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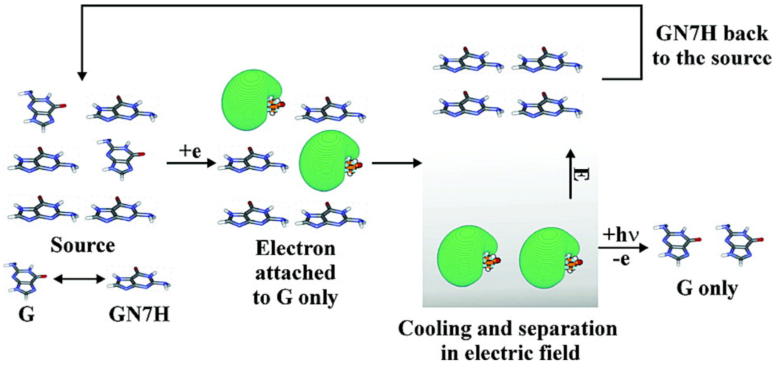

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Valence and Dipole-Bound Anions of the Most Stable Tautomers of Guanine

Maciej Haranczyk[†,‡] and Maciej Gutowski*[,†]

Contribution from the Chemical Sciences Division, Pacific Northwest National Laboratory, Richland, Washington 99352, and Department of Chemistry, University of Gdansk, 80-952 Gdansk, Poland

Received June 8, 2004; E-mail: maciej.gutowski@pnl.gov

Abstract: Anionic states of guanine, which is the only nucleic acid base of which the anions have not yet been studied in either photoelectron spectroscopic (PES) or Rydberg electron transfer (RET) experiments, have been characterized for the four most stable tautomers of neutral guanine using a broad spectrum of electronic structure methods from the density functional theory, with the B3LYP exchange−correlation functional, to the coupled-cluster method, with single, double, and perturbative triple excitations. Both valence and dipole-bound anionic states were addressed. We identified some of the difficulties facing future PES or RET experiments on the anion of guanine. Even if guanine is successfully transferred to the gas phase without thermal decomposition, it is critical to have the canonical amino−oxo (G) and both amino−hydroxy (GH and GHN7H) tautomers in the beam, not only the most stable, a noncanonical, amino−oxo tautomer (GN7H), as the latter does not support an adiabatically bound anionic state. We also suggested a scheme for enrichment of gas-phase guanine with the canonical tautomer, which is not the most stable in the gas phase, but which is of main interest due to its biological relevance. The tautomers G, GN7H, and GHN7H support vertically bound *valence* anionic states with the CCSD(T) value of vertical detachment energy of +0.58, +0.21, and +0.39 eV, respectively. These anionic states are, however, adiabatically unbound and thus metastable. The vertical electronic stability of these valence anionic states is accompanied by serious “buckling” of the molecular skeleton. The G and GHN7H tautomers support *dipole-bound* states with the CCSD(T) values of adiabatic electron affinity of 65 and 36 meV, respectively. A contribution from higher-than-second-order correlation terms represents, respectively, 48 and 68% of the total vertical electron detachment energy determined at the CCSD(T) level.

1. Introduction

The nucleic acid bases (NABs) are elementary building blocks of DNA, which is responsible for storing genetic information in cells. Low-energy electrons and hydroxyl radicals are among the most reactive species formed upon interaction of high-energy radiation with living cells. Low-energy electrons might become trapped on nucleic acid bases, and the resulting radical anions might participate in chemical reactions which can lead to DNA damage.[1] For example, the recent experiments of Sanche and co-workers suggested that anionic states cause single- and double-strand breaks.[2] Furthermore, the charged nucleic acid bases play a key role in the electron and hole transfer phenomena in DNA.[3−6]

The results of an ESR study of the relative distribution of ion radicals formed in γ-irradiated DNA suggested that the anion is divided between the pyrimidine bases, but the excess electron is not localized on guanine.[7] The reason is that the relative electron affinities favor cytosine and thymine over guanine and adenine.

In the past, a large number of theoretical and experimental studies were focused on determination of electron affinity of NABs in the gas or condensed phases. Anions of hydrated NABs are believed to support an excess electron on a valence-type molecular orbital, as suggested by many experimental[8] as well as theoretical data.[9] However, the existence of stable anions of NABs in the gas phase has long been a point of discussion. Computational studies conducted as early as the 1960s had predicted negative values of adiabatic electron affinity (AEA).[10−12]

[†] Pacific Northwest National Laboratory.

[‡] University of Gdansk.

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An important development occurred in mid 90s when Adamowicz and co-workers found stable but loosely bound anionic states supported primarily by the large dipole moments of neutral NABs.[13−15]

These insightful theoretical predictions were followed by experimental studies aiming to characterize anions of NABs in the gas phase. Bowen and co-workers studied uracil and thymine by negative ion photoelectron spectroscopy (PES).[16] The adiabatic electron affinities were found to be 93 ± 7 meV for uracil and 69 ± 7 meV for thymine and were assigned to dipole-bound states. Desfrancois, Abdoul-Carime, and Schermann produced gas-phase anions of NABs in charge-exchange collisions with laser-excited Rydberg atoms and reported the following values of AEA: 54 ± 35 meV for uracil, 68 ± 20 meV for thymine, and 12 ± 5 meV for adenine.[17] The latter authors also concluded that uracil and thymine have positive electron affinities for valence anionic states. Schlag and co-workers presented photodetachment−photoelectron spectra of the pyrimidine NABs.[18] They found a dipole-bound state of uracil at 86 ± 8 meV, thymine at 62 ± 8 meV, and cytosine at 85 ± 8 meV.

An important evolution of anions of NABs occurs upon solvation, as reported by Bowen and co-workers.[19] A transformation from the dipole-bound to covalent anion of uracil was demonstrated upon solvation by a single noble gas atom or water molecule. Their photoelectron spectra show that complexes of uracil with argon or krypton support only dipole-bound anions, but a complex of uracil with a more polarizable xenon atom can support both a dipole-bound and valence anionic state that can be distinguished easily by different values of electron vertical detachment energy (VDE) and the shape of the PES feature. The anionic complex of uracil and water was found to exist only as a valence anion. This study has convincingly demonstrated that anions of NABs might exist in dipole-bound states in the gas phase but convert to valence anions upon solvation.

Valence anionic states of NABs were probed in low-energy electron transmission spectroscopy experiments of Burrow and collaborators.[20] They reported a vertical attachment energy (VAE) of −0.46 eV for guanine and assigned it to an enol (amino−hydroxy) tautomer. The negative value means that the probed anionic state is unbound with respect to the neutral at the optimal geometry of the neutral.

The past computational studies were focused primarily on valence anionic states of the canonical tautomer of guanine.[9,21,22] The values of adiabatic electron affinity (AEA) were obtained primarily with the density functional theory (DFT) method using different exchange−correlation functionals and basis sets.[21,22] All but one suggested a negative value of the AEA (i.e., the anion was less stable than the neutral). The most recent study on electron affinities of NABs questioned the previously reported values of the AEA of guanine.[9] Sevilla and co-workers suggested that inclusion of diffuse functions in the basis set can result in contamination of the valence state with the dipole-bound state. In their calculations, they used only small 6-31G(D) and D95V(D) basis sets that do not provide a sufficient extendedness to support a dipole-bound state, and they reported a negative value of the AEA of −0.75 eV for the canonical tautomer of guanine with the B3LYP exchange−correlation functional.

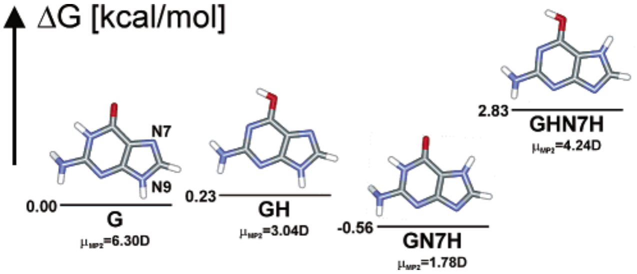

Figure 1. Tautomers of neutral guanine. Relative Gibbs free energy determined at the CCSD(T)/aug-cc-pVDZ level using the MP2/aug-cc-pVDZ geometries and thermal corrections.

The dipole-bound states of guanine were studied by Adamowicz et al.[15] In their 1994 study, they showed that the two tautomers of guanine, denoted G and GH in Figure 1, have positive electron affinities, 0.034 and 0.00038 eV, respectively, as determined at the MP2/6-31+G*X level of theory using the SCF/3-21+GX geometry (where X stands for a set of three sp shells with very small exponents). The relative energies of tautomers of neutral guanine were also presented. A difference in stability between the oxo−amino (G) and hydroxy−amino (GH) forms was found to be only 0.1 kcal/mol[23] at the MP2/6-31++G**//SCF/6-31++G** level. Adamowicz and co-workers concluded that the significant difference in the AEA values for the oxo−amino and hydroxy−amino tautomers should lead to a significant difference in the tautomeric equilibrium between the neutral and anionic guanine in the gas phase.

Many theoretical studies were devoted to the tautomers of neutral guanine[24−29] Four low-energy tautomers were identified (two amino−oxo and two amino−hydroxy; see Figure 1), with an amino−oxo form having hydrogen at N7 (GN7H) being the most stable. In a recent paper, Hobza and co-workers determined relative energies of tautomers of guanine characterized at the CCSD(T)/aug-cc-pVDZ level of theory using geometries obtained with the RI-MP2/TZVPP method.[24] The GN7H tautomer was found to be 0.69 kcal/mol lower in energy than the canonical tautomer (amino−oxo N9−H, denoted as G in Figure 1) and 0.44 kcal/mol lower in terms of Gibbs free energy. Amino−hydroxy tautomers, denoted GH and GHN7H (see Figure 1), are less stable than the amino−oxo tautomers. Experimental and theoretical results are consistent, and four

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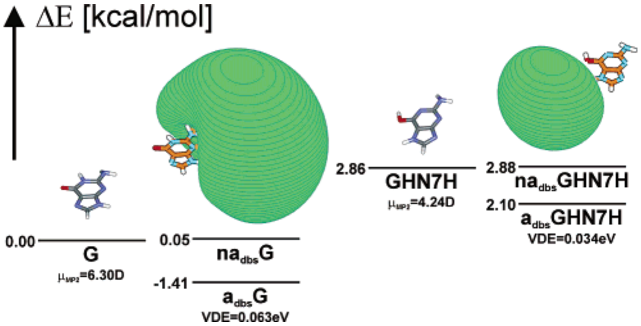

Figure 2. Dipole-bound anionic states of guanine. Singly occupied orbitals plotted with a spacing of 0.003 bohr$^{-3/2}$.

tautomeric forms of guanine have recently been detected in the gas phase.[30,31]

In this paper, we focus on both valence and dipole-bound anionic states of guanine. Guanine is the only NAB of which the anions have not yet been characterized in either PES or Rydberg electron transfer (RET) experiments. Recent efforts to determine properties of anionic guanine in the PES and RET experiments failed because guanine readily decomposes at elevated temperatures.[32] Guanine and other NABs also undergo dissociation upon an excess electron attachment. Guanine, however, dissociates into molecular fragments, whereas other bases undergo primarily a detachment of a NH hydrogen atom.[33]

In view of the instability of guanine in the gas-phase experiments, theory provides indispensable tools for characterizing valence and dipole-bound anionic states of various tautomers of guanine. Our study covers electron binding to the G, GH, GN7H, and GHN7H tautomers, and electronically bound states are characterized at the coupled-cluster level of theory with single, double, and noniterative triple excitations (CCSD(T)) and basis sets of aug-cc-pVDZ quality. An important finding is that the valence anionic states are adiabatically unbound, though the G, GN7H, and GHN7H tautomers support vertically bound valence anionic states; that is, the anion is more stable than the neutral at the equilibrium anionic geometry. We also demonstrate that a dipole-bound anionic state supported by the canonical tautomer G is more stable than the most stable neutral tautomer GN7H accompanied by a free electron. The GN7H tautomer does not support a dipole-bound state. Thus, the excess electron binding compensates the inherent instability of the canonical tautomer with respect to GN7H. Finally, within the PCM model of hydration,[34,35] all four tautomers support adiabatically bound valence anionic states. Trying to assist future PES and RET gas-phase experiments, we suggest that it is critical to have the G, GHN7H, and GH tautomers in the beam, not only the most stable GN7H tautomer, as the latter does not support a bound anionic state. We also suggest an experimental procedure for how to enrich the gas-phase guanine with the canonical tautomer G.

2. Methods

We use the notation of Adamowicz et al.[15] for the tautomers of guanine. The canonical tautomer, amino−oxo N9−H, is named “G”, and its amino−hydroxy form is called “GH”. Another amino−oxo N7−H tautomer and its amino−hydroxy counterpart are called “GN7H” and “GHN7H”, respectively (see Figure 1). Additional prefixes “a” and “na” are used to distinguish properties of the anion and neutral, respectively, determined at the minimum energy structure of the anion (Figures 2 and 3). Finally, the “val” or “dbs” subscript discriminates between the valence and dipole-bound anionic states.

The gas-phase geometries of neutral and anionic tautomers of guanine were optimized using the density functional method with the B3LYP exchange−correlation functional[36−38] and the second-order Møller−Plesset (MP2) method. The 6-311+G** and augmented correlation-consistent polarization double-ζ (aug-cc-pVDZ) basis sets[39] were used in the B3LYP and MP2 calculations, respectively. In calculations for dipole-bound anions, the aug-cc-pVDZ set was supplemented with five additional s and p functions placed on the H−N9 and H−N7 hydrogen of the G and GHN7H tautomer, respectively. The exponents of the extra diffuse functions form a geometric sequence with a progression constant of 1/3.2,[40] and the sequence starts from the smallest s exponent in the original aug-cc-pVDZ basis set. The spin contamination was negligible for dipole-bound anions and relatively small for valence anions. Indeed, the value of S^2 for valence anions described with the UHF and UB3LYP wave functions did not exceed 0.83 and 0.76, respectively.

The most accurate electronic energies for the neutral and anionic guanine were calculated at the coupled-cluster level of theory with single, double, and perturbative triple excitations (CCSD(T))[41] with the aug-cc-pVDZ basis set at the optimal MP2 geometries. The open-shell CCSD(T) calculations were carried out at the R/UCCSD(T) level. In this approach, a restricted open-shell Hartree−Fock calculation was initially performed to generate the set of molecular orbitals, and the spin constraint was relaxed in the coupled-cluster calculation.[42−44] The relative energies of the anion with respect to the neutral were corrected for zero-point vibrations; the relative free energies were obtained by including the zero-point vibration energy, thermal corrections, and entropy terms calculated at either the B3LYP or MP2 levels for T = 298 K and p = 1 atm in the harmonic oscillator rigid rotor approximation.

For dipole-bound anions, we applied a standard approach for analysis of the values of VDE.[45−47] First, the VDE was calculated at the Koopmans’ theorem level (D^{KT}) and then supplemented with orbital

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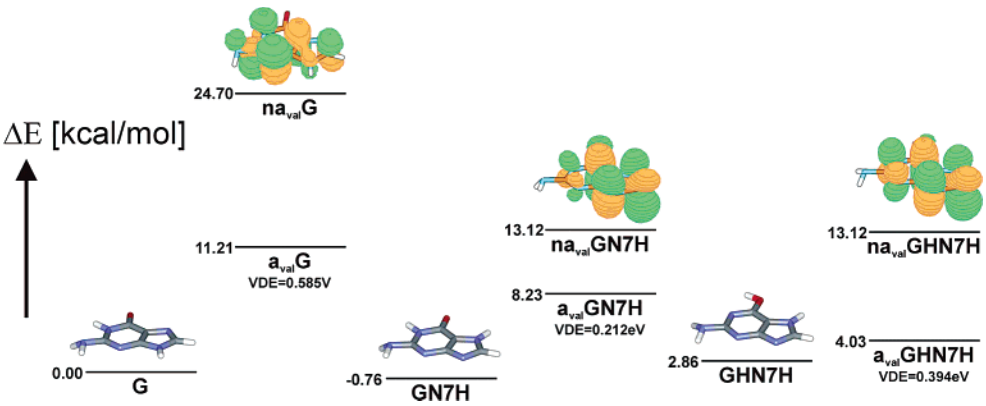

Figure 3. Vertically bound valence-type anionic states of guanine. Singly occupied orbitals plotted with a spacing of 0.02 bohr$^{-3/2}$.

relaxation and electron-correlation contributions. The polarization of the neutral (N) by the excess electron and the effect of back-polarization are taken into account when the SCF calculation is performed for the anion, and the accompanying induction effects are given by

$$\Delta D_{\mathrm{ind}}^{\mathrm{SCF}} = D^{\mathrm{SCF}} - D^{\mathrm{KT}} \tag{1}$$

where

$$D^{\mathrm{SCF}} = E_{\mathrm{N}}^{\mathrm{SCF}} - E_{\mathrm{A}}^{\mathrm{SCF}} \tag{2}$$

and $E_{\mathrm{N}}^{\mathrm{SCF}}$ and $E_{\mathrm{A}}^{\mathrm{SCF}}$ are the SCF energy of the neutral and the anion, respectively.

The dispersion interaction between the loosely bound electron (lbe) and N was extracted from the MP2 contribution to D. The dispersion term is a second-order correction with respect to the fluctuation−interaction operator,[45] and it is approximated here by $\Delta D_{\mathrm{disp}}^{\mathrm{MP2}}$, which takes into account proper permutational symmetry for all electrons in the anion

$$\epsilon_{\mathrm{disp}}^{(02)} \approx \sum_{a\in N}\sum_{r<s} \frac{|\langle \phi_{\mathrm{a}}\phi_{\mathrm{lbe}}||\phi_{\mathrm{r}}\phi_{\mathrm{s}}\rangle|^2}{e_{\mathrm{a}} + e_{\mathrm{lbe}} - e_{\mathrm{r}} - e_{\mathrm{s}}} = -\Delta D_{disp}^{MP2} \tag{3}$$

where φ_{a} and φ_{lbe} are spin orbitals occupied in the UHF wave function; φ_{r} and φ_{s} are unoccupied spin orbitals, and e is the corresponding orbital energy.

The total MP2 contribution to D defined as

$$\Delta D^{\mathrm{MP2}} = D^{\mathrm{MP2}} - D^{\mathrm{SCF}} \tag{4}$$

is naturally split into the dispersion and nondispersion terms

$$\Delta D^{\mathrm{MP2}} = \Delta D_{\mathrm{disp}}^{\mathrm{MP2}} + \Delta D_{\mathrm{no-disp}}^{\mathrm{MP2}} \tag{5}$$

with the latter being dominated by the correlation correction to the static Coulomb interaction between the lbe and the charge distribution of N.

Finally, a higher-order correlation contribution to D from single and double excitations is obtained by subtracting the MP2 result from the coupled-cluster CCSD result

$$\Delta HO^{\mathrm{SD}} = D^{\mathrm{CCSD}} - D^{MP2} \tag{6}$$

and an approximate contribution from triple excitations is obtained by subtracting the CCSD and CCSD(T) values of D

$$\Delta HO^{\mathrm{T}} = D^{\mathrm{CCSD(T)}} - D^{\mathrm{CCSD}} \tag{7}$$

The 1s orbitals of carbon, nitrogen, and oxygen were excluded from electron correlation treatments throughout this study.

Guanine in the gas phase does not support a bound valence anionic state at the geometry of the neutral.[20] A question that we address in this study is whether the regions of the potential energy surface that support a bound valence anion are also minima. In other words, are there minimum energy structures at which the anion is vertically bound? What intramolecular distortions are required to render the anionic state bound with respect to the neutral, and what energetic effects are accompanying these distortions? Answering these questions will allow the determination of whether the anions are adiabatically or only vertically bound, or not bound at all.

Sevilla et al. addressed a problem[9] of which set of atomic orbitals should be used in calculations of valence anions of polar molecules, such as guanine, which are characterized by negative values of vertical electron affinity, that is, the valence anion is unbound with respect to the neutral at the optimal geometry of the neutral, but which support dipole-bound anionic states. The latter anionic states are typically bound by less than 70 meV even for molecules with dipole moments as large as 6 D. There is a dilemma as to which basis set should be used in calculations for the valence anionic state. On one hand, it is known that extended basis sets supplemented with basis functions with small exponents are required to properly describe diffuse charge distributions of molecular anions.[48] On the other hand, optimization of the wave function for an unbound anion of a polar molecule might converge to a solution which is contaminated with a dipole-bound contribution if an extended basis set is used. Indeed, Sevilla et al. reported such a behavior in the B3LYP calculations with 6-31+G* and D95V+(D) basis sets for the valence anion of guanine. In consequence, they could only estimate the values of vertical and adiabatic electron affinity of guanine in the gas phase from the results obtained with sets of compact basis functions and basis set saturation trends for other nucleic acid bases.

Our approach to this basis set dilemma is different. We deal only with the regions of the potential energy surface in which the valence anion is vertically bound with respect to the neutral. Then, we perform calculations with standard basis sets that contain basis functions with small exponents. As we are dealing with bound anionic states, these basis functions contribute to the proper description of the anionic charge distribution but do not lead to a collapse to the dipole-bound state, which is usually less strongly bound than the valence anionic state. We believe that dealing with unbound valence anionic states is not straightforward when using conventional electronic structure methods based on variational principle, and the results may be dependent on the quality of the basis set. Special treatments, such as the stabilization method or the complex coordinate technique, provide means to extract resonance positions and widths.[48,49]

We applied the following approach to identify minimum energy structures of valence anions of guanine, which might be vertically bound in the gas phase. Initial B3LYP/6-311+G** calculations were per-

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Table 1. Relative Energies (kcal/mol) for the Tautomers of Neutral Guanine Determined at the B3LYP, MP2, and CCSD(T) Levels

	B3LYP				MP2				CCSD(T)				Ref 24	
tautomer	ΔE	$\Delta E + \Delta E^0_{vib}$	ΔH	ΔG	ΔE	$\Delta E + \Delta E^0_{vib}$	ΔH	ΔG	ΔE	$\Delta E + \Delta E^0_{vib}$	ΔH	ΔG	ΔE	ΔG
G	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
GH	0.63	0.65	0.62	0.74	0.34	0.29	0.23	0.42	0.15	0.09	0.04	0.23	0.22	0.12
GN7H	−0.76	−0.62	−0.65	−0.61	−0.72	−0.54	−0.57	−0.51	−0.76	−0.58	−0.62	−0.56	−0.69	−0.44
GHN7H	3.41	3.29	3.30	3.35	3.13	2.99	2.97	3.10	2.86	2.72	2.70	2.83	3.01	2.85

formed for the anion of hydrated guanine, using the PCM model[34,35] and water's dielectric constant $\epsilon = 78$. For all four tautomers, nonplanarity of the neutral guanine is limited to the $N2H_2$ group. It is known, however, that "buckling" of the ring of a nucleic acid base might increase the electronic stability of the anion because the excess electron occupies a π* orbital.[50] Thus, our energy minimizations for the anion of hydrated guanine were initiated from buckled structures. Some of the converged structures were indeed strongly nonplanar. These geometries as well as converged orbitals of the hydrated anion were used as initial guesses in geometry optimizations for the gas-phase anions.

The DFT and MP2 geometry optimizations were performed with Gaussian98,[39] the numerical MP2 frequency calculations with NWChem,[51] and the CCSD(T) calculations with the MOLPRO[52] package. The codes were run on Intel/P4Xeon workstations, SGI Altix server, and a cluster of dual Intel Itanium2 nodes with Quadrics interconnect. Molden was used for visualization of singly occupied molecular orbitals.[53]

Table 2. Adiabatic Electron Affinities (meV) Determined at the MP2, CCSD, and CCSD(T) Levels for Vertically Bound Valence and Dipole-Bound Anions[a]

	MP2		CCSD	CCSD(T)
	AEA−ΔE^0_{vib}	AEA	AEA	AEA
Dipole-Bound Anions				
G	32	36	56	65
GHN7H	10	13	30	36
Valence Anions				
G	−655	−628	−524	−486
GN7H	−756	−683	−592	−529
GHN7H	−622	−560	−422	−383

[a] AEA−ΔE^0_{vib} is the adiabatic electron affinity uncorrected for the difference in zero-point vibration energies between the neutral and the anion.

Table 3. Electron Vertical Detachment Energies (meV) and Their Decompositions (eqs 1−7)

	G	GHN7H	G	GN7H	GHN7H
anion type	dbs	dbs	val	val	val
D^{KT}	20.00	3.00	<0	<0	<0
ΔD^{SCF}_{ind}	2.00	1.00	N/A	N/A	N/A
D^{SCF}	22.00	4.00	379.00	105.00	335.00
ΔD^{MP2}_{disp}	21.65	8.35	N/A	N/A	N/A
$\Delta D^{MP2}_{no-disp}$	−10.65	−1.35	N/A	N/A	N/A
ΔD^{MP2}	11.00	7.00	74.00	−41.00	−76.00
D^{MP2}	33.00	11.00	453.00	64.00	259.00
ΔHO^{SD}	22.00	17.00	206.00	200.00	210.00
D^{CCSD}	55.00	28.00	659.00	264.00	469.00
ΔHO^{T}	8.00	6.00	−74.00	−52.00	−75.00
$D^{CCSD(T)}$	63.00	34.00	585.00	212.00	394.00

3. Results

3.1. Tautomers of Neutral Guanine. The amino−oxo N7−H tautomer (GN7H) is the most stable at every level of theory in terms of energy, enthalpy, and Gibbs free energy (Table 1 and Figure 1). At the CCSD(T)/aug-cc-pVDZ//MP2-aug-cc-pVDZ level, the canonical tautomer G is only 0.76 kcal/mol less stable in terms of energy. The amino−hydroxy GH and GHN7H tautomers follow by being less stable than G by 0.15 and 2.86 kcal/mol, respectively. In terms of Gibbs free energy, a difference in stability between G and GN7H is only 0.56 kcal/mol, and the amino−hydroxy tautomers are again less stable than the amino−oxo forms. Our results are in excellent agreement with the results of Hobza et al. which were calculated at the same CCSD(T)/aug-cc-pVDZ level but using the RI-MP2/TZVPP geometry.[24] Lower-level methods, such as MP2 and B3LYP, predict correctly not only the relative ordering of tautomers but also the quantitative energy differences, with deviations from the CCSD(T) results being larger for the amino−hydroxy tautomers,[54] but still not exceeding 0.6 kcal/mol.

In agreement with previous calculations,[15] the largest dipole moments of 6.3 and 4.2 D were found for the G and GHN7H tautomers, respectively (see Figure 1). A dipole moment of 1.78 D for GN7H is too small to support a dipole-bound state, whereas a dipole moment of 3.0 D for GH can support an anionic state, though previous calculations indicated that the electron-binding energy is <1 meV.[15] Thus, only dipole-bound states of G and GHN7H are studied here (see Tables 2 and 3 and Figure 2).

The results for neutral tautomers of guanine point to additional difficulties facing future PES or RET experiments on the anion of guanine. We expect that a barrier for the G ↔ GN7H tautomerization is high if not assisted by another molecule.[55] Even if guanine is successfully transferred to the gas phase without thermal decomposition, it is critical to have the G, GH, and GHN7H tautomers in the beam, not only the most stable GN7H tautomer as the latter does not support a bound anionic state and a long-lived anion cannot be formed in the course of excess electron attachment. When thermal contributions to the relative Gibbs energy are ignored, the energy difference of 0.58 kcal/mol between the G and GN7H tautomers implies that at $T = 100$ K, only 5% of guanine will populate the G tautomer.

3.2. Dipole-Bound Anions. The CCSD(T) value of adiabatic electron affinity for the canonical tautomer was found to be 65

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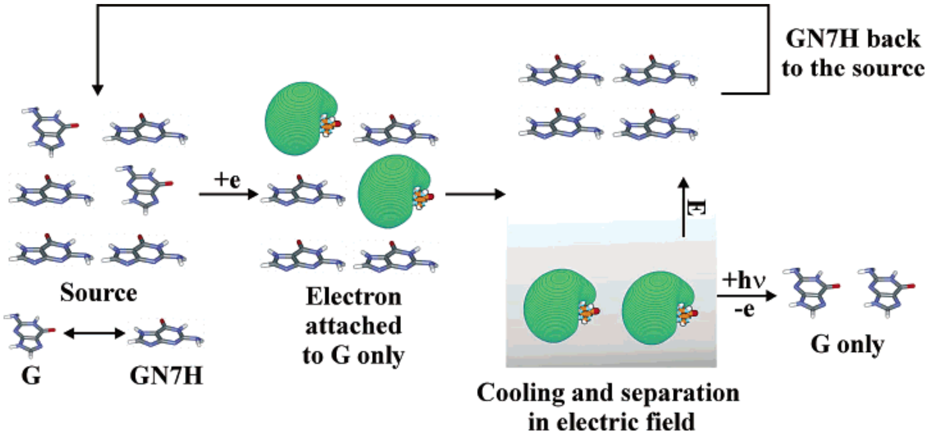

Figure 4. Scheme for the enrichment of gas-phase guanine with the biologically relevant G tautomer.

meV (see Table 2). This value is almost two times larger than the MP2 value, with the latter being in good agreement with that presented by Adamowicz and co-workers (34 meV).[15] There is only a small geometrical reorganization from the optimal geometry of the neutral to the optimal geometry of the dipole-bound anion. This may be inferred from the following: (i) a contribution from zero-point vibrations to the AEA is only 4 meV, (ii) the VDE is only 2 meV larger than the AEA, and (iii) the electronic energy of the neutral is increased by only 0.05 kcal/mol upon geometry relaxation induced by an excess electron attachment (see Figure 2).

The GHN7H tautomer with a dipole moment of 4.2 D also binds an excess electron, and the CCSD(T) value of the AEA is 36 meV (see Table 2). The MP2 value of the AEA is only 13 meV. Thus, correlation effects that go beyond the MP2 level are critical for dipole-bound anions of both tautomers. The energies of the anions of GHN7H and G differ by 3.5 kcal/mol (see Figure 2). Thus, the anionic beam in thermal equilibrium will be strongly dominated by the G tautomer.

We pointed out in Table 1 that the neutral tautomer GN7H is more stable than G by 0.58 kcal/mol at 0 K. However, the AEA of G is 1.50 kcal/mol, whereas the GN7H tautomer does not bind an electron adiabatically. Thus, the dipole-bound anion of G is more stable than the neutral of GN7H accompanied by a free electron.

In standard conditions, the gas-phase neutral guanine will be dominated by the GN7H tautomer, whereas the canonical tautomer G is of the main interest due to its biological relevance. The GN7H tautomer does not bind an excess electron, and a barrier for the G ↔ GN7H tautomerization is expected to be high. These properties suggest that there might be a possibility to enrich the population of the canonical tautomer through (i) transfer of guanine to the gas phase at temperatures that populate not only the GN7H but also the G tautomer, (ii) formation of anions of guanine, (iii) selection of the cooled-down long-lived species (i.e., primarily G^-), and (iv) soft photodetachment of an excess electron. The resulting guanine will populate primarily the G tautomer, and a small contamination will result from the GHN7H and, perhaps, GH tautomers. A scheme for the enrichment procedure is presented in Figure 4.

Table 4. Vertical Attachment Energies (VAE), Adiabatic Electron Affinities Uncorrected for the Zero-Point Vibration Term ($AEA-\Delta E^0_{vib}$), and Vertical Detachment Energies (VDE) Determined at the B3LYP/6-311+G** Level in Water[a]

tautomer	VAE	$AEA-\Delta E^0_{vib}$	VDE
G	0.90	1.41	2.65
GH	1.23	1.59	2.09
GN7H	1.30	1.76	1.96
GHN7H	1.45	1.86	2.03

[a] Effects of hydration simulated within the PCM model (all quantities are in eV).

A decomposition of vertical electron detachment energies into components defined by eqs 1−7 is presented in Table 3. The Koopmans' theorem contribution is followed by a small SCF induction term. The resulting values of D^{SCF} of 22 and 4 meV reproduce only 35 and 12% of the CCSD(T) value of D for G and GHN7H, respectively. For both anions, the MP2 dispersion contribution is larger than that of the Koopmans' theorem term, and the MP2 nondispersion term is destabilizing because the MP2 dipole moment of neutral guanine is smaller than the SCF dipole moment. The resulting values of D^{MP2} of 33 and 11 meV reproduce only 52 and 32% of $D^{CCSD(T)}$ for G and GHN7H, respectively. A contribution from higher-than-second-order correlation terms limited to single and double excitations is very significant and amounts to 22 and 17 meV for G and GHN7H, respectively. This is the dominant component of D for GHN7H. Relatively small contributions from triple excitations imply that the final CCSD(T) values of D of 63 and 34 meV for G and GHN7H, respectively, might be close to the methodologically converged result. An experimental verification of these theoretical predictions would be very important.

3.3. Valence Anions. Our search for vertically bound valence anionic states of guanine in the gas phase ended up with positive results for the G, GN7H, and GHN7H tautomers (see Tables 3 and 4, and Figure 3). The initial B3LYP/6-311+G** searches included two steps: (i) optimization for a hydrated valence anion using the PCM model and a buckled initial structure followed by (ii) reoptimization for the gas-phase anion using the geometry and orbitals of the hydrated anion.

Hydration within the PCM model has a significant effect on the neutral and anionic guanine. First, the G tautomer becomes the most stable among the neutral hydrated species, with the GN7H tautomer being less stable by 0.9 kcal/mol. Second, for each tautomer, the hydrated anion becomes not only vertically but also adiabatically bound (see Table 4). This is consistent with the results presented by Sevilla and co-workers.[9] The largest values of AEA are reported for the GHN7H and GN7H tautomers, which are also characterized by the largest values of electron vertical attachment energy. All are characterized by large values of VDE, about +2 eV, but the result may be sensitive to the selection of solvation model. Adiabatic binding of the excess electron is the weakest for the G tautomer. The hydrated anions display nonplanarity limited to the six-member ring of G and GH and the five-member rings of GN7H and GHN7H.

A reoptimization of the anionic structures in the gas phase led to an important discovery. Three anions, G, GN7H, and GHN7H, remain vertically bound at the MP2 level, and the MP2/aug-cc-pVDZ optimized structures are characterized by the CCSD(T) values of VDE being +0.58, +0.21, and +0.39 eV, respectively (see Tables 2 and 3, and Figure 3). They remain, however, adiabatically unbound with the CCSD(T) values of AEA of −0.49, −0.53, and −0.38 eV, respectively. For all of these tautomers, the SOMO orbital has a π^* valence character. The existence of a vertically stable valence anion of G has not been reported heretofore. In this anion, the six-member ring is strongly buckled, and the $-NH_2$ group is strongly rotated out of the plane of the ring. This anion is a very shallow minimum on the PES since the energy barrier for buckling of the guanine ring, which separates the valence anion from the planar dipole-bound anion, was found to be only 0.55 and 0.66 kcal/mol at the MP2 and CCSD(T) levels, respectively. The barrier does not exist at the B3LYP/6-311++G** level, which explains why the valence anion of G has not been hitherto identified. Interestingly, a small barrier exists at the B3LYP/6-31G** level. The GH tautomer does not support a vertically bound valence anionic state. The theoretical predictions are consistent at the MP2, CCSD, and CCSD(T) levels (Tables 2−4), which strengthens our conclusion that the G, GN7H, and GHN7H tautomers support vertically, but not adiabatically, bound anions.

The vertical electronic stability of the anionic G, GN7H, and GHN7H tautomers is accompanied by serious geometrical relaxations with respect to the structure of the corresponding neutrals. The nonplanarity of neutral tautomers is limited to the $N2H_2$ group. The excess electron attachment leads, however, to a serious buckling of the six-member ring for G and the five-member rings for GN7H and GHN7H, where the excess electron is primarily localized (Figure 3). These geometrical distortions involve both the hydrogen and heavy atoms. The largest deviation from planarity is displayed by the following dihedral angles [deviation from 0° (for G) and 180° (for GN7H and GHN7H) is considered here as a measure of nonplanarity]: (i) in G^-, the dihedral angles C6−N1−C2−N3 and N1−C2−N3−C4 are −37 and 27°, respectively; (ii) in $GN7H^-$, both dihedral angles, C4−C5−N7−H and C4−N9−C8−H, are equal to 147°; (iii) in $GHN7H^-$, the same dihedral angles are 140 and 149°, respectively. Thus, it is not surprising that the energy of the neutral is much higher at the optimal anionic geometry than at the minimum energy structure of the neutral. Indeed, these energy increases are 24.7, 13.9, and 10.3 kcal/mol for the G, GN7H, and GHN7H tautomers, respectively (Figure 3). The corresponding values of VDE are only 13.5, 4.9, and 9.1 kcal/mol, respectively, which renders the anionic states adiabatically unbound. Strong distortions of molecular frameworks are characteristic for valence anionic states but not for dipole-bound anionic states (compare Figures 2 and 3).

4. Summary

We characterized valence and dipole-bound anionic states of the four most stable tautomers of guanine using a broad spectrum of electronic structure methods from the density functional theory, with the B3LYP exchange−correlation functional, to the coupled-cluster method, with single, double, and perturbative triple excitations. Our main findings include the following:

(1) We developed an approach for the identification of weakly bound valence anions that do not bind an electron at the geometry of the neutral. Initial wave function and geometry optimizations are performed in a polar solvent. This approach guarantees electronic stability of the anion for a broad range of geometries, including the geometry of the neutral. The structure and wave function of the hydrated anion are then used as initial guesses in characterization of the gas-phase anion.

(2) Tautomers G, GN7H, and GHN7H support vertically bound valence anionic states in the gas phase, with the CCSD(T) value of vertical detachment energy of +0.58, +0.21, and +0.39 eV, respectively. These anionic states are, however, adiabatically unbound, and the CCSD(T) values of the adiabatic electron affinity are −0.49, −0.53, and −0.38 eV, respectively. The vertical electronic stability of these valence anionic states is accompanied by serious buckling of the molecular skeleton, in particular, in the region of the six-member ring of G and the five-member rings of GN7H and GHN7H. These are molecular fragments where the excess electron is primarily localized.

(3) The G and GHN7H tautomers support dipole-bound states, with the CCSD(T) values of the adiabatic electron affinity of 65 and 36 meV, respectively. A contribution from higher-than-second-order correlation terms is very significant and represents 48 and 68% of the total electron vertical detachment energy determined at the CCSD(T) level, respectively.

(4) The results for neutral tautomers of guanine point to additional difficulties facing future PES or RET experiments on the anion of guanine. Even if guanine is successfully transferred to the gas phase without thermal decomposition, it is critical to have the G, GHN7H, and GH tautomers in the beam, not only the most stable GN7H tautomer as the latter does not support a bound anionic state.

(5) In standard conditions, the gas-phase guanine will be dominated by the most stable tautomer, GN7H, whereas the canonical G tautomer is of main interest due to its biological relevance. There is, however, a possibility to enrich the population of the canonical tautomer in the gas phase through (i) transfer of guanine to the gas phase at temperatures that populate not only the GN7H but also the G tautomer, (ii) formation of anions of guanine, (iii) selection of the cooled-down long-lived species (i.e., primarily G^-) because GN7H does not bind an electron, and (iv) soft photodetachment of an excess electron. The resulting guanine will populate primarily the G tautomer, and a small contamination will result from the GHN7H tautomer.

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Supporting Information Available: Selected MP2/aug-cc-pVDZ geometries and CCSD(T) energies for the neutral and anionic tautomers of guanine. This material is available free of charge via the Internet at http://pubs.acs.org.

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