

The Effect of Conjugation on the Competition Between Internal Conversion and Electron Detachment: A Comparison Between Green Fluorescent and Red Kaede Protein Chromophores

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15 Detachment: A Comparison between Green
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20 Fluorescent and Red Kaede Protein Chromophores
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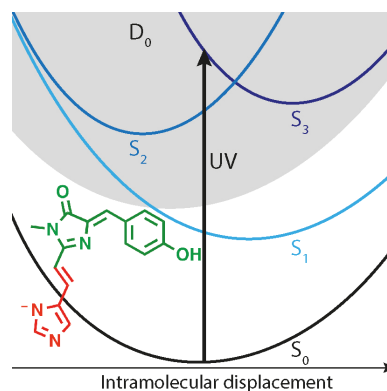
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ABSTRACT. Kaede, an analogue of green fluorescent protein (GFP), is a green-to-red photoconvertible fluorescent protein used as an *in vivo* ‘optical highlighter’ in bioimaging. The fluorescence quantum yield of the red Kaede protein is lower than that of GFP, suggesting that increasing the conjugation modifies the electronic relaxation pathway. Using a combination of anion photoelectron spectroscopy and electronic structure calculations, we find that the isolated red Kaede protein chromophore in the gas phase is deprotonated at the imidazole ring, unlike the GFP chromophore that is deprotonated at the phenol ring. We find evidence of an efficient electronic relaxation pathway from higher lying electronically excited states to the S_1 state of the red Kaede chromophore that is not accessible in the GFP chromophore. Rapid autodetachment from high lying vibrational states of S_1 is found to compete efficiently with internal conversion to the ground electronic state.

TOC GRAPHICS



KEYWORDS. Spectroscopy, Computational Chemistry, Photochemistry, Non-radiative decay.

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Green fluorescent proteins (GFP) and its family of variants are used widely as non-invasive fluorescent probes for *in vivo* monitoring of biological and biochemical processes.¹⁻⁶ The wild-type GFP chromophore, *p*-hydroxybenzylidene-2,3-dimethylimidazolinone (*p*HBDI, Fig. 1), is formed by the cyclisation and oxidation of Ser⁶⁵-Tyr⁶⁶-Gly⁶⁷ amino acid residues and is embedded within a β -barrel protein structure.^{1,4,7-10} The chromophore exists in deprotonated anionic (*p*HBDI⁻) or neutral forms and excitation of either of these leads to fluorescence from the deprotonated anionic chromophore at around 508 nm, with a quantum yield of $\Phi = 0.79$ ¹¹⁻¹⁴ (the neutral form deprotonates upon photoexcitation, yielding the anionic form).^{11,15} An interesting feature of the isolated GFP chromophore is that it is non-fluorescent, in both solution and gas-phases,^{12,14,16-17} as a result of efficient ultrafast non-radiative decay pathways being accessible in the absence of the protein.¹⁸

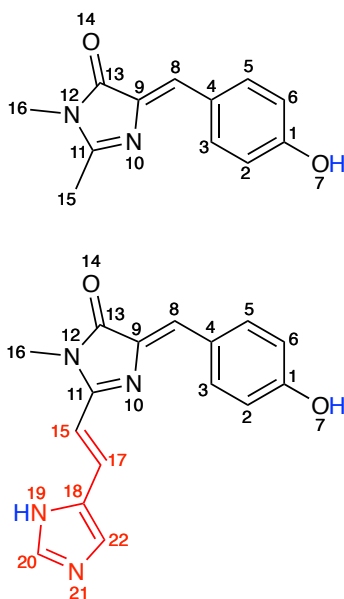


Fig. 1 Structure of the model GFP chromophore, *p*-hydroxybenzylidene-2,3-dimethylimidazolinone (*p*HBDI) (top) and the model rKaede chromophore (bottom). Possible deprotonation sites are highlighted in blue.

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3 For multi-labelling experiments, GFP variants with high visual contrast are desirable.¹⁹⁻²⁰
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5 Kaede, an analogue of GFP, is a green-to-red photoconvertible fluorescent protein.^{19,21-22} It has a
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7 GFP-like chromophore, thus fluorescing green (green Kaede) following irradiation at 480 nm.¹⁹⁻²²
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9 Upon exposure to ultraviolet (UV) light (350 – 420 nm), green Kaede converts efficiently and
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11 irreversibly into a red fluorescent form (rKaede).¹⁹⁻²¹ This green-to-red fluorescence conversion
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13 produces an easily distinguishable bright and stable red colour that is not present in the un-
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15 irradiated sample.^{1,19} Selective UV irradiation of cells expressing the Kaede protein enables it to
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17 be used as an *in vivo* ‘optical highlighter’ in bioimaging.^{1,19,21} Importantly, the excitation
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19 wavelengths needed to generate the red or green fluorescence do not induce photoconversion.¹⁹
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24 The green-to-red photoconversion of Kaede has been the subject of several studies.^{21,23} Briefly,
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26 UV light causes a C_α-N_α bond cleavage of the green Kaede chromophore, which is followed by
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28 deprotonation which in turn leads to the extended π-conjugated system that red-shifts the
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30 emission.^{21,23} The green Kaede chromophore, made up of a tripeptide of His⁶²-Tyr⁶³-Gly⁶⁴,^{21,23} is
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32 similar to that of GFP; however, relatively little is known about the photophysics of the isolated
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34 model rKaede chromophore, 2-[(1E)-2-(5-imidazolyl)ethenyl]-4-(p-hydroxybenzylidene)-5-
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36 imidazolinone (Fig. 1).²¹ Since the fluorescence quantum yield of the rKaede protein, Φ = 0.33,
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38 is lower than that of GFP,¹⁹ it seems likely that non-radiative decay pathways play a more
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40 important role in the excited state dynamics of the rKaede protein.
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46 The aim of this combined photoelectron spectroscopy and computational study of the rKaede
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48 chromophore is to shed new light on how the extended conjugation affects non-radiative
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50 processes in the gas-phase. Understanding the intrinsic properties of the rKaede chromophore is
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52 important as it is a first step towards understanding such processes in the protein; for example,
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54 the higher lying electronic states of the GFP chromophore in the gas-phase undergo efficient
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3 electron detachment and in the protein are resonant with a quasi-continuum of solvated electron
4 states, enhancing electron transfer from GFP to the solvent.²⁴
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8 Several recent experimental and theoretical investigations of *p*HBDI⁻ in the gas-phase have
9 identified two dominant competing radiationless relaxation channels – fragmentation, following
10 IC back to the ground electronic state, and electron detachment.^{16,18,24-34} Experimental
11 photoelectron spectroscopy studies and quantum chemistry calculations of gas-phase *p*HBDI⁻
12 have revealed that both direct and indirect electron detachment processes play an important role
13 in the deactivation of isolated *p*HBDI⁻.^{16,18,24,26-35} Close to the detachment threshold, around 355
14 nm, direct photodetachment dominates. This wavelength corresponds to a minimum in the
15 overall action absorption spectrum, lying above the maximum absorption cross-section to the
16 first, bright electronically excited state, but below the onset of significant absorption cross-
17 section to higher-lying electronically excited states. In fact, vibrationally-resolved photoelectron
18 spectra of cold *p*HBDI⁻ recorded at 355 nm have confirmed the adiabatic detachment threshold
19 to be 2.73 eV (454 nm)²⁷ in agreement with calculations.³⁶ Above the photodetachment threshold,
20 in the 350 – 315 nm photoexcitation range, indirect electron emission via resonant excitation of
21 higher lying electronically excited states is also possible. Although there are many excited states
22 and competing non-adiabatic decay pathways, the electron emission is dominated by a single,
23 optically bright, excited state shape resonance that is strongly coupled to the electronic
24 continuum.^{24,37}
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48 The rKaede chromophore has two deprotonation states: the O(-) form which is deprotonated at
49 the O₇ position on the phenol group (as in *p*-HBDI⁻), or the N(-) form which is deprotonated at
50 the N₁₉ or N₂₁ positions on the imidazole group. Studies of the wild-type rKaede protein have
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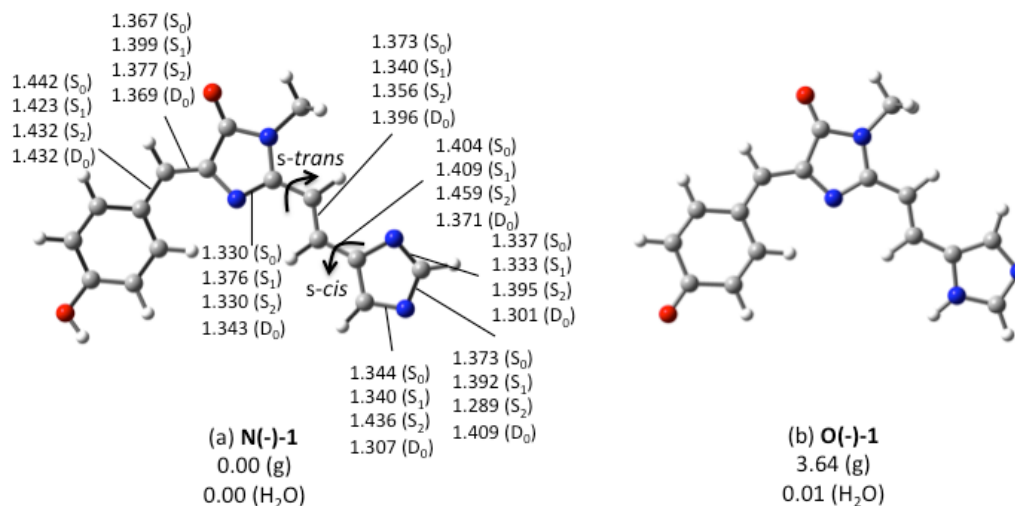


Fig. 2 Structures of (a) N(-)-1 and (b) O(-)-1 conformers of the rKaede chromophore anion. Representative bondlengths of the N(-)-1 S₀, S₁ and D₀ minima obtained with different methods (see text) given in Å. Relative energies in the gas phase (g) and in water in kcal mol⁻¹ at the bottom of the figure.

revealed the chromophore in the protein to be deprotonated at the phenolic oxygen.^{21,23} The pK_a of unsubstituted imidazole in water (14.52)³⁸ is higher than that of phenol (9.95), suggesting that the phenoxy form might be the more stable form of the deprotonated isolated chromophore in the gas phase; however, MP2 calculations on seven N(-) and O(-) rKaede isomers with different side chain conformations indicate that the N(-) form is more stable in the gas phase (see Computational Details and Table S1 in the Supporting Information). The most stable N(-) conformer at the MP2/aug-cc-pvtz level, labeled N(-)-1 (see Figure 2a), is planar and has *E* conformation along the C₁₆-C₁₇ bond and *s-trans* and *s-cis* conformation along the C₁₁-C₁₅ and C₁₇-C₁₈ bonds, respectively, and it is approximately 2 kcal mol⁻¹ more stable than the other N(-) isomers. This arrangement was also found in an NMR study of a fragment of the Kaede protein

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3 containing the red chromophore.²¹ In turn, the most stable O(-) conformer, O(-)-1 (Figure 2b),
4 has *E, s-trans, s-trans* conformation and is 3.6 kcal mol⁻¹ higher in energy than N(-)-1. These
5 values are internal energies because calculation of the entropic contribution is not practical at this
6 level of theory; however, our assignment of N(-)-1 as the predominant gas-phase is confirmed by
7 the calculated vertical detachment energies (VDEs) and the photoelectron spectroscopy data (see
8 next section).
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18 The relative stabilities in water have been estimated at the PCM/MP2/aug-cc-pvtz level.³⁹ This
19 approach does not consider specific H bonds but gives a first approximation of the solvation
20 effect. O(-)-1 is stabilized compared with N(-)-1, and the two isomers have virtually the same
21 energy, the difference being less than 0.01 kcal mol⁻¹ (see SI). This suggests that in water there
22 may be an equilibrium between the two forms. Overall, the deprotonation state of the rKaede
23 chromophore is very sensitive to the environment, which is consistent with the pH dependence of
24 the absorption spectrum of the red protein.¹⁹ The stabilization of O(-)-1 in water is due to its
25 larger dipole moment, 16.5 Debye compared to 9.7 Debye for N(-)-1 in the gas phase, and the
26 deprotonation of the phenol ring found in the protein is probably a result of the neighboring
27 residues, which favor the electronic density distribution of the O(-) form.
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Table 1 Vertical π,π^* excitation energies E_{ex} , and corresponding wavelengths λ , for the first five singlet excited states, S_1 - S_5 ,^a of the N-deprotonated rKaede chromophore (N(-)-1) at the MS-CASPT2, TD-CAM-B3LYP and CC2 levels of theory. Oscillator strengths f are in parentheses. The CASSCF/CASPT2 orbitals are presented in Fig. 3. S_1 vertical excitations of the O-deprotonated species (O(-)-1) and MS-CASPT2 data for p -HBDI⁻ included for comparison.

	MS-CASPT2(14,14)/ ANO-L ^b			TD-CAM-B3LYP/ 6-311++G(3df,3pd)		CC2/cc-pvtz ^d	
	E_{ex}/eV (f)	λ/nm	Character ^c	E_{ex}/eV (f)	λ/nm	E_{ex}/eV (f)	λ/nm
S_1	2.49 (1.138) O(-): ^c 2.24 (1.03) HBDI: 2.77 (1.157)	499	H→L (0.62)	2.66 (1.266) O(-): ^c 2.48 (1.28)	466	2.49 (1.048) O(-): ^c 2.04 (1.14)	497
S_2	3.66 (0.029) HBDI: 3.99 (0.038)	338	H-2→L (0.26) H,H→L,L (0.25)	3.86 (0.277)	321	3.79 (0.347)	327
S_3	4.07 (0.063) HBDI: 4.10 (0.073)	304	H-2→L (0.24) H→L+1 (0.24)	4.03 (0.009)	307	4.02 (0.016)	309
S_4	4.25 (0.215) HBDI: 4.78 (0.013)	291	H→L+1 (0.24) H-1→L (0.23)	4.21 (0.100)	295	4.13 (0.158)	300
S_5	4.28 (0.149) ^f HBDI: 4.89 (0.020)	290	H→L+2 (0.31) H-3→L (0.18)	4.44 (0.077)	279	4.21 (0.060)	294

^a n,π^* states not included in the numbering. ^bExcitation energies obtained at the SA-8-MS-CASPT2(14,14)/ANO-L level. SA-8-MS-CASPT2(16,14)/ANO-S data for p -HBDI⁻ included for comparison. ^cState character based on the PM-CASCI expansion from the MS-CASPT2 wave function. Squared coefficients given in brackets. ^d(n,π^*) states: 3.78 and 3.94 eV. ^e S_1 vertical excitation of the O-deprotonated form (O(-)-1 in Figure 2). ^fObtained at the SA-11-MS-CASPT2(14,14)/ANO-L level.

Electronic structure of the rKaede chromophore. The vertical π,π^* excitation energies of N(-)-1, computed at the MS-CASPT2, TD-CAM-B3LYP and CC2 levels are presented in Table 1, and the corresponding orbitals in Figure 3. All methods agree in a bright lowest vertical

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3 excitation (oscillator strength 1.05-1.27) corresponding to the HOMO→LUMO transition. The
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6 excitation energy of S_1 at the MS-CASPT2 and CC2 levels is 2.49 eV, while the TD-CAM-
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8 B3LYP value is somewhat higher, 2.66 eV. For comparison, the S_1 energy of the O-deprotonated
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10 form is 0.2-0.4 eV lower (2.24 eV at the MS-CASPT2 level). At the MS-CASPT2 level, S_2 of the
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12 N(-)-1 form has predominantly HOMO-2→LUMO character and appears at 3.66 eV. The S_2
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14 energies are higher with TD-CAMB3LYP and CC2 (3.86 and 3.79 eV) because of the partial
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16 double-excitation character that cannot be reproduced by TD-DFT or CC2. Because of this, S_2 is
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18 only weakly absorbing at the MS-CASPT2 level (oscillator strength 0.029), while the oscillator
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20 strength at the TD-CAMB3LYP and CC2 levels is larger. There are three additional states
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22 between 3.9 and 4.5 eV, approximately, with the following energies at the MS-CASPT2 level:
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24 4.07, 4.25 and 4.28 eV. Compared to the *p*-HBDF⁻ anion, the MS-CASPT2 S_1 - S_5 excitations of
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26 the rKaede chromophore are shifted to lower energies by 0.2 - 0.6 eV. For S_1 , the red shifts are
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28 approximately 0.3 eV and 0.5 eV for the N(-1)-1 and O(-)-1 isomers, respectively. This is
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30 consistent with the usual assumption that extended conjugation causes a red shift in the
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32 absorption. The lowest n,π^* states appear at 3.78 and 3.94 eV at the CC2 level and are not
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34 considered further because they have oscillator strengths < 0.001 and are only weakly coupled to
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36 the electron detachment continuum due to their Feshbach resonance character.
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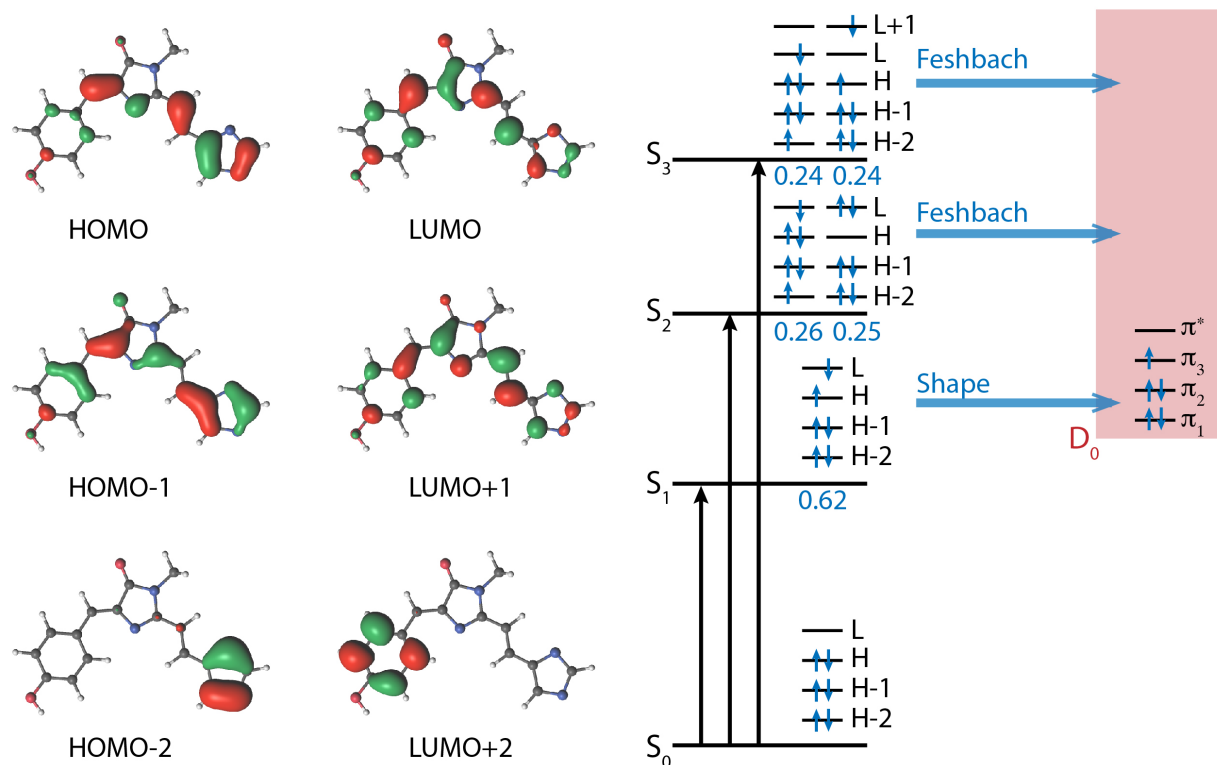


Fig. 3. Main CASSCF/MS-CASPT2 molecular orbitals involved in the transitions to the first three excited singlet electronic states of the rKaede chromophore and a schematic energy level diagram showing the resonance character (horizontal blue arrows) of these electronic states with respect to the D_0 electronic continuum.

The MS-CASPT2 vertical S_1 energies of the deprotonated forms in water (see SI for details) have been calculated to be 2.52 and 2.76 eV for O(-)-1 and N(-)-1. These values are in good agreement with the experimental band maximum of 2.55 eV, even though the calculations do not include vibronic effects which often shift the calculated absorption band to the red.⁴⁰

The excited states were optimized at the CC2/cc-pvtz level of theory,⁴¹⁻⁴² and the energies were recalculated with MS-CASPT2. Our discussion is based on the MS-CASPT2 values, but there is overall good agreement between the relative energies of the two methods for all minima (see

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3 Table SI2 for a comparison of the two methods). All optimized structures were planar. The
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5 calculated band origin (0-0 transition) of N(-)-1 in the gas phase is 2.42 eV (513 nm) at the MS-
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7 CASPT2 level, which corresponds to a relaxation energy of approximately 0.1 eV. The most
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9 significant structural changes at the S_1 minimum are stretches of the C_8-C_9 , $N_{10}-C_{11}$ and $C_{15}-C_{17}$
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11 bonds by 0.03 - 0.05 Å (see bond lengths in Figure 2a). This is consistent with the nodal
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13 structure of the orbitals involved in the excitation (H and L in Figure 3), which are delocalized
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15 along the conjugated system. The S_2 state has a relaxation energy of 0.30 eV, and the relative
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17 MS-CASPT2 energy of the S_2 minimum 3.36 eV. The main changes in the bond lengths involve
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19 the imidazole ring, where the excitation is localized (see the H-2 orbital in Figure 3). At this
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21 structure, the energy of S_1 is 3.03 eV. The S_2/S_1 energy gap is reduced from 1.17 eV at the
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23 Franck-Condon structure to 0.33 eV at the S_2 minimum, which suggests that there may be a near-
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25 lying conical intersection facilitating $S_2 \rightarrow S_1$ internal conversion. Finally, optimization of S_3 at
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27 the CC2 level of theory leads to a state inversion and a minimum on S_2 with a relative MS-
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29 CASPT2 energy of 3.66 eV. At this structure, the S_3 energy is 3.75 eV. This suggests that
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31 excitation of S_3 will result in rapid internal conversion to S_2 , and we postulate that this will be
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33 followed by further decay to S_1 , like what is predicted to happen after S_2 excitation.
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41 The photoelectron spectra of the deprotonated anionic model rKaede chromophore were
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43 recorded at 355, 350 and 315 nm as a function of electron kinetic energy (eKE) and plotted as a
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45 function of electron binding energy, $eBE = h\nu - eKE$ (Figure 4, solid black lines). The
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47 corresponding photoelectron spectra of $p\text{HBDI}^-$ are also presented for comparison (shaded grey)
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49 and are consistent with previous experimental photoelectron spectra measured by several groups,
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51 including our own group.^{18,29-32,43} It is clear that the rising edges of the photoelectron spectra for
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the rKaede and *p*HBDI⁻ anions are independent of the laser wavelengths employed, a signature of direct electron detachment.

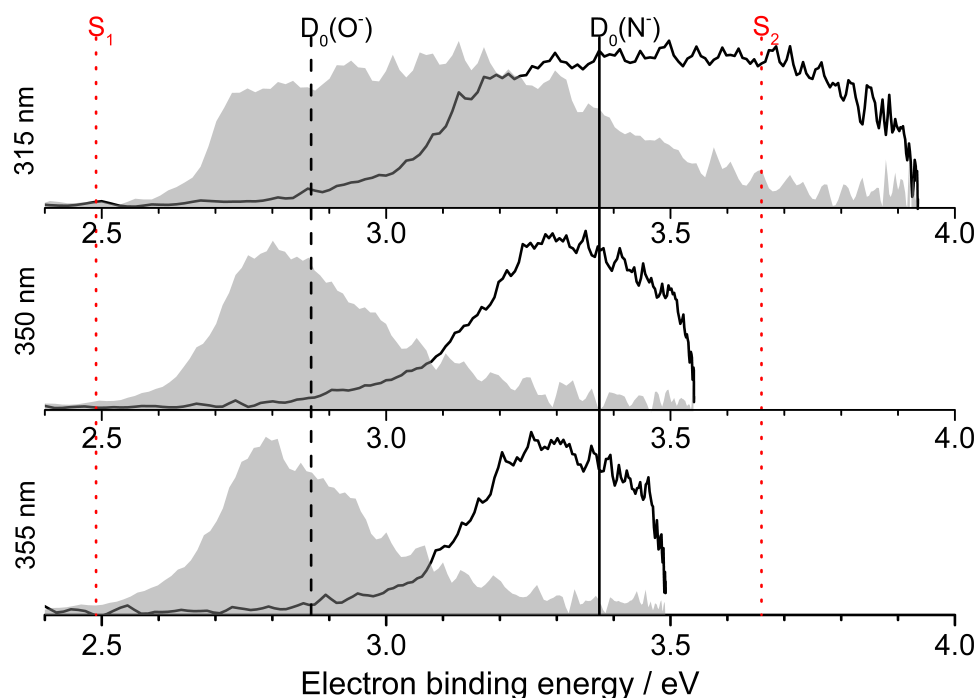


Fig. 4. Photoelectron spectra of the rKaede chromophore recorded at 355 nm (3.49 eV), 350 nm (3.54 eV) and 315 nm (3.94 eV) (solid black lines) compared with photoelectron spectra of *p*HBDI⁻ (shaded grey). All spectra have been normalised to their maximum intensities. Black vertical lines mark the calculated VDEs of the N(-)-1 (solid) and O(-)-1 (dashed) forms of the rKaede chromophore, and dotted red vertical lines mark the vertical excitation energies of the first 2 excited singlet states of the deprotonated Kaede chromophore.

The eBE corresponding to the maximum intensities of the 355 nm spectra for the deprotonated rKaede chromophore and *p*HBDI⁻ were estimated as the maxima of Gaussian functions fitted to the rising edges of the experimental spectra. The eBE estimated in this way for *p*HBDI⁻ is $2.8 \pm$

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3 0.1 eV, which is close to the adiabatic detachment energy of 2.73 ± 0.1 eV determined from high
4 resolution photoelectron spectra of vibrationally cold $p\text{HBDI}^-$.²⁷ The eBE for the rKaede anion is
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6 estimated to be 3.3 ± 0.1 eV, which is in good agreement with the value of 3.38 eV calculated
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8 both with EPT/6-311++G(3dp,3df) and MS-CASPT2/ANO-L (see Computational Details in the
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10 SI). The VDE calculated for O(-)-1 at the EPT level is 2.87 eV, which is sufficiently lower than
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12 the values estimated from experiment and calculated for N(-)-1, to support our suggestion that
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14 the rKaede chromophore is generated in its N-deprotonated form during electrospray ionization
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16 from methanol or methanol–water solutions. The 0.4 eV blue shift of the VDE for the rKaede
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18 chromophore compared to $p\text{HBDI}^-$ can be rationalized in terms of the increased conjugation
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20 having a greater stabilizing effect on the anion than the neutral radical.
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27 The slopes of the rising edges of the rKaede chromophore spectra are much shallower than
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29 those of $p\text{HBDI}^-$, hinting at a larger difference between the VDE and adiabatic detachment
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31 energy (ADE) for the rKaede chromophore than for $p\text{HBDI}^-$. This is indeed the case; the VDE
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33 and ADE for the rKaede chromophore at the MS-CASPT2 level are 3.38 and 3.15 eV, where the
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35 minimum of the ionized species was optimized at the B2PLYPD/cc-pvtz level of theory.⁴⁴ The
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37 calculated relaxation energy upon ionization, 0.23 eV, is in good agreement with experiment
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39 (Fig. 4) and contrasts with $p\text{HBDI}^-$ for which calculations have determined that $\text{ADE} \approx$
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41 VDE .^{24,26,31-32,37} At the optimized D_0 minimum, the main structural changes with respect to S_0 are
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43 found in the imidazole ring (see bond lengths in Figure 2), which is consistent with the ring
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45 having a formal negative charge in the N(-)-1 anion.
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51 As the photon energy increases, the broad features in the photoelectron spectra change shape
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53 on the high eBE side, characteristic of indirect photodetachment processes following resonant
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55 excitation of a higher lying electronically excited state (autodetachment). This broadening has
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3 been observed before in $p\text{HBDI}^-$ and it was rationalized in terms of resonant excitation of a
4 higher lying excited $^1\pi\pi^*$ state, which has excited shape resonance character with respect to the
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6 lowest electronic continuum, and some contribution from a $1^1n\pi^*$ state, which is a Feshbach
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8 resonance. Similar effects have been observed in photoelectron spectra of deprotonated
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10 photoactive yellow protein (PYP) chromophore anions following resonant excitation of the
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12 higher lying $2^1\pi\pi^*$ state, which also has excited shape resonance character with respect to the
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14 lowest electronic continuum.^{30,43}
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20 The photoelectron spectra of the rKaede chromophore all have significant intensities at low
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22 eKE (high eBE), unlike the photoelectron spectra of $p\text{HBDI}^-$. However, the low eKE electrons
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24 do not have the characteristic exponential shape that is a signature of thermionic emission from
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26 the ground electronic state, nor do they have an intensity step that might indicate opening of a
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28 higher lying electron continuum. In fact, the VDE of D_1 is calculated to be 4.70 eV at the MS-
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30 CASPT2 level for the rKaede chromophore, which is significantly higher than the highest photon
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32 energy used in our experiments (3.94 eV), suggesting that direct detachment to the D_1 continuum
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37 is unlikely.
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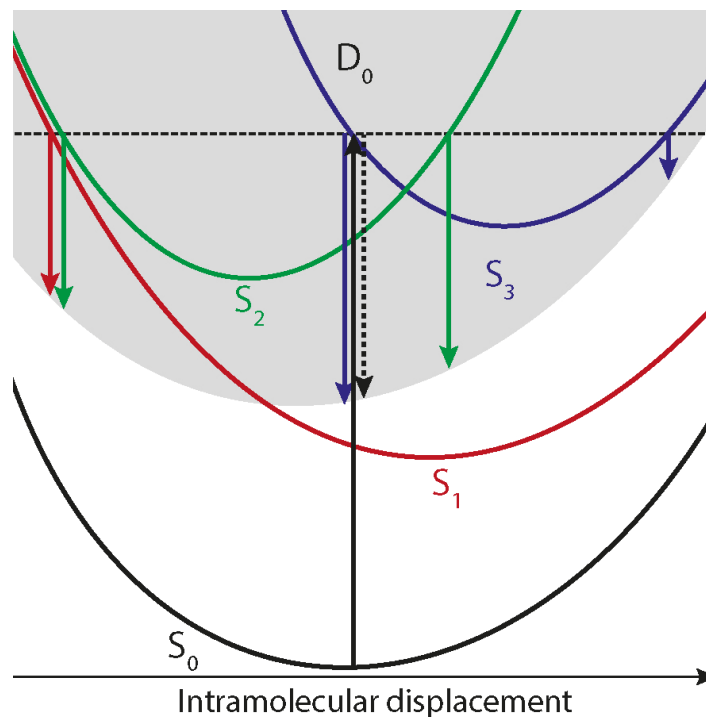


Fig. 5. Schematic potential energy level diagram illustrating competing electron detachment processes following photoexcitation of the S_3 state of the rKaede protein chromophore. The horizontal dashed line represents the final state energy and the solid grey shading represents the D_0 continuum. The solid black vertical arrow represents photoexcitation of the S_3 state. The dotted black vertical arrow represents direct detachment. Autodetachment to the D_0 continuum is possible from electronically excited S_3 , S_2 and S_1 states (vertical blue, green and red arrows, respectively) from any point along the intramolecular displacement coordinate lying in the D_0 continuum.

In Fig. 5, the possible electronic relaxation and electron emission processes following photoexcitation of the S_3 state of the rKaede protein chromophore are shown on a schematic

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3 potential energy diagram. The S_3 and S_2 states have a Feshbach resonance character with respect
4 to the D_0 continuum, whereas the S_1 state is predominantly a shape resonance. Thus, S_3 and S_2
5 are only weakly coupled to the electronic continuum. Moreover, the S_3 and S_2 optimizations
6 suggest that excitation of S_3 will be followed by rapid, sequential internal conversion to S_2 and
7 S_1 . Therefore, internal conversion to S_1 is likely to be more efficient than autodetachment from
8 either S_3 and S_2 . This is similar to the efficient and rapid internal conversion that has been
9 observed to occur through a series of conical intersections between excited states, that are
10 unbound with respect to electron detachment, in *para*-benzoquinone.⁴⁵ Because S_1 is a shape
11 resonance with respect to the D_0 continuum, the coupling between S_1 and D_0 is strong and
12 autodetachment from S_1 to D_0 will be fast. The absence of an exponential tail of low eKE
13 electrons, characteristic of thermionic emission from the hot electronic ground state, suggests
14 that autodetachment from high vibrational levels of S_1 is faster than internal conversion to the
15 electronic ground state. This in turn suggests that autodetachment from high lying vibrational
16 states in S_1 is responsible for the continuum of low eKE electrons observed in the 315 nm
17 photoelectron spectrum of rKaede. It is worth noting that S_4 and S_5 may also contribute to the
18 continuum of low eKE in the 315 nm spectrum of rKaede by similar rapid internal conversion
19 through a series of conical intersections to S_1 .

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The continuum of low eKE (high eBE) electrons seems likely to be a signature of
autodetachment from high vibrational levels of a low lying excited electronic state and indeed
such a continuum is also observed in the static photoelectron spectrum of *para*-benzoquinone, in
addition to the exponential tail arising from thermionic emission from a hot ground state.⁴⁵ A
continuum of low eKE electrons is not observed in the 315 nm photoelectron spectrum of
*p*HBDI⁻, although a broadening of the photoelectron spectrum towards high eBE is observed.

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3 This is readily understood in terms of the characters of the excited states. In $p\text{HBDF}^-$, the S_1 , S_2
4 and S_3 states are shape, Feshbach and excited-shape resonances, respectively, with respect to the
5 D_0 continuum.³⁷ Thus, in $p\text{HBDF}^-$ the S_3 state that is accessible at 315 nm is so strongly coupled
6 to the D_0 electronic continuum that it will undergo rapid autodetachment, resulting in a
7 broadening of the photoelectron spectrum to lower eKEs (higher eBE) but not to a continuum at
8 very low eKE.
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11 In summary, the comparison between UV photoelectron spectra of the rKaede protein
12 chromophore and the GFP chromophore suggests that there is an efficient electronic relaxation
13 pathway from higher lying electronically excited states to the S_1 state in the rKaede chromophore
14 that is not in operation in the GFP chromophore. Specifically, relaxation of S_2 facilitates $S_2 \rightarrow S_1$
15 internal conversion after excitation to S_2 and S_3 . This is a result of increasing the conjugation,
16 since the state that facilitates internal conversion to S_1 (S_2 at the Franck-Condon geometry) has
17 H-2->L configuration, *i.e.* it involves an occupied orbital on the imidazole ring which is not
18 present in $p\text{HBDF}^-$. Therefore, the extension of the $p\text{HBDF}^-$ chromophore with the imidazole
19 group causes the appearance of an additional state that is responsible for the suppression of
20 autodetachment from S_2 , suggesting that electron transfer from rKaede to the solvent will be less
21 efficient than in GFP. We believe this may be a general effect in large chromophores. This work
22 highlights the importance of detailed spectroscopic and dynamical studies of the rKaede protein
23 and of other green-to-red photoconvertible proteins so we may improve our understanding of
24 how to improve the properties of fluorescent protein optical markers that are not only used in the
25 biological and biomedical sciences as genetically coded fluorescent markers but are also
26 important tools for super resolution imaging.⁴⁶⁻⁴⁷
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3 **Supporting Information:** Computational details, experimental methods and Cartesian
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6 coordinates for N(-)-1 structures.
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