_2 loadings. Our results are in better agreement with their data

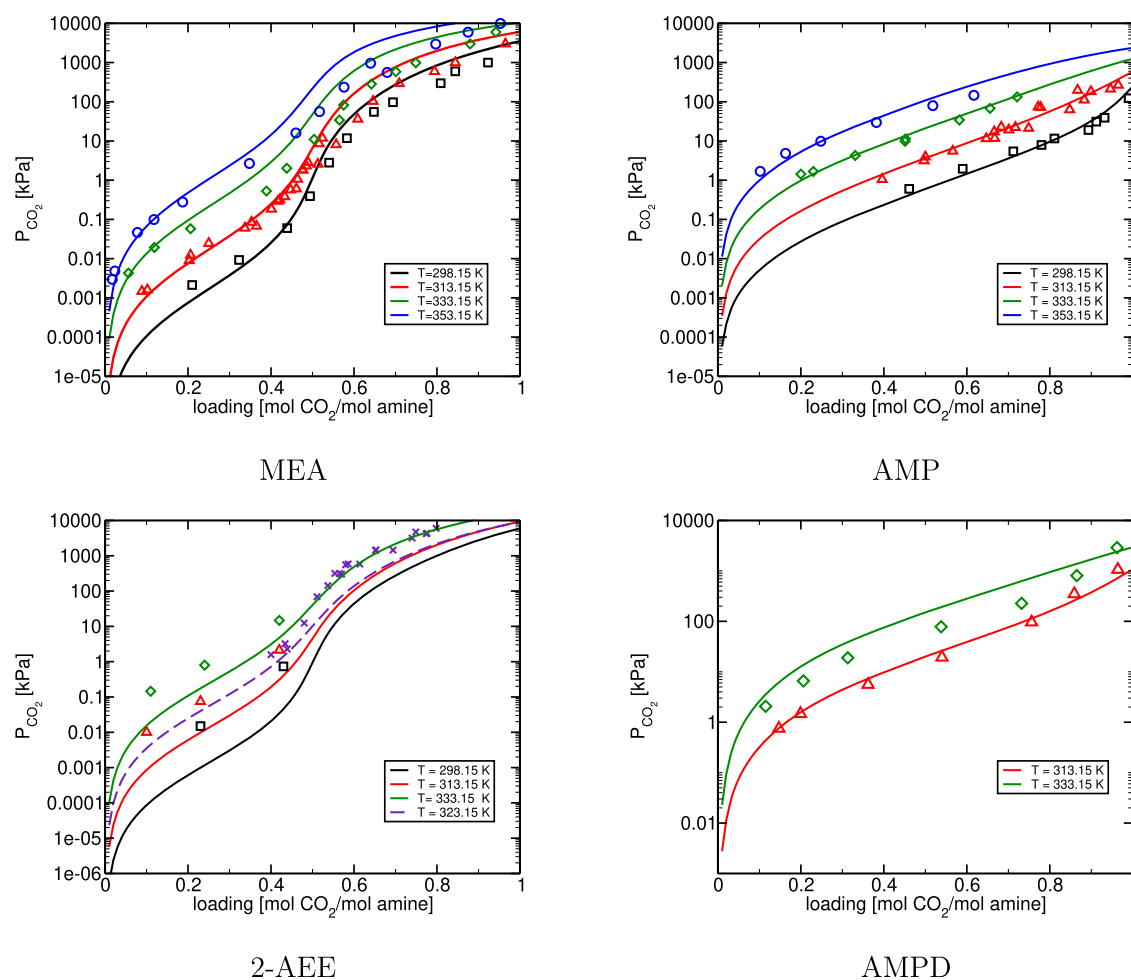


Figure 5. Comparison of the CO_2 partial pressures in 30 weight% MEA, AMP, AMPD and 60% 2-AEE aqueous solutions using the Henry Law based ideal-solution model at different temperatures with experimental data.^{78,92–95} In the case of 2-AEE, stars indicate the experimental data of Martin et al.⁹³ and the other symbols are data of Al-Juaied et al.⁷⁸ (65 wt % 2-AEE).

(open blue circles) than those of Hilliard⁹¹ (filled blue circles), which appear to under-predict the $\text{HCO}_3^-/\text{CO}_3^{2-}$ concentrations. The inset shows that the Jakobsen et al.⁹⁰ HCO_3^- concentrations (open circles) agree well with our results, but their CO_3^{2-} concentrations are higher than ours (although both are quite small) at high loadings. This is consistent with the suggestion of the Jakobsen group that their +NMR speciation data did not obey electroneutrality, which they attributed to possible over-estimation of the CO_3^{2-} concentration. At higher loadings, our $\text{HCO}_3^-/\text{CO}_3^{2-}$ results are in excellent agreement with the data of both Böttinger et al.⁷¹ and Jakobsen et al.⁹⁰

Finally, our results for the MEA carbamate species are in excellent agreement with those of Böttinger et al.⁷¹ (filled squares), Jakobsen et al.⁹⁰ (open circles), and Hilliard (filled circles) at loadings up to about 0.6. At higher loadings, our predictions are in agreement with the data of Böttinger et al., who used a combination of ^{13}C and ^1H NMR procedures with the goal of obtaining more accurate carbamate concentrations. The Jakobsen et al. data are significantly higher.

In contrast to MEA, which is a carbamate forming species, AMP is a sterically hindered amine and forms only very small amounts of carbamate due to the electronic effect of the methyl groups around the nitrogen. As shown in the right panel of Figure 3, this is well captured by our simulations. Our predicted concentration of the $\text{HCO}_3^-/\text{CO}_3^{2-}$ pair is in agreement with the Ciftja et al. measurements, whereas the AMP carbamate concentrations are significantly higher. The disagreement of AMPCO_2^- concentration with the experimental NMR-based data of Ciftja et al.⁷⁴ can be justified in part by the fact that these concentrations are very small and that the speciation fraction data reported by Ciftja et al. do not obey electroneutrality, resulting in the likelihood that the carbamate concentrations are subject to significant uncertainties.

Finally, Figure 4 shows our predicted compositions for the other alkanolamines studied, for which no experimental data exist in the literature. If and when NMR experiments are performed for these solvents, we expect that species concentrations lower than about 0.005 will be either difficult to obtain accurately or undetectable. For example, for AMPD this is expected to be the case for the carbamate species, which will make the experimental determination of its pK_2 value very difficult.

4.7. CO_2 Solubility. The equilibrium solubility of CO_2 is expressed in terms of its partial pressure, P_{CO_2} , in the vapor phase as a function of the total loading (both in its free and chemically bound solution forms) in the solution phase. It is determined from the equality of the chemical potentials of its free solution form and in the vapor phase in reaction R6. At the relatively low total pressures typically involved, the vapor phase may be treated as an ideal gas, which yields the following equation for the P_{CO_2} :

$$P_{\text{CO}_2} = \left(\frac{RT}{100P^0} \right) \left(\frac{\bar{p}_{\text{solv}}(T, \bar{P})}{1000} \right) m_{\text{CO}_2} \exp \left(\frac{\mu_{\text{CO}_2}^{\text{res}, \text{NVT}; \infty}(T, \rho(T, \bar{P}))}{RT} \right) \quad (16)$$

The dependence of P_{CO_2} on loading at several temperatures considered is shown and compared with available experimental data in Figure 5 for 30 wt % MEA, AMP, AMPD and 60 wt % 2-

(2-aminoethoxy)ethanol (2-AEE). For 2-AP shown in Figure 6, we only found a single solubility measurement at 313.15 K, with

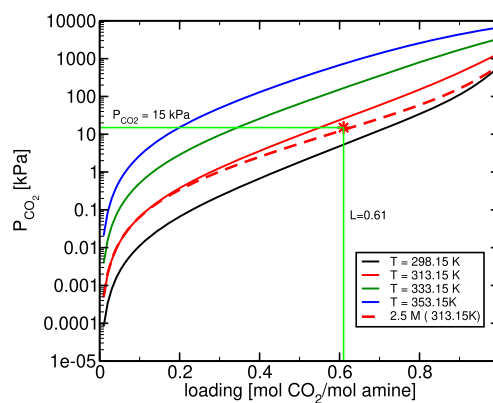


Figure 6. CO_2 solubility in 30 wt % (solid lines) and 16 wt % (dashed red line) 2-AP.

a CO_2 partial pressure of 15 kPa over 2 M (16 wt %) 2-AP aqueous solution.⁹⁶ It is seen that our predictions are in generally good agreement with the available experimental results.

5. EFFECT OF AMINE CONCENTRATION ON CO_2 SOLUBILITY

Optimizing the amine concentration in the solvent is an important parameter for PCC system design. Our equilibrium model can be used to predict the effect of the amine concentration on the CO_2 solubility, and representative results are shown in Figure 7. It can be seen that, for the carbamate forming amines (MEA, 1-AP, SAPD), the amine concentration has a small effect on the CO_2 solubility for loadings below 0.5. At higher loadings, amine solutions of lower concentration will have a higher CO_2 solubility, attributed to the change from carbamate formation to bicarbonate formation. This “salting out” effect is more pronounced for MEA, which is a strong carbamate forming species, whereas it is less pronounced for SAPD, which we found to be a mild carbamate forming molecule. Similar to MEA, 1-AP is a carbamate forming amine, and the concentration is predicted to have a small effect on the CO_2 solubility at low loadings, in qualitative accordance with the trend of the scattered experimental data points in that loading range.

6. UNCERTAINTY ANALYSIS

Consideration of the effects of uncertainties in input model parameters on its outputs is a generally important aspect of modeling.^{99–103} Experimental studies often use regression models to determine fundamental thermodynamic parameters such as the pK quantities shown in Table 1. These studies do not always provide uncertainty estimates for the pK values, but when they are provided, it is in the context of a particular combination of experimental and modeling approaches. A more reasonable indication of the uncertainty of experimentally determined pK values is the variation in the values obtained by different experimental groups using their different methodologies. In Section 4.2, we provided uncertainty estimates for our predictions.

Uncertainty analysis in the context of a nonlinear regression model of CO_2 reactive absorption has recently been considered

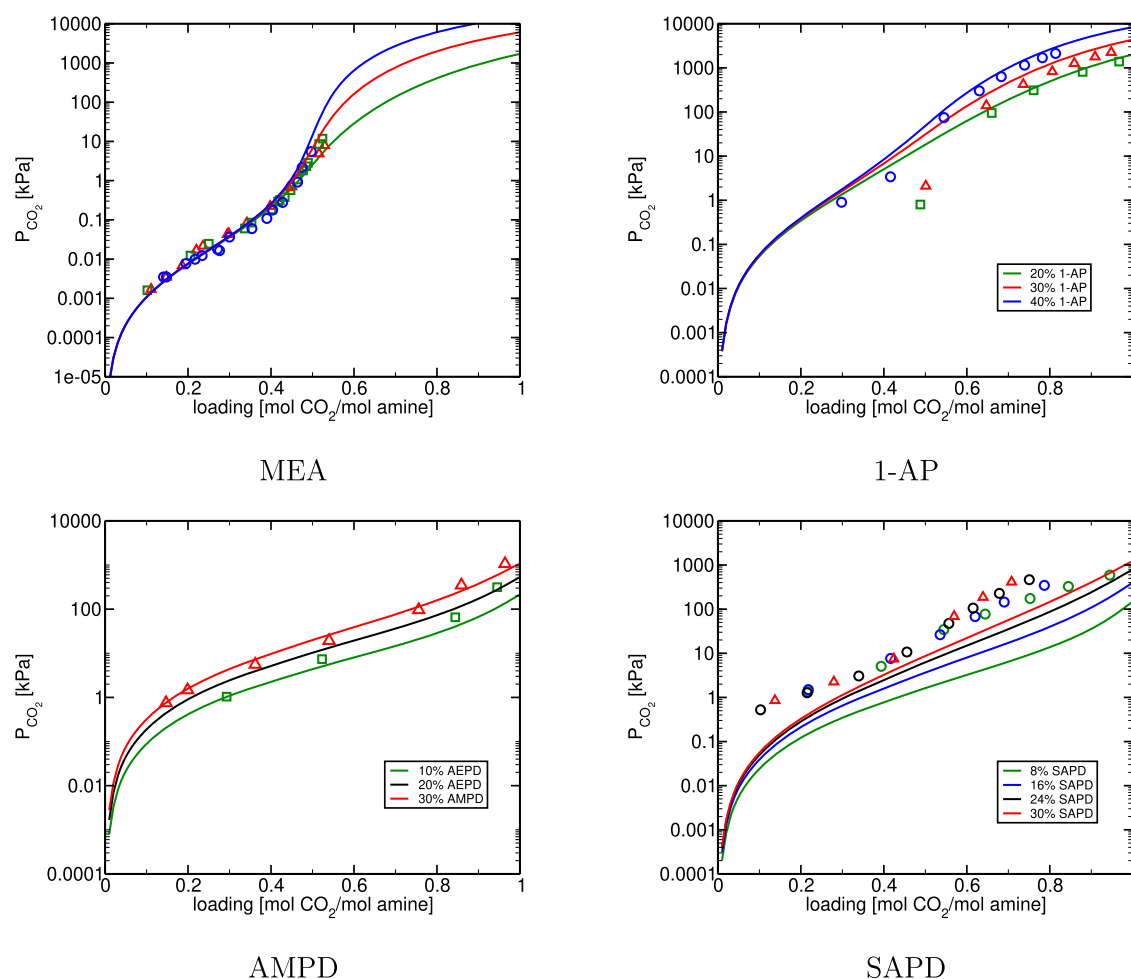


Figure 7. Effect of amine concentration on the CO_2 solubility of (a) MEA, (b) 1-AP, (c) AMPD, and (d) SAPD at 313.15 K, in comparison with experimental data.^{80,94,97,98}

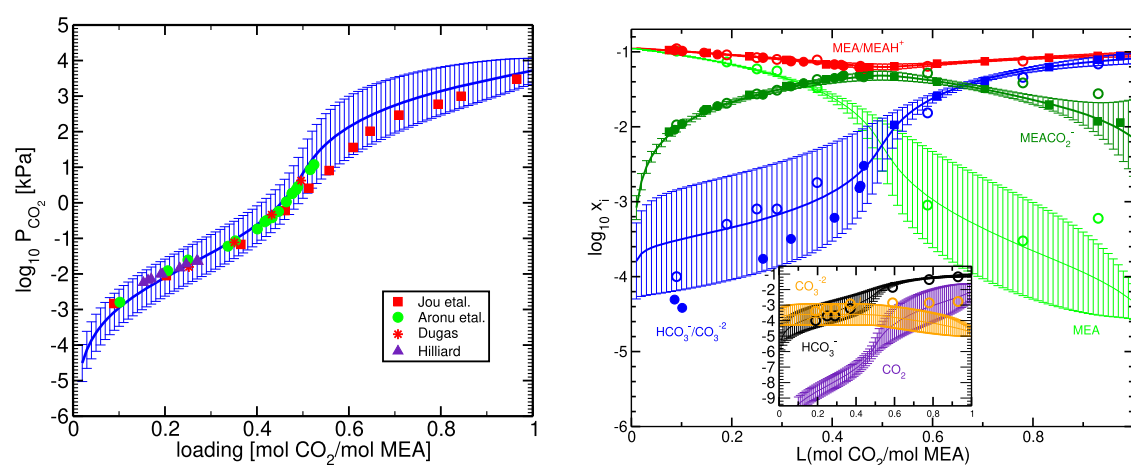


Figure 8. Left panel shows predicted values of P_{CO_2} in 30 wt % MEA at 313.15 K and their uncertainty intervals corresponding to one standard deviation, and comparison with experimental data.^{91,92,97,104} The right panel shows the predicted solution concentrations and their one standard deviation uncertainty intervals for CO_2 in 30 wt % MEA at 298.15 K, and comparison with the experimental data of Figure 3.

by Morgan et al.^{102,103} by propagating the regressed model parameter uncertainties through the model to its P_{CO_2} output value. Using a previous version of the molecular-based predictive methodology of this paper, our earlier MEA study⁴⁴ provided uncertainty estimates for both P_{CO_2} and the solution compositions by propagating the pK uncertainties to these

output quantities. Although the latter are important quantities, we are unaware of any other uncertainty study involving them.

The primary quantities used in our methodology to predict P_{CO_2} and speciation concentrations are the pK_1 and pK_2 values resulting from the ideal-gas free energy changes ΔG^0 and the species hydration free energies $\mu_i^{\text{res},\text{NVT};\infty}(T; P)$ in eqs 9–12.

We calculated uncertainty estimates by an empirical bootstrapping procedure by generating 1000 sets of (pK_1 , pK_2) values from independent normal distributions with means and variances given by the values in Table 1, and for each set we solved eq 1 for the resulting solution equilibrium compositions and P_{CO_2} as functions of the CO_2 loading. We then calculated the means and standard deviations of these compositions and P_{CO_2} values and expressed our uncertainties as one standard deviation of the predicted results.

Figure 8 shows representative results for the uncertainties of our predictions for P_{CO_2} for MEA at 313.15 K (left panel) and for the MEA solution compositions (right panel) at 298.15 K. We found no multiple sets of experimental P_{CO_2} and solution compositions at any common set of conditions, but we believe that the slight variations in the experimental temperatures do not significantly affect the results shown in the figures. The figures indicate that our predictions, and their precisions are compatible with the scatter of the experimental data. In the course of this study, we also found that pK_1 is the most important parameter at low loadings and that pK_2 is the most important at loadings greater than 0.5, for both P_{CO_2} and the solution species concentrations. We conclude from these figures that our predictive approach for the calculation of P_{CO_2} and the corresponding CO_2 -loaded solution concentrations provides results of similar quality to those determined experimentally.

7. SUMMARY AND CONCLUSIONS

We have developed a purely predictive methodology that requires no experimental data of any kind for the amine solvent for predicting P_{CO_2} and the corresponding CO_2 -loaded solution concentrations for the reactive absorption of CO_2 in a range of primary alkanolamine solvents. Our methodology is able to predict species concentrations of arbitrarily small magnitude, which are either difficult to measure or inaccessible experimentally. Since the reaction scheme is irrelevant for calculating equilibrium thermodynamic properties, ours was chosen to avoid the use of H^+ as a species, which is notoriously difficult to treat theoretically, due to the requirement to know the value of the hydration free energy of the proton as a function of temperature, an experimentally and theoretically elusive quantity. We applied our methodology to seven alkanolamine solvents and obtained excellent agreement with experimental results in cases when they are available, and made predictions in cases which have not yet been obtained.

Our algorithm entails the combination of the ideal-gas reaction standard free energies for the two reactions R1 and R2 using quantum mechanical methodology, and the calculation of hydration free energies for the solution species using classical force field methodology and standard molecular dynamics simulations. These quantities are appropriately translated to a macroscopically based thermodynamic model, from which P_{CO_2} and the solution concentrations are calculated by a free energy minimization algorithm.

We also calculated uncertainties for our predicted values of the relevant equilibrium constants, and for P_{CO_2} and the CO_2 loaded solution concentrations, by propagating the uncertainties in the ideal-gas quantities and hydration free energies through the equilibrium calculations to the final predicted quantities. We compared our predictions and their uncertainties with the corresponding experimental results obtained by different research groups (when these were available) and inferred the

experimental uncertainties from the scatter of the data. For all quantities (with the possible slight exception of the value of pK_1), we conclude that our methodology provides predictions in mutual agreement with those obtained experimentally within their mutual uncertainties.

Potential improvements to our approach, which may be required for more complex solvents, would entail more accurate and precise estimates of the ideal-gas reaction free energies and of the species hydration free energies. The recently developed (on-the-fly polarization) OTFP methodology for calculating hydration free energies is one possibility.^{105,106} In addition, for more complex solutions it may be necessary to account for the nonideal activity coefficient behavior in the Henry Law based chemical potential model used in this paper. Although we have found this to be unnecessary for the solutions arising in the systems considered here, these may be incorporated by means of the ideal solution chemical potential extrapolation methodology of Smith and Qi.⁴⁹

We suggest that our algorithm provides a potentially cost-effective screening methodology for improved solvent selection, and current work is underway to apply it to other potential solvents and their mixtures.

■ ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acs.iecr.0c03738>.

Ideal-gas standard reaction free energies for reactions R1 and R2, fitted equilibrium constant expressions for R1 and R2, species $\mu_{res,NVT;\infty}$ values at several temperatures, values of quantities contributing to the equilibrium constants of reactions R1 and R2, and raw Gaussian16 output for the neutral, protonated and carbamate forms of the alkanolamines studied, and for the small molecules (PDF)

Gromacs topology and G4 geometry (ZIP)

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Notes

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