Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

Supporting Information: Analysis of Conformational Properties of Amine Ligands at the Gold/Water Interface with QM, MM and QM/MM simulations

Dongyue Liang,[†] Jiewei Hong,[†] Dong Fang,[†] Joseph W. Bennett,[‡] Sara E. Mason,[‡] Robert J. Hamers,[¶] and Qiang Cui[*,†]

†*Department of Chemistry and Theoretical Chemistry Institute, University of Wisconsin-Madison, 1101 University Avenue, Madison, WI 53706*

‡*Department of Chemistry, University of Iowa, 251 North Capitol Street, Iowa City, IA 52242*

¶*Department of Chemistry, University of Wisconsin-Madison, 1101 University Avenue, Madison, WI 53706*

E-mail: cui@chem.wisc.edu,Tel:(+1)-608-332-6584

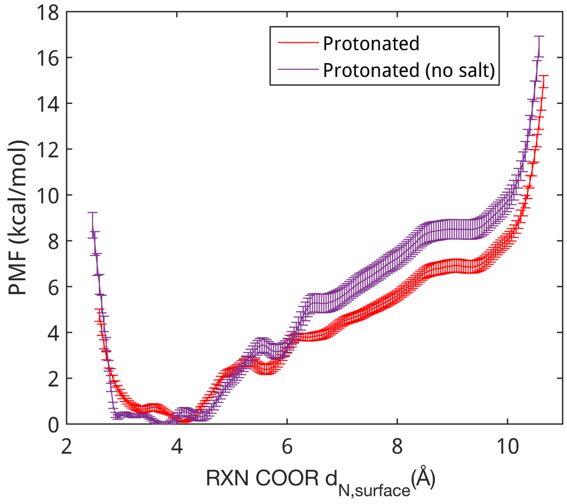
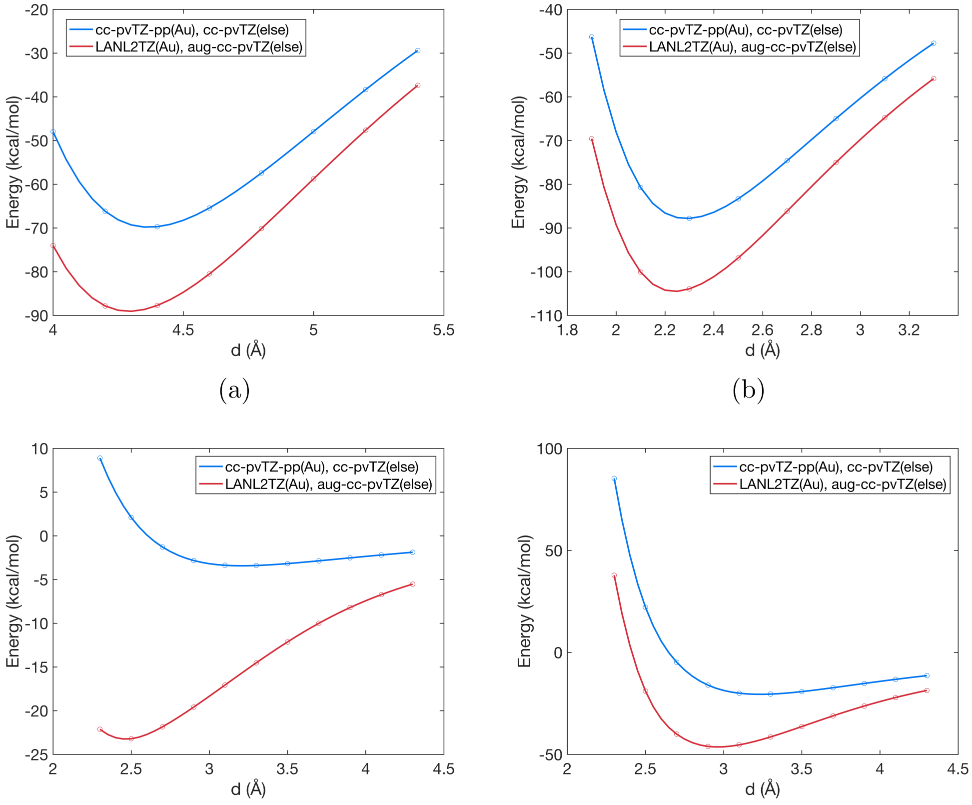


Figure S1: Potentials of mean force for a protonated amine at the (111) gold surface immerse in water with or without 150 M KCl salt. The result is used to test sensitivity of the ligand orientation to solution condition.

Table S1: T_1 diagnostic[1] for the CCSD(T) calculations reported in the main text [a]

(a)		(b)		(c)		(d)	
d(Å)	T_1 diag.	d(Å)	T_1 diag.	d(Å)	T_1 diag.	d(Å)	T_1 diag.
4.0	0.0246	1.9	0.0201	2.1	0.0248	2.3	0.0189
4.2	0.0247	2.1	0.0200	2.3	0.0223	2.5	0.0191
4.4	0.0249	2.3	0.0202	2.5	0.0215	2.7	0.0193
4.6	0.0253	2.5	0.0206	2.7	0.0212	2.9	0.0195
4.8	0.0260	2.7	0.0211	2.9	0.0210	3.1	0.0197
5.0	0.0273	2.9	0.0218	3.1	0.0208	3.3	0.0199
5.2	0.0290	3.1	0.0226	3.3	0.0207	3.5	0.0200
5.4	0.0313	3.3	0.0235	3.5	0.0206	3.7	0.0202
				3.7	0.0205	3.9	0.0203
				3.9	0.0204	4.1	0.0203
				4.1	0.0204	4.3	0.0204
				4.3	0.0203		

[a] (a-d) corresponds to the systems defined in Fig. 2 in the main text. Basis set: cc-pVTZ-pp for Au, with the g functions removed, cc-pVTZ for the main group elements.



(a) (b)

(c) (d)

Figure S2: CCSD(T) calculations of potential energy scans using different basis set for (a-b) covalent and (c-d) non-covalent interactions between the ligand and gold cluster systems illustrated in Fig. 2 of the main text. The x axis is defined accordingly. The g functions of cc-pVTZ-pp basis set are removed for Au. Similar to findings from previous benchmark calculations,[2,3] the Hay-Wadt pseudo-potential/basis set is not well suited for highly correlated calculations.

Table S2: Vertical binding energy (E_{bd}, in kcal/mol) calculated with CCSD(T) and different DFT functionals for the systems illustrated in Fig. 2 of the main text.[a]

Method	(a)	(b)	(c)	(d)
CCSD(T)	-87.7	-103.9	-14.5	-41.4
PBE	-71.8	-88.8	-3.1	-21.9
PBE-GD3	-74.3	-91.0	-6.4	-25.7
B3LYP	-60.3	-82.1	-0.6	-18.6
B3LYP-GD3	-64.9	-85.9	-6.2	-25.2
M06	-68.8	-88.9	-5.1	-21.9
M06-GD3	-69.3	-89.6	-5.9	-22.8
PBE0	-68.4	-88.7	-2.1	-21.4
PBE0-GD3	-71.2	-91.1	-5.5	-25.4
B2PLYP	-50.2	-81.0	0.7	-17.0
B2PLYP-GD3	-54.5	-84.0	-2.0	-20.3
CAM-B3LYP	-63.1	-90.0	-1.1	-20.1
CAM-B3LYP-GD3	-66.3	-92.7	-4.9	-24.6

[a] Compared to Table 1 in the main text, a smaller basis set is used: Lanl2TZ[4] for Au, aug-cc-pVTZ[5,6] for the main group elements. While the impact on the DFT results is modest, the CCSD(T) results deviate significantly from those with the cc-pVTZ-pp basis for Au; also see Fig. S2.

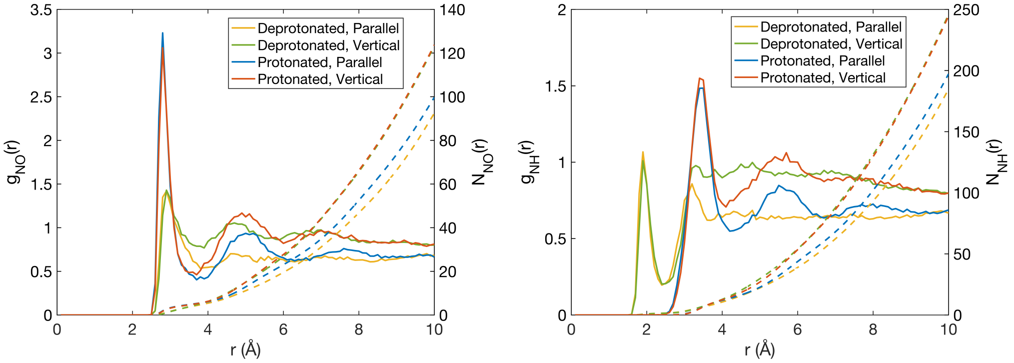
Table S3: Hirschfeld charges from gas phase QM/MM calculations[a]

Atom	Deprotonated Vertical	Deprotonated Parallel	Protonated Vertical	Protonated Parallel
1Au	-0.040	-0.017	-0.021	-0.057
2Au	-0.012	-0.026	-0.009	-0.068
3Au	-0.015	-0.021	-0.012	-0.012
4Au	0.018	0.038	0.000	-0.040
5Au	-0.024	-0.032	-0.007	-0.003
6Au	0.017	0.037	-0.010	0.016
7Au	0.022	0.010	0.018	0.005
8Au	-0.012	0.000	-0.034	-0.012
9Au	0.009	-0.021	0.032	0.024
10Au	0.020	0.037	0.002	0.034
11Au	0.001	0.039	-0.006	0.044
12Au	-0.039	-0.044	-0.053	-0.017
13Au	-0.029	-0.023	-0.009	0.018
14Au	-0.030	-0.031	-0.023	0.009
15Au	-0.041	-0.047	-0.023	0.007
16Au	0.025	0.010	0.028	0.005
17Au	0.031	0.047	0.028	0.033
18Au	0.026	0.029	0.024	0.029
19Au	0.006	0.006	0.010	0.013
20Au	0.029	0.025	0.041	0.037
21Au	0.028	0.040	0.026	0.042
22Au	0.042	0.043	0.044	0.048
23Au	0.022	0.018	0.035	0.037
24Au	-0.047	-0.039	0.000	0.028
25Au	-0.013	-0.008	0.007	0.015
26Au	-0.012	0.005	0.003	0.028
27Au	-0.002	-0.004	0.018	0.025
28Au	-0.017	-0.023	0.003	0.007
29Au	0.000	0.007	0.005	0.017
30Au	-0.024	-0.026	-0.010	0.001
31Au	-0.015	-0.013	0.012	0.021
32S	-0.006	-0.021	-0.049	-0.016
33C	-0.059	-0.065	-0.066	-0.064
34H	0.040	0.034	0.040	0.036
35H	0.051	0.055	0.048	0.060
36C	-0.067	-0.068	-0.061	-0.064
37H	0.043	0.045	0.047	0.051
38H	0.035	0.024	0.039	0.027
39C	-0.074	-0.078	-0.061	-0.067
40H	0.035	0.037	0.051	0.050
41H	0.034	0.021	0.052	0.030
42C	-0.019	-0.021	0.031	0.014
43H	0.044	0.045	0.080	0.070
44H	0.043	0.023	0.081	0.043
45N	-0.250	-0.236	0.033	0.009
46H	0.113	0.075	0.204	0.125
47H	0.113	0.113	0.204	0.188
48H	-	-	0.208	0.176

[a] The QM is PBE-GD3, with LanL2DZ for Au and 6-31G(d) for main group elements. 7Au, 9Au and 11Au are the three Au atoms closest to the S in the ligand.

Table S4: Hirshfeld charges of the ligand from periodic DFT calculations

Atom	Deprotonated Vertical	Deprotonated Parallel	Protonated Vertical	Protonated [a] Parallel
S	-0.0340	-0.0073	-0.0360	0.0028
C	-0.0600	-0.0806	-0.0630	-0.0784
H	0.0403	0.0494	0.0420	0.0545
H	0.0526	0.0018	0.0506	0.0025
C	-0.0749	-0.0743	-0.0728	-0.0705
H	-0.0019	-0.0126	-0.0020	-0.0114
H	0.0170	0.0401	0.0217	0.0457
C	-0.0582	-0.0706	-0.0531	-0.0673
H	0.0413	-0.0014	0.0455	0.0021
H	0.0392	0.0387	0.0511	0.0467
C	0.0159	-0.0110	0.0480	0.0164
H	0.0409	0.0123	0.0631	0.0302
H	0.0573	0.0575	0.0861	0.0763
N	-0.2099	-0.1732	-0.0044	-0.0126
H	0.1342	0.1076	0.1979	0.1787
H	0.0882	0.0484	0.1885	0.0944
H	-	-	0.1623	0.1273



(a) (b)

Figure S3: Radial distribution functions of the water oxygen and hydrogen around the amine nitrogen ($g_{NO}(r), g_{NH}(r)$) from the MM-PMF windows for the corresponding free energy minima, which contains 5 ns sampling. The dashed lines indicate the integrated radial distribution functions, which give the number of water oxygen/hydrogen within a given distance from the amine nitrogen ($N_{NO}(r), N_{NH}(r)$). Compare to Fig. 9 in the main text.

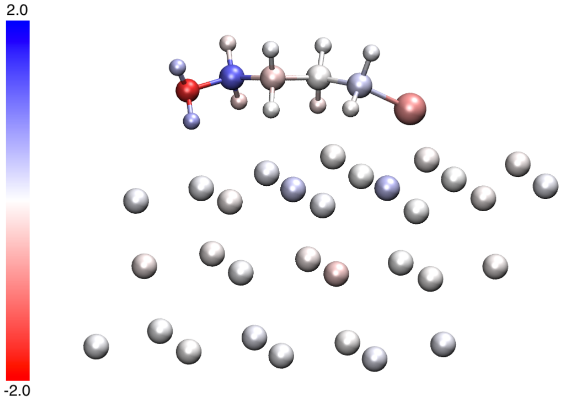


Figure S4: Illustration of extreme ESP charge distributions (using the MKUFF model[7,8]) occasionally sampled in the mean-field QM/MM simulations for the deprotonated amine ligand; e.g., -1.62*e* for the amine nitrogen and +1.19*e* for the connecting carbon. To compare various ESP charge schemes, a model system is set up to probe the interaction between an amine (lysine sidechain analog) and water. As shown in Table S5, different ESP schemes on average give similar descriptions for such interactions, regardless of the protonation state of the amine.

Table S5: Comparison of interaction energies (in kcal/mol) between a lysine sidechain analog and a water molecule from different QM and MM calculations[a]

System	PBE-GD3	CHARMM	MKUFF[7,8] R	MKUFF $R \times 1.2^b$	MKUFF $R/1.2^b$	HLYGat[9]
Protonated	2.12	1.15	1.57	1.57	1.60	1.53
Deprotonated	1.51	2.03	2.24	2.25	2.21	2.26

[a] The reference is based on HF/6-31G(d); for the deprotonated case, the HF interaction energies are multiplied by a factor of 1.16 to approximate the missing polarization effects, as done in the CHARMM force field parameterization procedure.[10] The shown values are the Root Mean Square Deviations from the HF reference for ∼150 randomly generated water configurations around the amine group in the lysine sidechain analog. In the MKUFF and HLYGat calculations, the lysine sidechain is described with the ESP charges, and the water is described with TIP3P. In general, the results show that DFT calculations, CHARMM force field and the ESP models give comparable descriptions for the lysine-water interactions. The major source of error of MM results comes from the cases with very short distances between the sidechain analog and water, where the repulsion becomes dominant. [b] The radii used to fit the ESP charges are scaled up or down from the UFF radii by a factor of 1.2.

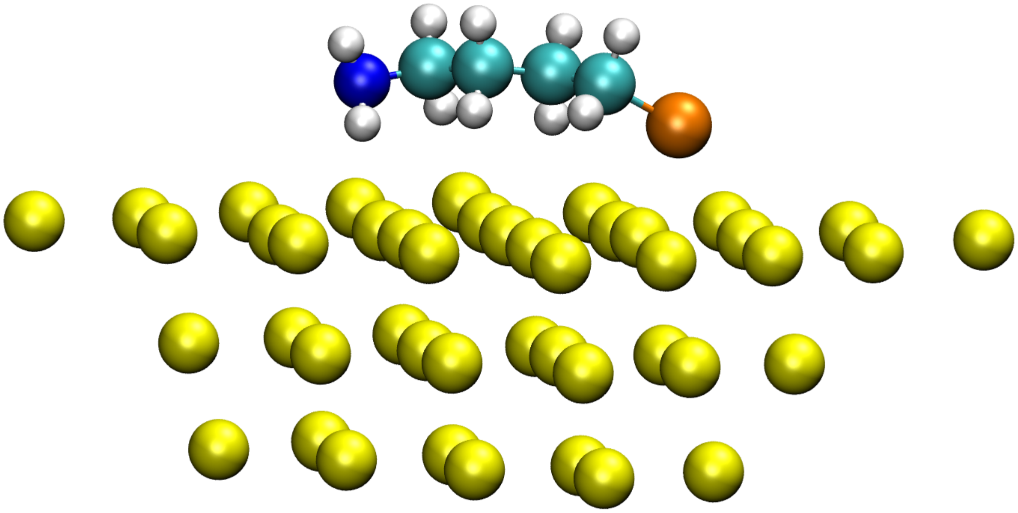


Figure S5: An illustration of the cluster model used for NMR chemical shift calculations. The structures are taken from gas phase QM/MM optimization results.

Table S6: Optimized gold-sulfur distances (in Å) between the ligand sulfur atom and three nearest gold atoms from QM/MM-MFEP calculations[a]

Atom	Deprotonated Vertical	Deprotonated Parallel	Protonated Vertical	Protonated Parallel
7Au	2.44	2.44	2.46	2.43
9Au	3.45	3.44	3.46	3.46
11Au	3.17	3.40	3.17	3.40

[a] The QM is PBE-GD3, with LanL2DZ for Au and 6-31G(d) for main group elements.

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