

Identification of the vibrational marker of tyrosine cation radical using ultrafast transient infrared spectroscopy of flavoprotein systems

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Abstract

Tryptophan and tyrosine radical intermediates play crucial roles in many biological charge transfer processes. Particularly in flavoprotein photochemistry, short-lived reaction intermediates can be studied by the complementary techniques of ultrafast visible and infrared spectroscopy. The spectral properties of tryptophan radical are well established, and the formation of neutral tyrosine radicals has been observed in many biological processes. However, only recently the formation of a cation tyrosine radical was observed by transient visible spectroscopy in a few systems. Here, we assigned the infrared vibrational markers of the cationic and neutral tyrosine radical at 1483 and 1502 cm⁻¹ (in deuterated buffer) respectively in a variant of the bacterial methyl transferase TrmFO, and in the native glucose oxidase. In addition, we studied a mutant of AppABLUF blue-light sensor domain from *Rhodobacter sphaeroides* in which only a direct formation of the neutral radical was observed. Our studies highlight the exquisite sensitivity of transient infrared spectroscopy to low concentrations of specific radicals.

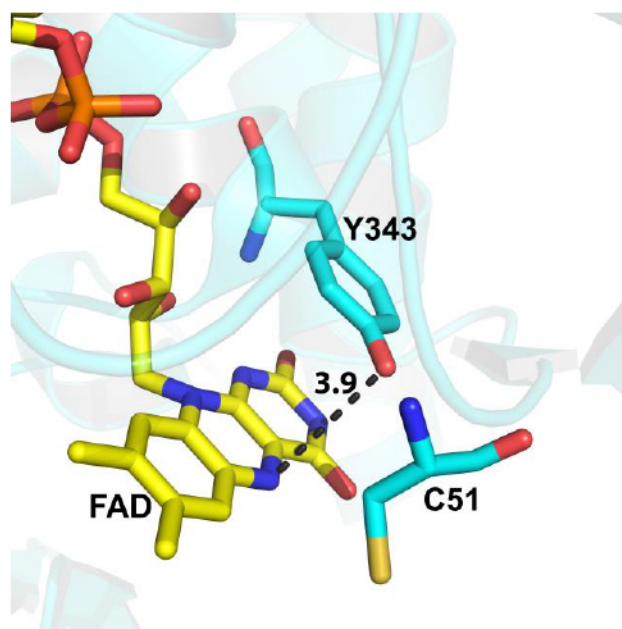
Introduction

Charge transfer processes are omnipresent in biological reaction pathways. Alongside specialized redox-active cofactors, in many cases amino acid residues – mostly aromatic residues like tryptophan and tyrosine – play important roles in reaction intermediates. Therefore, cationic and neutral radicals are thought to be important. They can be investigated using spectroscopic methods, including EPR, visible and infrared spectroscopy. The latter two can be combined with very high time resolution, allowing the characterization of very short-lived intermediates in photo-activatable systems. A prototypical example is the formation of tryptophan cation radicals during photoactivation of the flavo-photoenzyme DNA photolyase where sequential electron transfer involving three adjacent tryptophans occurs on the picosecond timescale.¹⁻⁵ The pKa of the tryptophan cation radical is ~4 and its deprotonation happens in a couple of hundreds of nanoseconds.² This process, and similar subsequently studied processes in the related cryptochrome blue-light sensors⁶⁻¹¹ have been extensively studied by polarization- and spectrally resolved transient visible spectroscopy. Transient infrared spectroscopy was successfully used to characterize protein dynamics, and activation mechanism of light dependent protein function.¹¹⁻¹⁴ The sensitivity of time-resolved infrared method allows us to visualize in the difference infrared spectra the vibrational modes of the chromophore or protein arising upon photoexcitation. Previously, we employed transient infrared spectroscopy to characterize the photocycle of the BLUF photoreceptor PixD, and we showed that the photoactivation mechanism of PixD involves a sequential formation of the anionic and neutral flavin radicals upon photoexcitation of the flavin chromophore, and the conserved tyrosine is the source of both electron and proton in the PCET mechanism.¹⁵

Tyrosine cation radicals may also play a role as reaction intermediates, but they are thought to be far less stable and more short-lived, or only occurring concomitant with proton transfer, as its pKa is ~ -2.¹⁶ The deprotonated, neutral, tyrosine radical has been observed as a relatively long-lived functional intermediate in a number of proteins, including photosystem II and type II ribonucleotide reductase^{17, 18}, and its visible¹⁹ and vibrational²⁰ spectroscopic characteristics have been determined. Yet, only recently Vos and co-workers used transient visible spectroscopy to identify a short-lived protonated cation radical after photoexcitation of flavin in non-photoactive flavoenzymes where tyrosine and the isoalloxazine ring systems

67 closely interact: in a variant of the bacterial flavoenzyme TrmFO²¹, a tRNA:m⁵U54-
68 methylase, and subsequently in native glucose oxidase.²²

69
70 The available crystal structure²³ of the purified TrmFO shows a close cysteine at
71 position 51 (C51) in the *Thermus thermophilus* enzyme, which forms a stable adduct with the
72 flavin, a property mainly observed in LOV domains.²⁴ The adduct formation in LOV proteins
73 is triggered by light absorption of FMN and a nearby conserved cysteine forms an adduct with
74 the C4a atom of the flavin. Mutation to the conserved cysteine residue blocks the formation of
75 the adduct in LOV domains, resulting in a highly fluorescent protein. Contrary to the
76 observation in LOV domains, the adduct formed in TrmFO is highly fluorescent. Substitution
77 of C51 with alanine inhibits the adduct formation, yielding an almost non-fluorescent flavin
78 since a tyrosine residue (Y343) is very close and parallel to the isoalloxazine ring (Fig.1); this
79 is a favourable position of Y343 for making the electron transfer process very efficient and
80 the excited state of the flavin very short-lived, ~1 ps or less. In the same transient visible
81 studies²¹, Vos and co-workers assigned a photoproduct to the FAD•TyrOH^{•+} state, that
82 subsequently decayed in ~3 ps.



85
86 Fig. 1 Crystal structure of *Thermus thermophilus* TrmFO (pdb 3G5Q). In this study, the residue C51 was
87 mutated to A creating the C51A TrmFO mutant.

TrmFO system appears to be a good model system to investigate infrared properties of a tyrosine cation radical. Therefore, we performed transient infrared measurements both on TrmFO C51A and the C51A/Y343F double mutant. The substitution of tyrosine with phenylalanine was chosen to inhibit the electron transfer pathway. The results suggest the presence of parallel reaction schemes and the sensitivity of infrared spectroscopy to observe low concentrations of reaction intermediates. In addition, we expand our studies to glucose oxidase and BLUF proteins to further validate the presence of tyrosine cation radical in those systems.

Experimental Methods

Transient infrared absorption measurements

Ultrafast time-resolved IR (TRIR) spectra were measured at the STFC Central Laser Facility with ~ 100 fs time resolution.²⁵ TRIR spectra were acquired at 20 °C from 1300 – 1800 cm^{-1} at a resolution of 3 cm^{-1} per pixel. Data were obtained using a 50 μm path length cell while the sample was rastered with the help of a Lissajous scanner to minimize long-lived phototransformation (photobleaching, photodegradation and photoconversion). The excitation beam of the 450 nm, 100 fs, 5 kHz, pulses was focused to a spot size of ~ 100 μm and the pulse energy was kept around 500 nJ. Transient difference spectra (pump on – pump off) were recorded using the IR probe at time delays between 1 ps and 2 ns. After the measurements were recorded, the extent of phototransformation was shown to be negligible using absorbance spectroscopy. Spectra were calibrated relative to the IR transmission of a pure *cis* stilbene standard sample placed at the sample position. TRIR of light-adapted W104Y AppA BLUF domain were recorded under continuous illumination with $\sim 200\text{mW}$ of 450 nm light on the sample cell during the experiment.

Data were analyzed globally using the Glotaran software package.²⁶ In the case of global analysis, simultaneous fit is performed on the measured ΔA data, the pre-exponential factors (belonging to the different wavelengths) of each decay rate will give the decay associated spectra (DAS). An alternative way is to assume a sequential model ($A \rightarrow B \rightarrow C$) and solve the respective differential equations. The obtained evolution associated spectra (EAS) will show the evolution of spectra in time²⁷. All the data presented in the paper were fitted assuming a sequential scheme, the decay rates for the individual EAS spectra show the time needed to convert from one state to the other. Assuming the simplest $A \rightarrow B \rightarrow C$ scheme the decay rate of EAS1 is the time need to evolve from state A to state B, the spectrum of EAS1 is the spectrum belonging to state A.

Individual kinetics were fit using Origin 2020 from Originlab.

Protein expression and purification

The BLUF domain of AppA (AppA_{BLUF}: residues 5-125) was expressed in BL21(DE3) *Escherichia coli* cells. Protein expression and purification were performed in the dark as described previously²⁸. The W104Y AppA BLUF construct was obtained by site-directed mutagenesis performed using Phusion site-directed mutagenesis kit (NEB), wt AppA_{BLUF} in pET15b as a template and the following primers: 5'-CGCCGCTTTGCGGGATATCACATGCAGCTCTCC-3' and 5'-CTTGGCGATCGGTTCTCTGCGAGGATCTC-3'. All constructs were verified by DNA sequencing.

C51A and C51A/Y343F mutant proteins of TrmFO from *T. thermophilus* were heterologously expressed and purified as previously described.²¹ Glucose oxidase from *A. niger* was purchased from Sigma and dissolved in the same D2O buffer (50 mM NaH₂PO₄, 10 mM NaCl, pD 8.0) as the TrmFO and AppA W104Y mutants. All protein concentrations were kept to ~1mM and measured in Harrick cells using 50 μ m spacers between the CaF₂ windows; in this way ~80 μ l sample was used for one measurement.

Results

TrmFO mutants C51A/Y343F and C51A

In C51A/Y343F double mutant of TrmFO, the fluorescence quenchers nearby the flavin are absent, and the FAD* excited state decays in a multiphasic manner on the timescale of 30 ps and longer.²¹ Accordingly, TRIR spectra of C51A/Y343F mutant (Fig. 2A) resemble the TRIR spectra of oxidized flavin in solution (see Fig. S1) on the fs and ps timescale, and do not evolve with time, thus it can be assigned to FAD* vibrational modes. The negative vibrational

154 modes (bleaches) are assigned to the depletion of the ground state population of the flavin while
155 the positive peaks (called transients in this paper) are associated with vibrational modes of the
156 excited state of flavin or to protein modes. The 1547 cm^{-1} and 1581 cm^{-1} bleaches were assigned
157 to flavin ring modes, the $\sim 1700 \text{ cm}^{-1}$ bleach was earlier assigned as the vibration of the C4=O
158 carbonyl of flavin, the 1640-1650 cm^{-1} bleach was assigned as the C2=O stretch, and the 1380
159 cm^{-1} and 1415 cm^{-1} transients are vibrational markers of the excited state of the flavin (see
160 assignment of these peaks in the first paragraph of SI).^{12, 28-30}

161 The overlaid TRIR spectra of C51A/Y343F and C51A variants (Fig. 2C) illustrate that the
162 frequency of C4=O in the 1700 cm^{-1} region is blue shifted by approximately 8 cm^{-1} , from 1697
163 cm^{-1} in C51A mutant to 1705 cm^{-1} in C51A/Y343F. This suggests that the replacement of Y343
164 to phenylalanine decreases the hydrogen bonding around the C4 carbonyl of Flavin.

165 The kinetics of the ground state recovery observed at 1547 cm^{-1} (Fig. 2F) highlights
166 that the C51A mutant returns to the ground much faster (within a few ps) than the double
167 mutant. In C51A TrmFO, there is a faster charge transport to the tyrosine, followed by charge
168 recombination to the resting FAD state²¹, whereas in the C51A/Y343F mutant the flavin
169 fluorescence is far less quenched on this time scale.

170 The TRIR spectra of TrmFO C51A mutant evolve significantly (Fig. 2B), presumably
171 reflecting excited state decay, and charge transfer processes, which differ from those of the
172 C51A/Y343F mutant assigned to FAD*. At lower frequencies, the C51A spectra show two
173 broad transients around 1485-1505 cm^{-1} and 1515-1535 cm^{-1} which are not present in the
174 C51A/Y343F mutant. Hence, we propose that the appearance of these vibrational modes is
175 primarily related to the electron transfer process, which takes place from tyrosine 343 to the
176 flavin.

177 Based on previous infrared measurements on flavin radicals, the broad transient around 1515-
178 1535 cm^{-1} can *a priori* be interpreted relatively straightforward. It appears composed of two

shoulders – at 1518 cm^{-1} and 1528 cm^{-1} whose relative intensity varies in time, reflecting two distinct vibrational modes. In earlier work³¹, we used DFT calculations and infrared measurements to assign these two transients to the formation of the anionic, $\text{FAD}^{\bullet-}$, (1518 cm^{-1}) and neutral, $\text{FADH}^{\bullet}$, flavin radicals (1528 cm^{-1}). For example, in the case of PixD – a BLUF domain protein – the sequential formation of these two peaks shone light on the photoactivation process of the protein: first the anionic flavin radical ($\text{FAD}^{\bullet-}$) was formed within 2-3 ps followed by the protonation of the flavin, thus leading to the formation of the neutral flavin radical ($\text{FADH}^{\bullet}$) in $\sim 100\text{ ps}$.

A similar sequence appears to be observed in the case of the C51A mutant. A global analysis of the TRIR data yielded time constants of 1 ps and 3 ps, and a very small longer-lived phase (Fig. 2D), similar to the one observed by Nag et al²¹. Using a sequential scheme to fit data adequately, the evolution-associated spectra (EAS) obtained from the global fit are well separated (Fig. 2D). EAS1 is mainly dominated by the vibrational modes of $\text{FAD}^{\bullet-}$ – FAD (cf. Fig S1), as expected from our previous work using transient visible spectroscopy.²¹ However, we also observed a distinct transient formed at 1515 cm^{-1} , indicating that some $\text{FAD}^{\bullet-}$ is formed at very early times after excitation. This suggests that a fraction of the excited state decays, by flavin photoreduction, much faster than the time resolution of our system and the previously reported²¹ fluorescence experiments ($\sim 200\text{ fs}$). Indeed, the kinetics at 1515 cm^{-1} rise with the instrument response time.

EAS2 (3ps) includes a substantial transient at 1528 cm^{-1} which was assigned to $\text{FADH}^{\bullet}$. The kinetics of 1528 cm^{-1} transient (Fig. 2E) shows that this signal does not form instantly after excitation but in a sequential way, in $\sim 1\text{ ps}$ after the initial formation of the anionic radical. This is an unexpected result since $\text{FADH}^{\bullet}$ has a marked visible signature and was not observed ($<10\%$) in the visible transient absorption experiments^{21, 32}, where the 3-ps phase was assigned to recombination of $\text{FAD}^{\bullet-}$ and $\text{TyrOH}^{\bullet+}$. Therefore, it appears that

transient infrared method is exquisitely sensitive to even very minor amount of FADH[•] observed at 1528 cm⁻¹ in the C51A TrmFO mutant. Formation of FADH[•] implies the presence of a proton and a proton donor, this latter obviously must be the tyrosine. As the flavin is protonated as the result of the electron transfer process, one can talk about proton coupled electron transfer process (PCET) seen in many photoactive flavoproteins (Slr1694 BLUF, PaPB etc.)

A second difference between the EAS1 of the C51A mutant (Fig. 2D) and the expected pure excited state spectrum observed in the C51A/Y343F mutant (Fig. 2A) is the transient between 1475 and 1500 cm⁻¹, the maximum being around 1483 cm⁻¹. Based on the assessment that a tyrosine cation radical is formed along with FAD reduction²¹, we attribute the 1483 cm⁻¹ transient to the tyrosine cation radical associated with the fraction of FAD^{•-} formed within the instrument response (see above). In EAS2 (3-ps phase precursor) the 1483 cm⁻¹ transient is shifted towards 1500 cm⁻¹. We suggest that this may be due to the expected proton transfer of the tyrosine radical to the flavin anion, yielding the small amount of FADH[•] alluded to above, thus producing some neutral tyrosine radical. This is in accord with assignment of a 1502 cm⁻¹ mode to the TyrO[•]C-O[•] stretching vibration in a ribonucleotide reductase from *Bacillus cereus* by Raman spectroscopy¹⁸ and a 1504 cm⁻¹ FTIR band in PSII from *Synechocystis* sp. PCC 6803.¹⁷

Analysis of the EAS spectra of C51A mutant illustrates that the high frequency mode of the flavin (~ 1700 cm⁻¹) is upshifted by ~ 5 cm⁻¹ in EAS2 compared to EAS1 which reflects a less hydrogen bonded environment for the C4=O carbonyl of the flavin. It is expected since the deprotonation of the tyrosine perturbs the hydrogen bonding network around the flavin.

As mentioned above, the ground-state recovery in the C51A/Y343F double mutant is much slower than in the C51A mutant which it is expected since close by electron donor is absent. Nevertheless, the decay of unquenched flavin excited states is faster than expected,

229 indicating the presence of another electron donor allowing electron transfer on the tens and
230 hundreds of picoseconds timescale, presumably a Trp residue.²¹ Interestingly, all the IR
231 spectra of the C51A/Y343F protein are similar and devoid of any sign of tryptophan or flavin
232 radical formation. This indicates that if such radicals are formed on the timescale of our
233 experiments, they decay faster than they are formed or the yield of formation of these radicals
234 is under the detection limit of the present instrumentation. Experiments with additional
235 mutations are required to identify of other potential electron donors.

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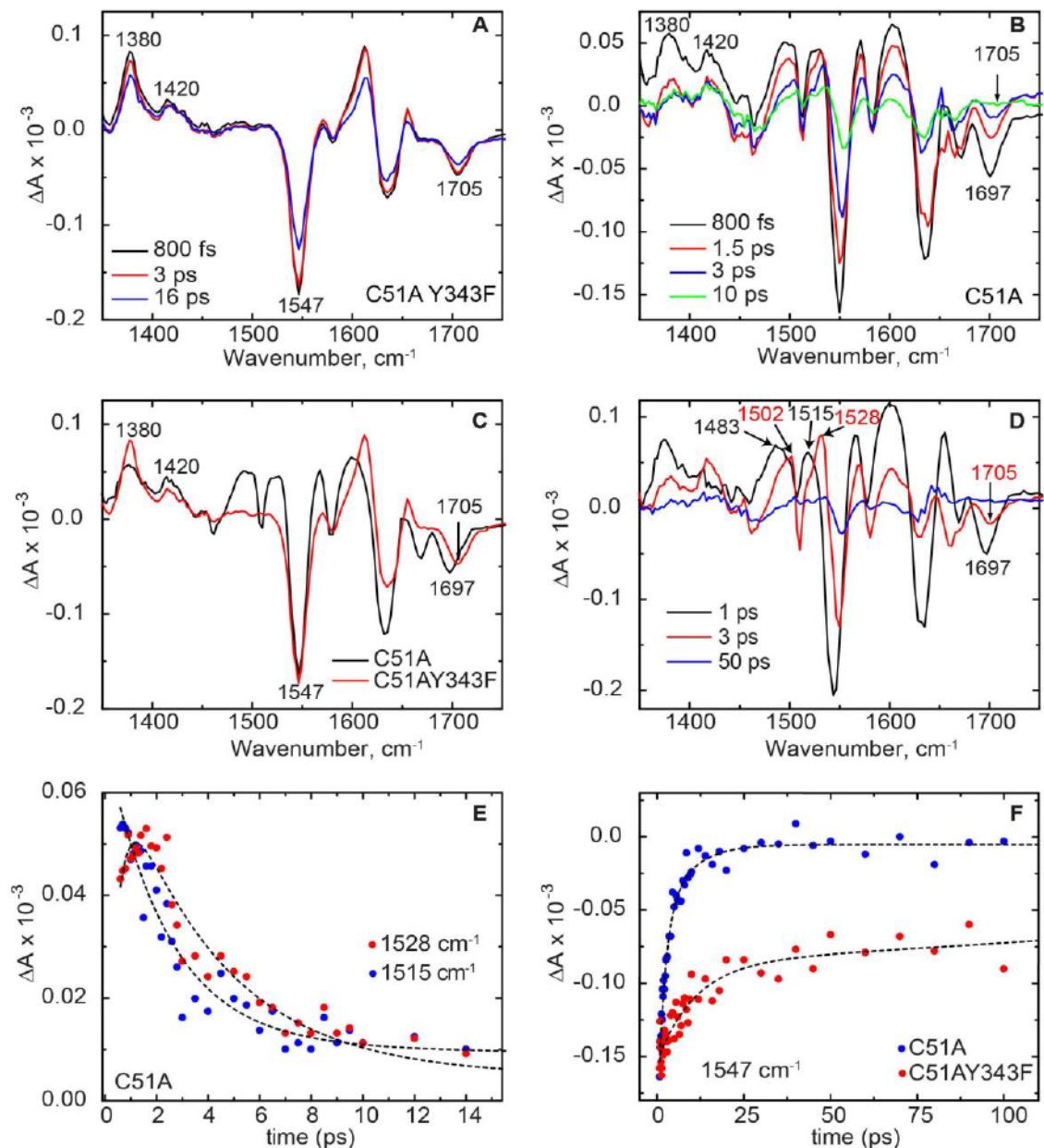


Fig 2. A) TRIR spectra measured on the C51AY343F mutant at different delays B) TRIR spectra measured on the C51A mutant at different delays C) Comparison of TRIR spectra measured on the C51A and C51AY343F mutants at 800 fs D) EAS spectra of the C51A mutant E) Kinetics measured on the C51A mutant at 1515 cm⁻¹ (blue) and 1528 cm⁻¹ (red) respectively F) Kinetics at 1547 cm⁻¹ in the C51A and C51AY343F mutant

Glucose oxidase

We collected new TRIR measurements on glucose oxidase (GOX) to further characterize the infrared vibrational markers observed for tyrosine cation and neutral radical. Previously, we published the TRIR spectra of glucose oxidase in three different redox states of flavin (oxidized, neutral and anionic radical) focusing on the vibrational markers of the neutral and anionic redox state as well as on the interpretation on the longer lived product states involving tryptophan.³¹ In the present study, we globally fit the data using a sequential model to obtain the EAS spectra of the measurements.

GOX contains two tyrosine residues close to the isoalloxazine ring of FAD (Fig. 3). We recently characterized the relatively complex photochemistry of glucose oxidase using transient visible absorption and fluorescence spectroscopy.²² We found evidence for multiphasic FAD* decay leading initially to the FAD*·TyrOH⁺ state in ~1 ps, and subsequently also to some FADH*·TyrO[·] in ~4 ps and to some TrpH⁺ in ~30ps, all these electron and proton transfer steps occur in competition with recombination reactions. In this light, we reinvestigated GOX by TRIR.

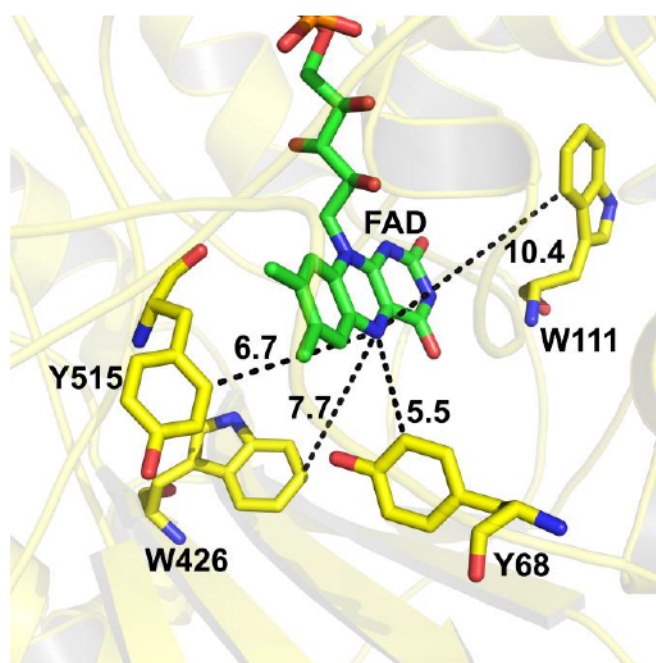


Fig 3. Structure of glucose oxidase (PDB: 1CF3) showing the distance of isoalloxazine ring and the potential electron donors.

The transient infrared spectra of glucose oxidase (Fig. 4A) resemble the TRIR data of C51A TrmFO mutant (Fig. 2B): at lower frequencies, we observe the transients around 1380 and 1420 cm^{-1} related to the excited state of the flavin, a broad transient around 1480 cm^{-1} and a well separated one at 1515 cm^{-1} , and a new transient peak appearing at 1528 cm^{-1} at later time delays. Fig. 4B depicts the result of a global fitting of TRIR dataset in terms EAS assuming a sequential model. The time constants of the fit, 1 ps, 3 ps, 36 ps and the asymptotic one agree with those of the visible data, with the limitation that in the infrared measurements we could not separate the pure excited state of the flavin. EAS1 (1 ps) and EAS2 (3ps) both contain spectral features ascribed to the excited flavin, as well as a 1483 cm^{-1} band and the flavin anionic peak (1515 cm^{-1}). Similarly to TrmFO, the tyrosine cation radical in GOX is formed in 1 ps upon excitation²², and in the TRIR of GOX the 1483 cm^{-1} band appears to reflect the vibrational mode of the tyrosine cation radical, in agreement with the above assignment for C51A TrmFO.

The EAS3 and EAS4 illustrate a poorly resolved shoulder at 1490 cm^{-1} , as well as a distinct shoulder at 1528 cm^{-1} which we assigned to FADH $\bullet$ state of flavin. In our earlier work³¹, we showed that electron transfer can also take place from one of the adjacent tryptophans (W426, W111), so the formation of the 1490 cm^{-1} band indicates the appearance of the tryptophan cation radical.

In our previous studies on AppA³⁰ and pixD mutants, the TRIR spectra reveal the 1488-1490 cm^{-1} peak arising from a photoinduced electron transfer processes, and we assigned this peak to the vibrational marker of the TrpH $\bullet^+$ radical (assignment of this peak in the PixD mutant can be found in the SI). Based on calculation, this mode is related to the Φ_{19a} mode of the phenyl ring (using the Wilson vibration nomenclature) and the C2-C3 stretch.^{33, 34} Resonance Raman spectroscopy was recently utilized to measure vibrational properties of tryptophan radicals, and it was found that the W5 $\bullet^+$ vibrational mode in water can be found at 1495 cm^{-1} while in D₂O is shifted to 1488 cm^{-1} .³⁵ Vibrational marker of tryptophan cation radical was firstly assigned by Blanco-Rodriguez et al³⁶., using the same time resolved transient infrared absorption system (ULTRA²⁵) what was used for this work. The authors assigned the Trp $\bullet^+$ feature at 1278 and 1497 cm^{-1} in the case of a model inorganic complex in DCM. This compares well (specially if we take into account the difference between the two solvents) with the expected 1490-1495 cm^{-1} .

The long phase (EAS4) contains a (poorly resolved) transient at 1502 cm^{-1} . Based on our observation of the visible transient data²², where the tyrosine neutral radical is stabilized for tens of picoseconds and longer, we conclude that the 1502 cm^{-1} band is related to the formation of the TyrO $\cdot$. In the visible transient data, tyrosine radical is already formed in the EAS3 (37 ps) phase, which is probably the case in the TRIR measurements, just the 1502 cm^{-1} transient is covered by the small bleach of FAD $\sim$ 1503 cm^{-1} .

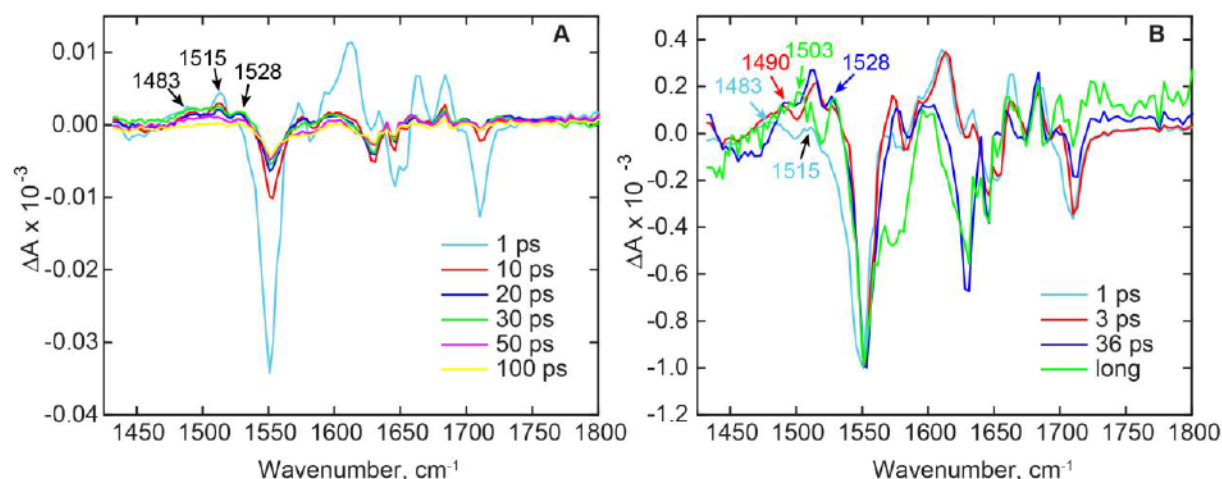


Fig 4. TRIR on glucose oxidase. A) TRIR spectra at different delays B) EAS spectra obtained from global analysis. Here, we normalized data here to highlight the vibrations.

Taken all data together, the infrared absorption data provide extra details of distinct vibrational modes for neutral and cation tyrosine radical along with flavin radicals and appear generally consistent with the visible transient absorption data.

W104Y AppA mutant

AppA regulates the biosynthesis of the photosynthetic genes in the bacterium *Rhodospirillum rubrum*. In the dark and at low oxygen level, AppA binds PpsR, a transcriptional antirepressor, while at high light intensity or oxygen level the AppA-PpsR complex dissociates, and PpsR blocks the production of the photosynthetic genes.^{37, 38} The primary photochemistry of AppA is driven by the reorganization of the hydrogen bonding network around the flavin upon blue light absorption, this small reorganization leads to a larger structural change in the protein.²⁶ Even though AppA is a photoactive flavoprotein, its function is not driven by electron transfer as flavin radical formation was not observed in the

dark-adapted state of the protein.³⁰ However electron transfer and radical formation are observed in the light-adapted protein³⁹, most likely due to a tryptophan residue (W104, the only close tryptophan in the protein) which moves closer to the flavin after blue light absorption.⁴⁰

In this work, we replaced the close tryptophan (W104) with a tyrosine; therefore, Y21 and Y104 are the only two potential electron donors to flavin (see Fig. 5). We performed measurements on the light adapted state of the W104Y mutant and our *a priori* expectation was that if we observe the build-up of an amino acid radical that must be a tyrosine radical.

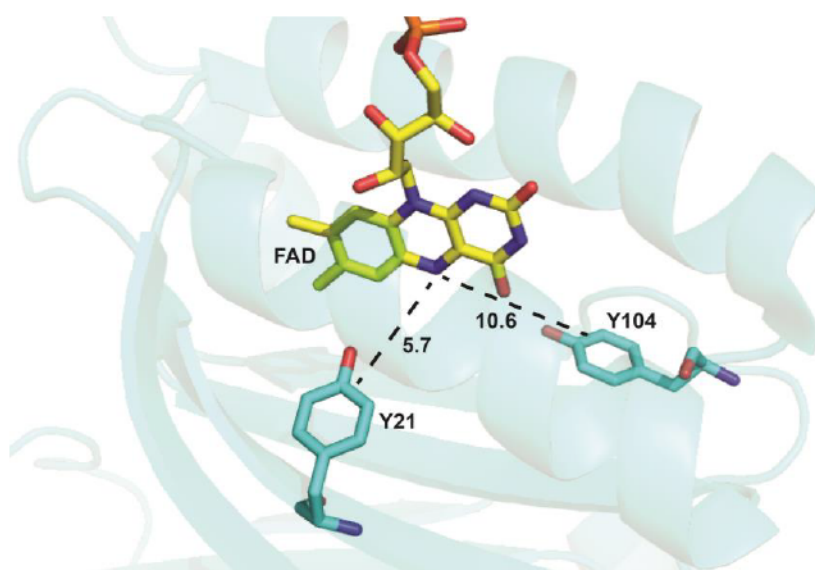


Fig. 5 Structure of AppA BLUF in light state (pdb: 2IYI) showing FAD and the two adjacent tyrosines. The position of Y104 is speculative, as the original structure contains a tryptophan at this position.

Apart from the dominant excited state transients at 1380 and 1415 cm^{-1} , the transient infrared spectra of the W104Y mutant (Fig. 6A) display the formation of transients at $\sim 1528 \text{ cm}^{-1}$ (neutral flavin radical) as well as at $\sim 1502 \text{ cm}^{-1}$. Both peaks were formed in approximately 2 ps as can be observed by the fits of these individual kinetics (Fig. 6 C-D). Based on our findings in C51A TrmFO mutant and GOX, the 1502 cm^{-1} vibrational mode can be assigned to a neutral tyrosine radical and the presence of the $\sim 1528 \text{ cm}^{-1}$ peak suggests that the W104Y mutant participates in proton coupled electron transfer (PCET), thus forming $\text{FADH}^\bullet$ and $\text{TyrO}^\bullet$ to some extent.

This assessment is corroborated by the global analysis (Fig. 6B). The EAS1 spectrum (2 ps) is dominated by vibrational modes of excited oxidized flavin. The EAS2 (40 ps) contains the appearance of both the formation of the neutral tyrosine radical as well as $\text{FADH}^\bullet$. In the final EAS, the high frequency bleach is shifted up $\sim 7 \text{ cm}^{-1}$, reflecting that the C4=O of the flavin loses some hydrogen bond after the flavin becomes protonated. This result can be explained

by the fact that tyrosine at 104 position is in hydrogen bonding distance to the flavin, and as it deprotonates the flavin loses that interaction, causing a substantial upshift of the C4=O stretch.

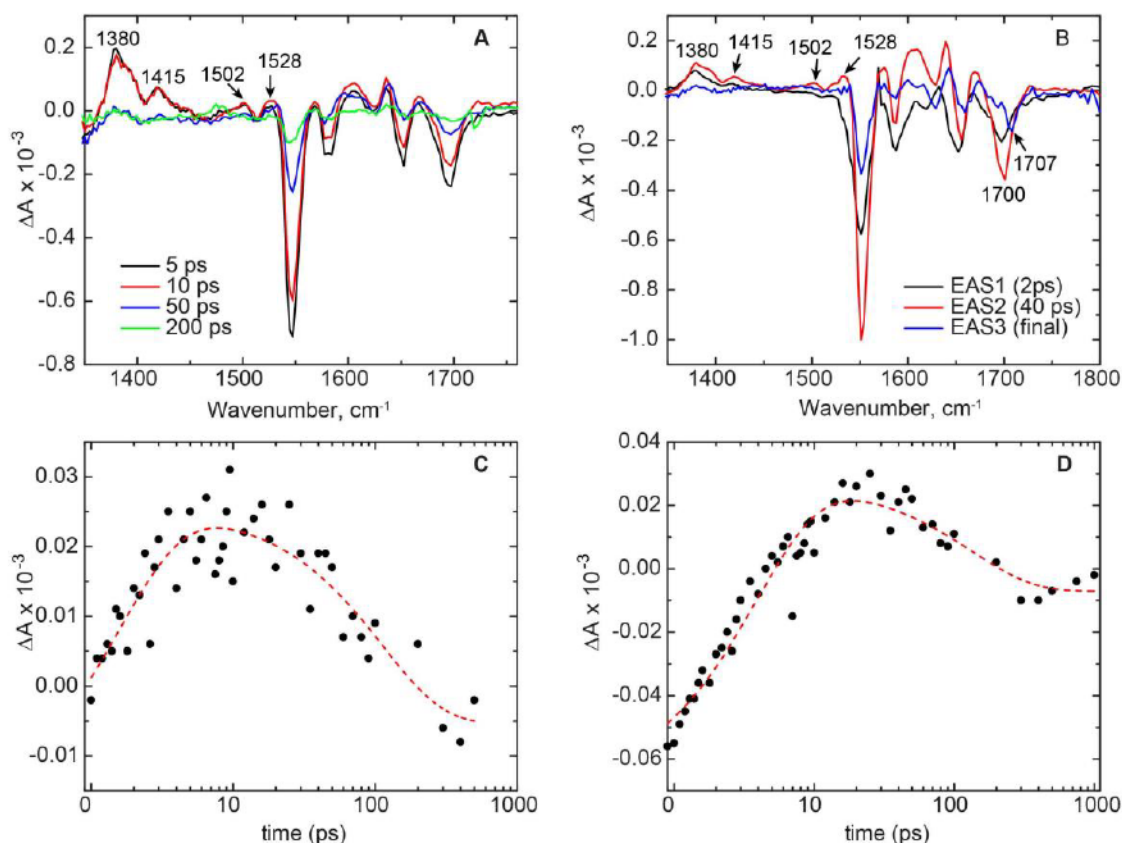


Fig 6. A) TRIR spectra measured on light-adapted state of W104Y AppABLUF at different delays B) EAS spectra from global analysis of the TRIR spectra measured on the W104Y AppA mutant C) Kinetics observed at 1502 cm^{-1} D) Kinetics observed at 1528 cm^{-1}

Indeed, we can conclude that activation of AppA W104Y mutant does not involve the sequential formation of charged radical species as observed in C51A TrmFO mutant and in GOX. Appearances of the neutral tyrosine radical and the neutral flavin radical peaks show evidence for a fraction of fast proton coupled electron transfer process, in which tyrosine is the proton donor.

Discussion

We employed ultrafast infrared absorption measurements to identify the vibrational markers of the cation and neutral tyrosine radical in C51A and C51A/Y343F variants of TrmFO. We further investigated the formation of the same radical in wild type GOX and W104Y AppABLUF mutant in the light state. Comparing our previous visible transient absorption data measured on TrmFO mutants and GOX with the infrared measurements, we identify the 1483 cm^{-1} vibrational mode as a vibrational marker of $\text{TyrOH}^{\bullet+}$. Tryptophan cation radical ($\text{TrpH}^{\bullet+}$) has a vibrational signature around 1488-1490 cm^{-1} . We were able to identify a vibrational marker for the neutral tyrosine radical at $\sim 1502 \text{ cm}^{-1}$. The exact position of both the tyrosine cation and neutral radical strongly depends on the hydrogen bonding environment, on the solvent, so their frequencies can differ in a water-based buffer as in this work the samples were dissolved in deuterated buffer. The observed shift in a water-based buffer is expected to be smaller in the case of the neutral tyrosine radical and more significant in the case of the tyrosine cation radical.

This finding is in good agreement with earlier assignments of this vibrational mode with the pioneering work on phenoxyl and tyrosine radicals. Time resolved Resonance Raman spectroscopy measurements – using 400 nm excitation – were done on phenoxyl radicals produced in aqueous solutions by pulse radiolysis. These measurements found a strong Raman peak at 1505 cm^{-1} which the authors assigned to the C=O stretch of the phenol group.⁴¹ A strong vibration for the tyrosine radical was found using UV Resonance Raman spectroscopy at 1510 cm^{-1} .²⁰

The role of tyrosine as electron donor in Photosystem II was first proved by Gerken, Brettel et. al using a nanosecond UV flash photolysis system; the authors proved that due to the electron transfer neutral tyrosine radical is formed⁴². Formation of neutral tyrosine radical in Photosystem II from *Synechocystis sp.* PCC 6803 was investigated by difference FTIR and the vibrational marker of $\text{Tyr}_D^{\bullet}$ and $\text{Tyr}_Z^{\bullet}$ radicals were found at 1503 cm^{-1} and 1512 cm^{-1} respectively.¹⁷ Calculations performed in the case of phenoxyl ($\text{PhO}^{\bullet}$) and tyrosine radical ($\text{TyrO}^{\bullet}$) revealed that the experimentally determined vibrational mode stands for the ν_{7a} C-O stretching of the phenol ring (see Table S1 and Fig. S4).

Using these new findings on the vibrational feature of neutral and cation tyrosine radical, we characterized the photochemistry of AppA W104Y mutant which was tailored to enhance and identify the formation of tyrosine radicals. This mutation altered significantly the photochemistry of the protein but as expected from earlier work^{40, 43} it did not stop the

formation of the light adapted state, except it altered the dark-adapted state recovery to ~ 100 fold faster compared to WT AppA. Blue-light irradiation of BLUF domain proteins results in a ~ 10 nm shift of the 447 nm absorption peak of flavin due the reorganization of the hydrogen bonding network around the isoalloxazine ring. Stopping the irradiation, the absorption peak turns back to the original value in dark-adapted state. This recovery from light-adapted to dark-adapted state happens in ~ 30 minutes in AppA and much faster (couple of seconds) in PixD or OaPAC. Replacement of W104 suppresses the red shift in the full-length protein⁴³ and results in a faster recovery of the dark-adapted state in the BLUF domain; in W104A the recovery was 80-fold faster than in wild type.⁴⁴

We performed transient infrared measurements on the light state of W104Y, and we observed one step formation of neutral tyrosine radical accompanying with a neutral flavin radical at ~2 ps after excitation. This suggests that in this mutant proton coupled electron transfer occurs, with both the electron and proton donor being a tyrosine. PCET is not unexpected during the photoactivation of photoactive flavoproteins, especially if the primary electron donor is a tyrosine. Proton coupled electron transfer was observed for example in the case of two BLUF domain proteins, PixD¹⁵ and PapB.⁴⁵ In the case of PixD, we observed a sequential radical formation: first, Y8 donated an electron to the flavin and FAD^{•-} radical formed, neutral flavin radical was formed concomitantly in ~ 100 ps.¹⁵ Based on theoretical calculations, in the case of PixD protonation of the flavin happens sequentially: after excitation the tyrosine gives a proton to an adjacent glutamine which finally protonates the flavin, stabilizing the neutral radical state.^{46, 47} In the case of PaPB, a BLUF protein found in the purple bacterium *Rhodospseudomonas palustris*, FADH[•] was formed directly – as in the case of the AppA W104Y mutant – via a proton coupled electron transfer process.³⁸

Our experimental data indicate that excitation of flavin in C51A TrmFO mutant also leads to a sequential proton coupled electron transfer to a very small extent (<10%), like in some of the BLUF domain proteins: tyrosine 343 gives an electron to the flavin forming the anionic flavin radical, subsequently fast deprotonation of the tyrosine leads to the protonation of the neutral flavin radical. We also have seen evidence for proton coupled electron transfer in GOX, where an electron is transferred upon excitation from one of the close tyrosines, followed by a proton transfer – from the tyrosine which gave the electron – stabilizing the FADH[•] state of flavin. Photochemistry of GOX was observed to be heterogenous and complex since besides the tyrosines, one of the close tryptophans can also donate an electron to the excited flavin. Altogether, this work exemplifies how extremely sensitive and selective

TRIR method is in elucidating even minor reaction pathways involving aromatic residue radicals.

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Conflict of interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

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