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Photoelectron Spectroscopy of Oppositely Charged Molecular Switches in the Aqueous Phase: Theory and Experiment

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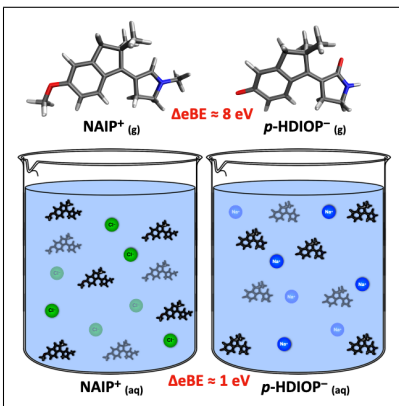
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Abstract

XUV photoelectron spectroscopy (XPS) is a powerful method for investigating electronic structures of molecules. However, the correct interpretation of results in condensed phase requires theoretical models that account for solvation. Here we present experimental aqueous-phase XPS of two organic biomimetic molecular switches, NAIP and *p*-HDIOP. They are structurally similar, but have opposite charges and thus present a stringent benchmark for solvation models which need to reproduce the observed $\Delta eBE = 1.1$ eV difference in electron binding energy compared to the 8 eV difference predicted in the gas phase. We present calculations using implicit and explicit solvent models. The latter employs the Average Solvent Electrostatic Configuration and Free Energy Gradient (ASEC-FEG) approach. Both non-equilibrium polarizable continuum models and ASEC-FEG calculations give vertical binding energies in good agreement with the experiment for three different computational protocols. Counterions, explicitly accounted for in ASEC-FEG, contribute to the stabilization of molecular states and reduction of ΔeBE upon solvation.

TOC Graphic



Keywords

photoelectron spectroscopy, electronic structure, molecular environment, biomimetic photo-switches

XUV photoelectron spectroscopy (XPS) is a powerful analytical method to study electronic structure of molecules. While originally a gas-phase or solid-state surface technique, developments in experimental technologies such as liquid microjets^{1,2} and ambient pressure instruments³ have extended XPS to the solution phase, where many chemical and biological systems reside. The past decade has seen several applications of static XPS to biologically-relevant organic molecules⁴⁻⁶ as well as time-resolved XPS to small inorganic and organic molecules⁷⁻¹²

Experimentally, the interpretation of solution-phase XPS is complicated by several factors. The well-resolved vibronic peaks readily observed in gas-phase spectra are broadened, shifted, and merged together in solution, resulting in broad bands that are more difficult to connect to theoretical quantities such as vertical binding energies, adiabatic binding energies, and Franck-Condon factors. Scattering and gas-liquid interface effects also complicate the interpretation of XPS spectra. Predicting solution-phase binding energies from first principles can also be challenging; quantum chemical computations must treat the initial and ionized states of the system in a balanced way and capture both short- and long-range solute-solvent interactions either through a large (or periodic) solvent box,¹³⁻¹⁸ non-equilibrium continuum solvation,¹⁹⁻²⁴ or a mix of explicit and implicit solvation.²⁴⁻²⁶

Here we report for the first time the experimental XPS spectra and calculated electron binding energies of two molecular switches. The first switch is the methoxy N-alkyl-indanylidene-pyrrolinium (dMe-MeO-NAIP, from now on referred to as NAIP). This switch is demethylated on C5 of the pyrroline compared to the previously investigated compound of ref. 27. The second switch is *para*-hydroxydimethylindanylidene-oxopyrrolidine (*p*-HDIOP). These molecules, shown in Fig. 1, are biomimetic switches designed to mimic the ultrafast photo-isomerization of the retinal protonated Schiff base (rPSB) chromophore of rhodopsin^{27,28} or the anionic chromophore of the green fluorescent protein,²⁹ respectively. Photo-isomerisation of these switches occurs on sub-picosecond time scales in methanol, within 300 fs for NAIP³⁰ and 400 fs for (*p*-HDIOP),²⁹ but with a relatively low quantum

efficiency in the 20% range. NMR analysis has shown that before illumination, NAIP is predominantly ($> 95\%$) in the E form,²⁸ and p -HDIOP also adopts the E isomer in the ground state.²⁹ For the purpose of this study, we consider them as model benchmark systems for studying the effect of solvation on electronic binding energies. Importantly, NAIP and p -HDIOP are structurally similar, but they are oppositely charged. NAIP is positively charged, becoming a 2+ ion upon photoionization, while p -HDIOP is negatively charged, becoming neutral upon photodetachment. Because of this difference, their electron binding energies are very different in the gas phase. However, the experiments reported in this manuscript find that this difference is reduced to just 1.1 eV in the aqueous phase due to solvation effects. This poses a challenge to computations, which must capture the large and opposite solvent effect on the binding energies of the two molecules.

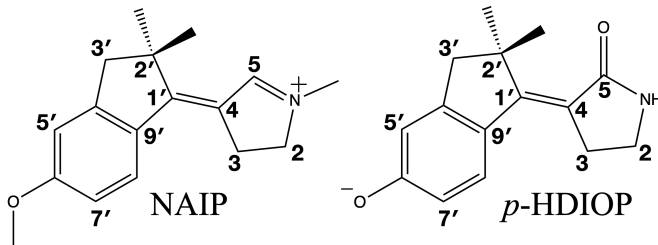


Figure 1: Structures of E -NAIP and E - p -HDIOP.

Computational Methods

Vertical binding energies (E^v) were first computed using three different electronic structure methods, introduced as **M1**, **M2**, and **M3** below. The goal of using three methods is not to compare their accuracy, but rather to check whether solvation effects computed for those three different methods are generally reproduced.

For each method we also report adiabatic binding energies (E_{ee}^a). Fig. 2 schematically presents the definitions of E^v , E_{ee}^a , and E_{00}^a . E^v is a difference between the final (ionized)

state energy and the initial state energy both computed at the equilibrium geometry of the initial state. E_{ee}^a is a difference between the final (ionized) state energy and the initial state energy each computed at the equilibrium geometry of the corresponding state. E_{00}^a are adiabatic energies that account for the zero-point vibrational energy (ZPVE) correction for each state obtained from frequency calculations. In the case of **M1**, 0-0 binding energies (E_{00}^a) are also computed.

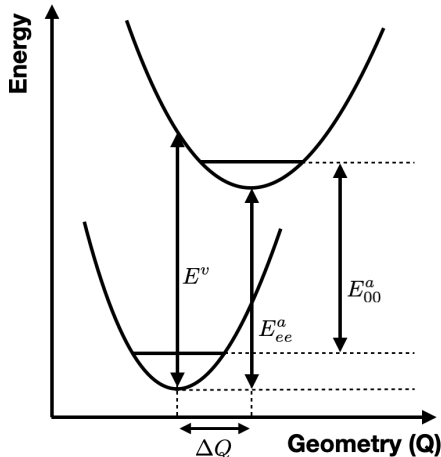


Figure 2: Schematic representation of vertical (E^v), adiabatic (E_{ee}^a), and 0-0 (E_{00}^a) binding energies. ΔQ represents the geometric displacement of the equilibrium structure of the ionized molecule compared to its initial state.

Method 1 (M1): Gas-phase geometries and frequencies were obtained using the PBE0 density functional^{31,32} and 6-311+G* basis set. E^v and E_{ee}^a were computed using the Δ SCF approach. E_{00}^a was computed with Δ SCF after taking the sum of electronic and zero-point vibrational energies for each of the initial and final states at their respective equilibrium geometries. **M1** calculations were carried out with Q-Chem 5.4.³³

Method 2 (M2): Gas-phase geometries were optimized using the ω B97X-D density functional³⁴ and cc-pVDZ correlation-consistent basis set.³⁵ E^v and E_{ee}^a were computed using equation-of-motion ionization-potential coupled-cluster with single and double excitations (EOM-IP-CCSD) and the cc-pVDZ basis set. EOM-IP-CCSD computes ionized states from a coupled cluster reference wave function using an electron-annihilating excitation operator.^{36,37} To make the calculations tractable, the single-precision implementation³⁸

of EOM-IP-CCSD and Frozen Natural Orbital (FNO) truncation³⁹ were employed. **M2** calculations were carried out with Q-Chem 5.4.³³

Method 3 (M3): E^v and E_{ee}^a were computed with the second-order perturbation theory corrected complete-active-space self-consistent field (CASPT2//CASSCF) method.^{40,41} The CASPT2//CASSCF approach has been regularly employed to study NAIP, *p*-HDIOP, and rPSB, and has been shown to benefit from a cancellation of errors that makes it suitable for modeling the excitation energies and photo-isomerization mechanism of those systems.^{29,42–45}

Methods **M1** and **M2** or similar protocols have been used in multiple instances for computing electron binding energies, with benchmarks indicating typical errors of 0.1–0.2 eV relative to experiments for molecules that do not have strong electron correlation.^{6,17,46–51} CASPT2 and related multi-reference methods have also been used to compute binding energies accurately in systems ranging from small metal clusters^{52,53} to other biologically relevant molecules.^{54,55}

Vertical and adiabatic binding energies were computed using ΔE 's computed with CASPT2. Geometry optimizations were carried with CASSCF and the 6-31G* basis set, while energies of the initial and final (ionized) states were computed using CASPT2 single point calculations with the ANO-L-VDZP basis set.⁵⁶ For both molecular switches, an active space of 12 electrons in 11 orbitals was used for the initial state and 11 electrons in 11 orbitals for the ionized state. The CASSCF orbital with single occupancy in the ionized state are shown in Fig. 3. In both *E*-NAIP and *E*-*p*-HDIOP, the ionization occurs from π orbitals, whether in the gas phase or in solution. No state-averaging was employed for the CASSCF wave function, and a single-state CASPT2 was used for each of the initial and ionized states. The Cholesky decomposition was used for CASPT2.⁵⁷ **M3** calculations were carried out in OpenMolcas version 22.10.⁵⁸

The effect of solvation on the computed electron binding energies was computed using both implicit and explicit solvent models. For **M1**, the E^v , E_{ee}^a , and E_{00}^a calculations were repeated using the conductor-like polarizable continuum model (C-PCM) to account for

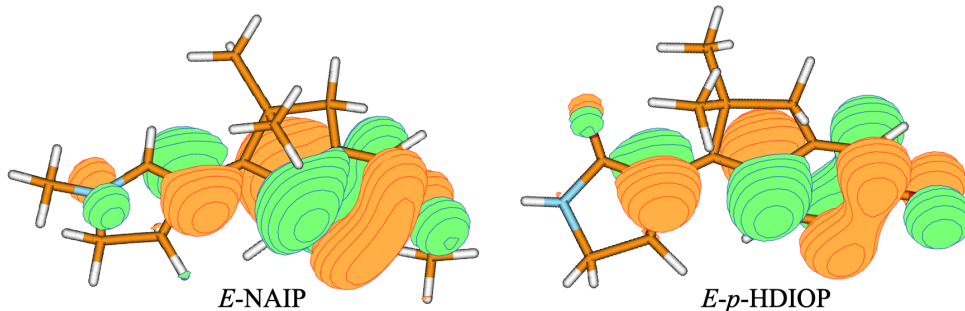


Figure 3: CASSCF molecular orbital having single occupancy for *E*-NAIP (left) and *E*-*p*-HDIOP (right) in the ionized state. The orbital CASSCF occupancies are between 1.01 – 1.02. The figures were generated using Molden.⁵⁹

the effect of the water solvent dielectric.^{60,61} By default, these models allow both the fast (e.g., polarization) and slow (e.g., orientational) components of solvent response to relax and are labeled equilibrium PCM (e-PCM). e-PCM is not suitable for computing vertical binding energies (E^v), where only the fast component of the solvent polarization remains in equilibrium with the sudden ionization but the slow component is effectively frozen.¹⁹ Therefore, we also computed E^v using a non-equilibrium formulation of PCM (ne-PCM) using the Marcus-Brady-Carr state-specific approach.^{20,21,62-64}

For **M2**, EOM-IP-CCSD ne-PCM calculations were computed using a zeroth-order treatment that uses solvent-polarized molecular orbitals for the EOM-IP-CCSD calculations.⁶⁴

Explicit solvent calculations were performed using the Average Solvent Electrostatic Configuration and Free Energy Gradient (ASEC-FEG) quantum mechanical / molecular mechanical (QM/MM) approach. The theoretical details of this method have been described previously.⁶⁵⁻⁷³ The details of the model set-up and methodology is presented in the Supporting Information. Briefly, the quantum chemical optimization and energy calculations are performed iteratively in the field of a time-averaged environment of the solution obtained from MD snapshots. Water molecules and counterions (Na^+ in the case of *p*-HDIOP and Cl^- in the case of NAIP) are included explicitly in the MD and ASEC-FEG QM/MM calculations. Their presence not only ensures a globally neutral system before ionization, but also accounts for the electrostatic interaction between the solute and the counterion in an aver-

aged way.⁷² The ASEC-FEG approach is related to other methods that simulate QM energies in a conformationally sampled solvent environment such as ASEP/MD,⁷⁴ MESS-E,⁷⁵ and QM-NBB.⁷⁶ MD simulations were carried out using GROMACS 2022.3,^{77,78} while QM/MM calculations were carried out using the OpenMolcas⁷⁹ and Tinker 6.3⁸⁰ interface,⁸¹ treating the molecular switches at the QM level of theory and the ASEC solvent and counterion at the MM level of theory. The QM subsystem was optimized at the CASSCF/6-31G* level of theory. As with the gas-phase calculations, CASSCF employed a 12 electron in 11 orbital active space and no state averaging.

For each of *p*-HDIOP and NAIP, the ASEC configurations (taken from the last iteration of ASEC-FEG protocol) were exported to Q-Chem, and PBE0/6-311+G* ΔSCF and EOM-IP-CCSD/cc-pVDZ binding energies were computed in that ASEC charge environment.

Test calculations were also carried out where solution ions (Na⁺ for *p*-HDIOP and Cl⁻ for NAIP) were deleted for each step of the ASEC-FEG protocol to compute the CASTP2 ionization energies in the absence of ions. The results are shown in the Results section as **M3-no ion**.

Radial Distribution Functions (RDFs) for the counterions were computed with periodic boundary conditions using the gmx rdf tool in GROMACS.^{77,78} The cumulative number (CN), a normalized integral of the RDF that, in this case, indicates the probability of finding the counterion within distance *r*, was also generated.

Experimental Methods

The two molecular switches were prepared and characterized according to procedures reported in the literature (see ref. 82 for NAIP and ref. 29 for *p*-HDIOP).

The spectroscopy experiments were performed at the XUV monochromator beamline described previously.^{9,11,83} In short, XUV light is produced by high-order harmonic generation (HHG) driven by a Ti:Sa femtosecond multi-mJ laser source with the central wavelength of

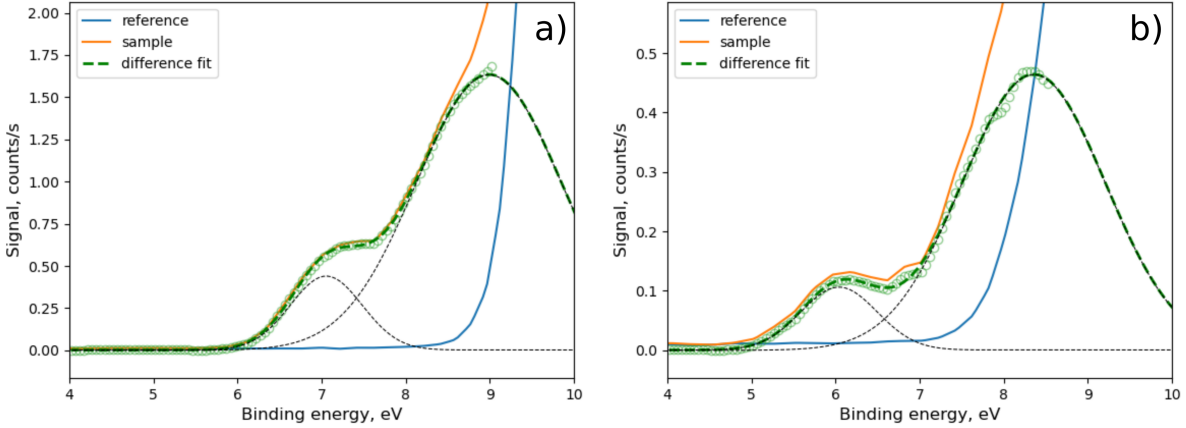


Figure 4: a) Photoelectron spectrum of NAIP. The sample and solvent spectra are shown as orange and blue lines, respectively. The difference spectrum (green open circles) shows two bands and is well described by two Gaussian profiles (green dashed curve). The individual Gaussians are shown with black dashed lines. The central binding energies of the two bands are 7.1 eV and 9.0 eV. b) Photoelectron spectrum of *p*-HDIOP. The central binding energies of the two bands are 6.0 eV and 8.4 eV.

795 nm. The HHG spectrum generated in Argon is monochromatized by a grating-based grazing incidence monochromator. The monochromator preserves the duration of XUV pulses, which is important for time-resolved experiments performed at the beamline,^{9,11} but is not relevant for the present static measurements. As described in ref. 9, the XUV monochromator beamline is coupled to a microliquid jet endstation equipped with a “magnetic bottle” time-of-flight spectrometer. For the present measurements the harmonic 15 (photon energy of 23.4 eV) was chosen.

As discussed in the literature⁸⁴ determining binding energies in liquid jet photoelectron spectroscopy requires suppression of the steaming potential, which is generated if the solvent has low conductivity. Following the earlier work, we added 10 mM of NaCl (Sigma-Aldrich) to ultrapure water before preparing sample solutions. The remaining systematic error in the measured photoelectron kinetic energies (e.g. due to incomplete suppression) were eliminated by a calibration procedure using the base solvent solution and harmonics 15 (23.4 eV), 17 (26.4 eV) and 19 (29.6 eV), which allows determining the residual shift of the liquid water $1b_1$ band with respect to the literature value. The photoelectron energy resolution in the

experiment is limited by the bandwidth of the source (about 300 meV FWHM⁸³) while the resolution of the time-of-flight spectrometer is better than 100 meV.⁹ The observed bands in liquid phase are broadened due to different solvation structures and vibrational excitation upon ionization.

It is worth emphasizing that direct comparison of the computed and experimentally determined binding energies is complicated by elastic and inelastic scattering of the photoelectrons by the solvent. Scattering arises from a complex interplay of multiple factors, including solubility of the switches (related to probing depth), energy of the ionizing radiation, solvent, and angle of detection of the electrons.^{6,85–88} It can be argued that inelastic scattering may only allow higher energy electrons to escape the solvent and therefore give a higher apparent binding energy than the true one. However, given that the photoelectron spectra can be fitted accurately using Gaussian curves in Fig. 4, this suggests that scattering is not significant enough to distort the spectra.⁶ In any case, it is expected that the effect of electron loss is on the same order of magnitude as the experimental uncertainty at the ionizing radiation energy employed (23.4 eV, 16–17 eV above the ionization/detachment threshold for the two switches). Another factor is the sensitivity of the binding energy to the degree of solvation of the molecular switches; the switches near the air–water interface may have different binding energies compared to the bulk. However, a recent computational study indicates that the binding energy of ions is relatively insensitive to a bulk versus interfacial solvation.⁸⁹ Finally, the computational methods employed here also have limitations; while implicit solvation may miss specific details of the solvent-solute interactions, the ASEC-FEG approach used here treats the solvent with a fixed-charge force field and misses solvent polarization effects.

A 10 mM NaCl solution was prepared and used both for the NAIP sample preparation and for reference solvent measurements performed before and after the sample measurements, which is important for background suppression as discussed below. The NAIP sample thus contained 1.35 mM concentration of NAIP molecules, 10 mM of NaCl in pure water. The

total volume of the sample solution was 15 ml, which was sufficient for 15 minutes of signal accumulation at the flow rate of 0.4 ml/min after accounting for the volume of the sample delivery system. All the flasks and sample supply capillaries were covered by aluminium foil to prevent the compound isomerization under the laboratory light. The reference solvent measurements were accumulated for the same amount of time. The measured photoelectron spectrum of NAIP is shown in Fig. 4a) as an orange line together with the reference solvent spectrum (blue curve), plotted as a function of the binding energy (eBE, determined using the photon energy minus kinetic energy of the detected electrons). The open circles show the difference spectrum resulting from subtraction of the solvent signal. The green dashed line represents a fit line composed of two Gaussian profiles, which describe well the two bands observed in the range of 5 to 9 eV. The central binding energies of the two bands are 7.1 eV and 9.0 eV. The full widths at half maximum (FWHM) are 1.0 eV and 2.0 eV, respectively. The errors of the fits are on the order of 1% of the values, but systematic uncertainties (e.g. from the bandwidth of the XUV light) may be larger. From experience we conservatively estimate them to be on the order of 0.2–0.3 eV.

The anionic *p*-HDIOP solute requires a basic solution of the otherwise neutral chromophore. Therefore 100 mM of KOH was added to the water solvent, which also contained 10 mM of NaCl. This solution was used both for sample preparation and for reference measurements. The *p*-HDIOP sample thus contained 1.15 mM of *p*-HDIOP, 100 mM of KOH, 10 mM of NaCl in pure water. Other parameters of the measurement correspond to those of NAIP, as described above. The photoelectron spectra of *p*-HDIOP are shown in Fig. 4b). Two bands are again observed in the signal of the solute. The two-Gaussian fit yields the central band positions of 6.0 eV and 8.4 eV with the FWHM of 1.1 eV and 2.0 eV, respectively. The solvent spectrum in Fig. 4b) is different from that of Fig. 4a) due to the weak OH⁻ band observed in the range of 7-8 eV binding energies. This signal is removed by the solvent signal subtraction.

The remainder of this manuscript will focus on the first electron binding energy. The

results of the gas-phase, PCM, and ASEC *ab initio* calculations for the three electronic structure methods are summarized in Table 1 along with the experimental results.

Table 1: Computed binding energies of NAIP and *p*-HDIOP

Method ¹	Energy ²	Solvation ³	<i>E</i> -NAIP (eV)	<i>Z</i> -NAIP (eV)	<i>E-p</i> -HDIOP (eV)	<i>Z-p</i> -HDIOP (eV)	$\Delta(E\text{-NAIP} - E\text{-}p\text{-HDIOP})$
M1	E^v	None	10.6	10.6	2.8	2.6	7.8
M2	E^v	None	10.4	10.5	2.2	2.0	8.2
M3	E^v	None	10.7	10.8	2.8	2.7	7.9
M1	E_{ee}^a	None	10.5	10.5	2.7	2.5	7.8
M2	E_{ee}^a	None	10.3	10.3	2.1	1.9	8.1
M3	E_{ee}^a	None	10.6	10.6	2.7	2.6	7.9
M1	E_{00}^a	None	10.5	10.5	2.7	2.5	7.8
M1	E^v	e-PCM	6.0	6.0	4.5	4.5	1.5
M1	E^v	ne-PCM	6.9	6.9	5.5	5.5	1.4
M2	E^v	ne-PCM	7.6	7.6	5.8	5.8	1.8
M1	E_{ee}^a	e-PCM	5.9	5.9	4.4	4.4	1.5
M1	E_{00}^a	e-PCM	5.9	5.9	4.5	4.4	1.4
M1	E^v	ASEC	7.7	7.7	6.7	6.7	1.0
M2	E^v	ASEC	7.7	7.6	6.3	6.3	1.4
M3	E^v	ASEC	7.8	7.8	7.0	7.0	0.8
M3-no ion	E^v	ASEC	8.4	8.4	6.3	6.4	2.1
Experiment			7.1	–	6.0	–	1.1

¹ M1 = Δ SCF, PBE0/6-311+G*; M2 = EOM-IP-CCSD// ω B97X-D/cc-pVDZ ; M3 = CASPT2/ANO-L-VDZP//CASSCF/6-31G*.

² E^v = Vertical binding energy, E_{ee}^a = Adiabatic binding energy, E_{00}^a = 0-0 binding energy.

³ e-PCM = equilibrium PCM; ne-PCM = non-equilibrium PCM; ASEC = Average solvent electrostatic configuration.

In the gas-phase calculations, NAIP and *p*-HDIOP have binding energies that differ by ca. 8 eV. This is not surprising considering their opposite charges; *p*-HDIOP is negatively charged and has a low photodetachment energy in the gas phase. NAIP is positively charged and its ionization to the 2+ charged state requires significantly more energy.

Upon solvation, the negatively charged *p*-HDIOP is stabilized more than the neutral final state, which increases its binding energy relative to the gas phase. Conversely, solvation of NAIP is likely to have a larger stabilizing effect on the final (2+) state compared to the initial (1+) state, reducing the binding energy. Solvation therefore is expected to have a large and opposite effect on the binding energies of the two molecular switches. Indeed, the experimental results and the calculations in Table 1 indicate that accounting for the solvent environment brings the binding energies of NAIP and *p*-HDIOP much closer together from 8 eV in the gas phase to ca. 1 eV in the aqueous phase.

Before discussing the effect of solvation, we look at the gas phase calculations to determine a suitable protocol for computing binding energies. The three electronic structure methods

give mostly consistent vertical and adiabatic binding energies in the gas phase. Methods **M1** and **M3** in particular agree with each other to within 0.1–0.2 eV in all cases. **M2** underestimates the binding energy of *p*-HDIOP compared to the other two methods. This can be attributed to the missing diffuse basis functions in the EOM-IP-CCSD/cc-pVDZ calculations. Diffuse basis functions are important for accurately determining the energy of the negatively charged initial state of *p*-HDIOP. Accounting for those diffuse functions should increase the binding energy of *p*-HDIOP.

Comparing *E*- and *Z*- isomers of NAIP and *p*-HDIOP. Previous studies have established that the *E*- stereoisomer is more stable than *Z*- for both NAIP and *p*-HDIOP.^{28,29} We computed E^v and E_{ee}^a for all four systems (*E*-NAIP, *Z*-NAIP, *E*-*p*-HDIOP, and *Z*-*p*-HDIOP). The computations show that binding energies for *E*- and *Z*- isomers for each of NAIP and *p*-HDIOP are close (within 0.1 eV for NAIP, and within 0.2 eV for *p*-HDIOP). Therefore, the stereoisomers cannot be resolved experimentally using photoelectron spectroscopy. The remainder of the discussion will focus on the *E*-NAIP and *E*-*p*-HDIOP stereoisomers.

Comparing vertical (E^v), adiabatic (E_{ee}^a), and 0-0 (E_{00}^a) binding energies. E_{ee}^a was computed using methods **M1**, **M2**, and **M3** in the gas phase. In all cases, the effect of geometry relaxation of the ionized state reduced the binding energy is limited to under 0.2 eV compared to E^v . We accounted for the effect of ZPVE on adiabatic excitation energies for method **M1**. The ZPVEs are similar for the initial and ionized states (within 0.05 eV) and therefore give E_{00}^a energies that are similar to E_{ee}^a .

Of the three quantities (E^v , E_{ee}^a , and E_{00}^a), only E_{00}^a has a direct connection to an experimental quantity. In a well-resolved spectrum for a vibrationally cold molecule, E_{00}^a corresponds to the lowest energy transition and marks the onset of the spectral band. The other two quantities are theoretical, although E^v can be (and often is) connected to the energy where the absorption or emission signal is at a maximum for that band.⁹⁰ Given the similarity of calculated E^v and E_{00}^a for each of *p*-HDIOP and NAIP, it appears that neither

switch undergoes significant structural rearrangement upon ionization. This is in contrast to the behavior of these switches in the first singlet excited state, which quickly leads to a strong relaxation along bond-length alternation and out-of-plane deformation modes.^{27,28,91–93} The remainder of the discussion will therefore focus on vertical binding energies (E^v), which will be compared to the experimentally determined central binding energies from the first bands in Fig. 4.

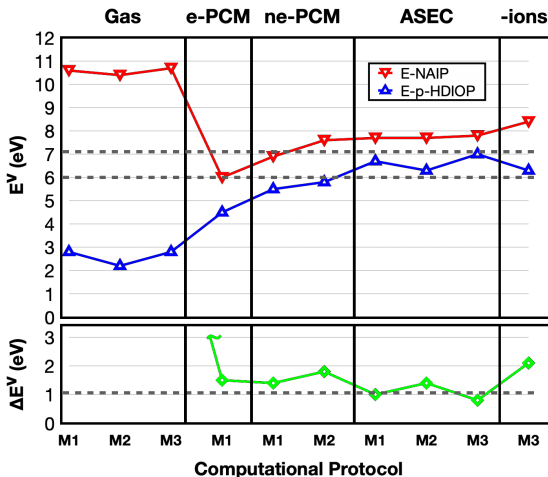


Figure 5: **Top.** Computed E^v s for E -NAIP (red) and E - p -HDIOP (blue) using the computational methods and solvation models as shown in Table 1. **Bottom.** A plot of the difference (green) in the E^v for E -NAIP and E - p -HDIOP (ΔE^v) as a function of the method and solvation model. The horizontal dashed lines indicate the experimental values.

Comparing solvation models. The E^v and ΔE^v results from Table 1 are plotted in Fig. 5. The binding energies of NAIP and p -HDIOP differ by ca. 8 eV in the gas phase. Using an equilibrium implicit PCM model decreases this ΔE^v to 1.5 eV for **M1**, which is comparable to the experimental difference of binding energies Δ eBE value of 1.1 eV. Using a polarizable continuum model therefore largely captures the effect of solvation on those two oppositely charged molecules. However, equilibrium PCM calculations underestimate the absolute binding energies of both switches relative to the experimental ones by over 1 eV. This is not surprising; e-PCM fully relaxes the solvent environment in the ionized state, which is an incorrect representation of the solvent response to sudden ionization.¹⁹ The ionized state energy is therefore overstabilized and the binding energy underestimated.

This underestimation of the binding energy is largely resolved by using a non-equilibrium PCM approach. ne-PCM calculations using both **M1** and **M2** give binding energies that are in better agreement with those obtained experimentally (within 0.5 eV). The computed ΔE^v s for **M1** using ne-PCM is also slightly improved, at 1.4 eV compared to the experimental 1.1 eV. For **M2**, the ΔE^v is overestimated, at 1.8 eV, but this could be explained again by the missing diffuse basis functions, which leads to an underestimation of the *p*-HDIOP binding energy.

ASEC-FEG QM/MM explicit solvent calculations further reduce the computed ΔE^v to 0.8–1.4 eV, in good agreement with the experimental ΔeBE . The result from **M1** is in particularly good agreement, at 1.0 eV, while **M2** overestimates ΔE^v (due to the basis set) and **M3** underestimates ΔE^v . Nonetheless, all three models are within 0.3 eV of the experimental ΔIE . On the other hand, while the ASEC-FEG QM/MM calculations give a ΔE^v that is in good agreement with the experiment, all three methods (**M1**, **M2**, and **M3**) overestimate the absolute binding energies of both NAIP and *p*-HDIOP by over 0.5 eV. This is on the order of magnitude of the effect of solvent polarization, which can exceed 0.5 eV,^{26,94,95} and is missing in the ASEC fixed charge model used here.

The effect of the counterion. Although both ne-PCM and ASEC-FEG give binding energies that are in reasonably good agreement with the experiment, it would be interesting to look at one of the aspects where the ASEC and PCM solvation models differ; ASEC includes not only explicit solvent, but also explicit counterions. The ASEC configuration samples the distribution of those ions from MD simulation. Fig. 6 shows the radial distribution functions (RDF) and cumulative number (CN) of the counterion relative to the center of mass of the switches computed from one of the MD simulations. From this distribution of charges, it is possible to estimate the effect of the ions using Coulomb’s law. Assuming a centro-symmetric potential interacting with a point charge of magnitude e , and in the

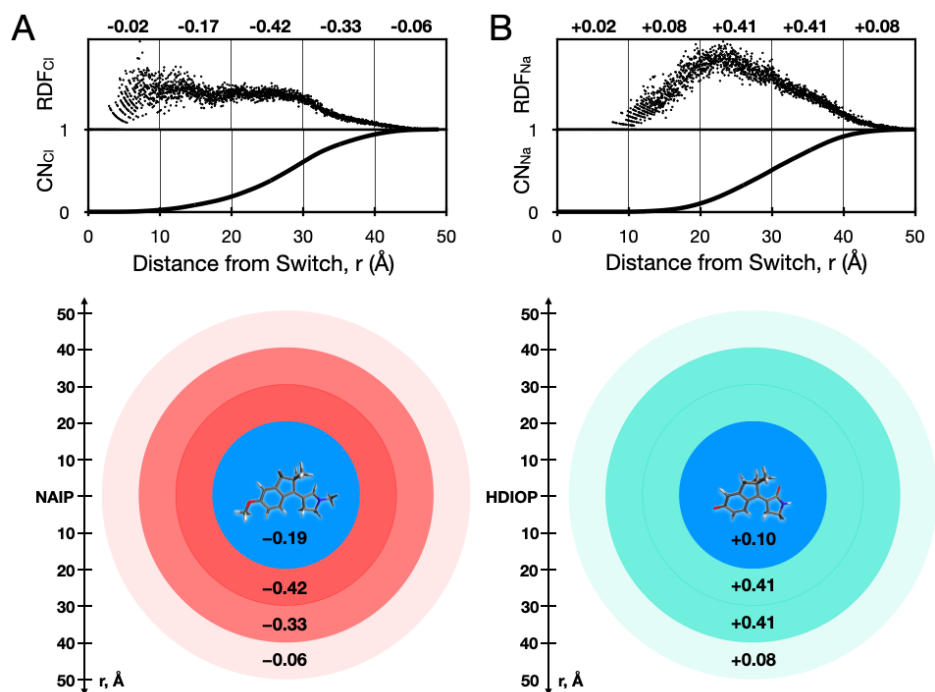


Figure 6: **Top.** Radial distribution functions (RDF) and cumulative number (CN) of the counterion for *E*-NAIP (**A**) and *Z-p*-HDIOP (**B**). The RDF and CN for each of the two systems were computed from a 4 ns MD simulation. The CN converges to 1 at a large radius because there is only one counterion, and therefore represents the probability of finding the counterion at a given value of r . The numbers at the top indicate the probability of finding the counterion in each 10 Å shell around the center of mass of the molecule, multiplied by the sign of the charge. **Bottom.** A schematic representation of an ASEC configuration that shows how the counterion is distributed. The blue circle represents the water solvent ASEC configuration, which is explicitly included in the QM/MM calculations for up to 20 Å. The surrounding concentric circles represent the counterions that interact at a long range with the solute. The color and shading of each shell relates to the total charge within that spherical shell, based on the CNs computed from an MD simulation.

absence of a dielectric medium:

$$V = -\frac{1}{4\pi\epsilon_0} \int \frac{\rho(r)}{r} d\tau \quad (1)$$

The $\rho(r)$ term can be represented using the CN plots in Fig. 6. Integrating the expression above using these CN plots gives an energy of 0.52 eV for the interaction between Na^+ ions and the negatively charged *p*-HDIOP, and 0.60 eV for the interaction between Cl^- ions and positively charged NAIP. Considering that this charge interaction will stabilize the 2+ ionized state more than the 1+ initial state in NAIP, but will instead stabilize the -1 initial state in *p*-HDIOP more than the neutral state, the direct effect of counterions on ΔE^v is over 1 eV. Indeed, we find that simply deleting the counterions and repeating the QM/MM calculations increases the computed ΔE^v from 0.8 eV to 2.1 eV (**M3-no ion** in Table 1).

Of course, deleting the counterions does not give a realistic representation of the effect they have on the binding energy. The calculations only account for a minimal number of counterions of the solute, while experimental solutions are more complex and contain NaCl and KOH for experimental purposes. Further, water molecules are arranged in such a way to screen the counterions and will rearrange in the absence of these counterion. If we account for the relative permittivity of water (78.4 at ambient conditions), the effect of the counterions on the binding energy of the molecular switches would be substantially diminished. However, NAIP and *p*-HDIOP are not point charges in a uniform dielectric field, and the counterion distribution is certainly not centro-symmetric. Therefore, counterions in the ASEC-FEG model may contribute to long-range electrostatic solute-counterion interactions that are missing in the PCM models, leading to a slightly lower computed $\Delta e\text{BE}$. Such long-range effects were found to be important in QM/MM calculations of proteins such as rhodopsins and flavoprotein photoreceptors,^{72,96} where counterions are distributed near the surface of the protein. More realistic models of the solute-ion interactions will be addressed in future work.

In conclusion, we have presented experimental XPS and computed binding energies of a positively charged molecule, NAIP, and a negatively charged molecule, *p*-HDIOP. These photo-switches pose a challenge to electronic structure calculations, which need to account for large and opposite solvation effects through suitable solvation models. Experimentally, the difference in electron binding energy (ΔeBE) between *p*-HDIOP and NAIP is 1.1 eV, compared to ca. 8 eV difference predicted in the gas phase. Non-equilibrium implicit (ne-PCM) solvation models capture a large part of the solvent effect and give both absolute and relative binding energies that are in good agreement with the experiments. Equilibrium (e-PCM) models reproduce the relative binding energies of the two switches relatively well ($\Delta\text{eBE}=1.5$ eV) but give underestimated binding energies by over 1 eV. ASEC-FEG explicit solvent models gives a ΔE^v of 0.8–1.4 eV, depending on the method, in closer agreement to the experimental ΔeBE . An advantage of the ASEC-FEG explicit solvent model is that it captures long-range electrostatic interactions with a time-averaged solvent and counterion environment. However, it misses fast polarization effects of the nearby solvent molecules, which are better captured by ne-PCM solvent models. The results presented in this work will serve as a solid basis for time-resolved XPS experiments, which are being performed in our laboratory.

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Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Supporting Information Available

The supporting information includes details of the QM/MM calculations, tables of computed absolute and vertical binding energies, and optimized coordinates for the ground and ionized states of the molecular switches.

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