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A Q63E *Rhodobacter sphaeroides* AppA BLUF domain mutant is locked in a pseudo light-excited signaling state

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Abstract

The AppA BLUF photoreceptor from *Rhodobacter sphaeroides* contains a conserved key residue, Gln63 that is thought to undergo a shift in hydrogen bonding interactions when a bound flavin is light excited. In this study we have characterized two substitution mutants of Gln63 (Q63E, Q63L) in the context of two constructs of the BLUF domain that have differing lengths, AppA1–126 and AppA17–133. Q63L mutations in both constructs exhibit a blue-shifted flavin absorption spectrum as well as a loss of the photocycle. Altered fluorescence emission and fluorescence quenching of the Q63L mutant indicates significant perturbations of hydrogen bonding to the flavin and surrounding amino acids which is confirmed by ^{1}H-^{15}N HSQC NMR spectroscopy. The Q63E substitution mutant is constitutively locked in a lit signaling state as evidenced by a permanent 3 nm red-shift of the flavin absorption, quenching of flavin fluorescence emission, analysis of ^{1}H-^{15}N HSQC spectra and the inability of full length AppA Q63E to bind to the PpsR repressor. The significance of these findings on the mechanism of light-induced output signaling is discussed.

Keywords

Flavin photoreceptor; blue light absorption; photocycle

AppA is a member of the “Blue-Light Using FAD” (BLUF) class of photoreceptors that is widely distributed among prokaryotes (1–2). BLUF photoreceptors were initially identified based on their involvement in regulating well known light-driven events such as phototaxis in cyanobacteria and algae (2–6) or, in case of AppA, the transcriptional control of genes required for photosynthesis (7–8). However, there are many non-photosynthetic species that contain BLUF photoreceptors of unknown function with well over 100 examples of BLUF containing proteins in genome databases. A BLUF domain connected to an EAL domain in YcgF from *E. coli* has been rather extensively studied (5, 9–13).

X-ray crystallographic studies have demonstrated that the BLUF domain is comprised of a well-conserved βαββαββ fold. The major structural differences among different BLUF structures are a slight variation in the length of the β5 strand and the conformation of the loop that connects the β4 and β5 strands. NMR studies on light and dark-adapted BLUF proteins also demonstrate that the β4–β5 loop is dynamic and undergoes a light-dependent conformational change (14–15). One controversial feature is the precise positions of the side chains of a conserved tryptophan and methionine residues in the β5 strand that are found in distinct orientations in various BLUF structures (17–19). The Andersen et al. (19) structure

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of an AppA BLUF domain comprised of residues 17–133 (AppA17–133) has Trp104 buried near the flavin and hydrogen bonded to Glu63 while Met106 is swung away from the flavin. This is in contrast to the crystal structure of an AppA BLUF domain containing residues 1–124 (AppA1–124 C20S mutant) by Jung et al. (17) where Trp104 is swung away from the flavin and solvent is exposed while Met106 is located near the flavin and within hydrogen bonding distance to Glu63. The different orientations of Trp104 and Met106 lead Andersen et al. (19) to propose a model where excitation of the flavin results in a hydrogen bond rearrangement between Gln63, the flavin and Trp104. This model has been studied using FTIR analyses, theoretical calculations and fast spectroscopy (2, 16, 20–24). In this model, the dark state BLUF domain is characterized by a hydrogen bond between Trp104 Nε1 indole proton and Gln63, with Gln63 also donating a hydrogen bond to N5 of FAD. Light excitation of the flavin initiates fast electron and proton transfer from a conserved tyrosine (Y21 in AppA) to the flavin. This is followed by Gln63 undergoing a ~180° rotation around the C^{γ}–C^{δ} bond breaking the hydrogen bond to Trp104 alowing Trp104 to swing away from Gln63. Gln63 is then proposed to form a new hydrogen bond with the carboxyamide protons donating hydrogen bonds to both N5 and C4=O of FAD, resulting in a pronounced spectral shift in the FAD absorption and fluorescence emission spectrum. Another variant of this model proposes that Met106 is hydrogen bonded to Gln63 in the dark state while Trp104 is bound to Gln63 in the lit state (17, 22). Finally, there is also a model based on theoretical thermodynamic calculations that proposes that flavin light excitation promotes Gln tautomerisation that subsequently allows Gln63 rotation and exchange of Trp104 with Met106 (23). Yet another model proposes Met106 and Trp104 exchange following Glu63 tautomerization without its rotation (24).

Analysis of the structural environment of Trp104 in solution was recently undertaken by Dragnea et al. (25) in the dark and lit states using a combination of NMR spectroscopy, absorption and steady state fluorescence spectroscopy, as well as collisional quenching of tryptophan fluorescence. These results indicated that Trp104 is indeed buried and likely hydrogen bonded to Gln63 in the AppA17–133 domain as described by the crystal structure of Anderson et al., (19) and that an AppA domain comprised of residues 1–126 (AppA1–126) has Trp104 far from Q63 as shown in the structure by Jung et al. (17). Furthermore, it was also demonstrated that Trp104 does not appreciably move when the flavin is light excited and that full length wild type AppA has Trp104 in a conformation far from Q63 as indicated by the structure of Jung et al. (17). These new findings call into question the relevance of the various models that invoke movement of Trp104 and therefore require a reassessment of the role of Gln63 in controlling a light generated output signal in AppA.

In this study, we characterize Gln63 mutants in the context of both AppA17–133 and AppA1–126 to assess the role of Gln63 in controlling the characteristic light mediated BLUF spectral shift and output signal. Using a combination of NMR, absorption and fluorescence spectroscopies, we show that a Q63L mutant exhibits permanent blue-shifted spectrum and that the structure takes on a non-native conformation independent on light conditions. This is in dramatic contrast to a Q63E mutant that is both spectrally and conformationally locked in light excited state. These results provide further evidence that Gln63 indeed has a critical role in conferring both the spectral properties and output signals of BLUF photoreceptors.

Methods

Mutant construction and protein purification

Q63L and Q63E mutations were introduced into genes encoding AppA1–126 (plasmid pTY-AppA126) and AppA17–133 (plasmid pTY-AppA17–133), as well as in the AppA full-length protein (pTY-AppA) using a QuickChange kit (Stratagene), appropriate primers and

their complements. Carrying a chitin binding domain as a tag, all proteins were purified using Chitin beads (New England Biolabs). The chitin tag was removed during 50 mM DTT incubation on Chitin beads overnight and proteins were further purified by size-exclusion chromatography on Superose 12 using ÄKTA FPLC system, in 20 mM Tris-HCl, pH 8.0, 100 mM NaCl.

Visible Spectral Analysis

Absorption spectra were recorded on a Beckman DU-640 spectrophotometer using a 1 cm path quartz cuvette. Fluorescence emission spectra from 310 to 570 nm were recorded on a PerkinElmer LS50B spectrofluorometer using dilute samples to avoid self-absorption (A_{280} = 0.02) that were excited at 295 nm. Fluorescence quenching experiments with acrylamide as a quencher were recorded on the same dilute samples as above with excitation at 295 nm and single point emission reading at 360 nm. With temperature controlled at 15°C, 2 mL samples were stirred and quenched by the additions of 8 M acrylamide added at regular intervals up to 250 μL (0.88 M acrylamide). For the light-excited protein, the strong white light was applied to the sample for ~ 30 s and the fluorescence signal was read immediately following irradiation.

For proteins with homogeneous fluorophore, the fluorescence quenching by acrylamide can be described by Stern-Volmer relationship (26):

$$F_o/F=(1+Ksv[Q])e^{V[Q]}$$

in which F_0 is the fluorescence intensity in the absence of quencher and F is the fluorescence intensity in the presence of various concentrations of quencher [Q]. K_{SV} and V are Stern-Volmer quenching constants used to describe dynamic and static quenching respectively. The correction for sample dilution and acrylamide absorption was taken into account in the fit. Each quenching curve was measured at least three times for reproducibility.

NMR chemical shift perturbation experiments

All NMR spectra were recorded on a Varian Inova 500 MHz spectrometer equipped with an inverse probe at 35 °C. ^{1}H-^{15}N HSQC spectra were recorded for WT, Q63E and Q63L AppA1–126 and AppA17–133 with a 160 X 512 *t*1 and *t*2 data points, respectively. All experiments were performed at ambient low light conditions, in which AppA WT does not get light-excited. The backbone assignments for WT AppA were obtained from previously published spectra (14). The majority of the resonance assignments (>95%) for the Q63E mutant were obtained by inspection and comparison with spectra obtained for the analogous WT protein. Q63L mutants exhibited large chemical shifts when compared to AppA WT or Q63E, which prevented peak assignment.

Size-exclusion chromatography and characterization of AppAwt or AppA Q63 mutant complexes with PpsR

PpsR was kindly purified and provided by Liang Yin in our laboratory. AppA wt, AppAQ63E or Q63L full-length proteins were eluted from chitin beads after overnight incubation with 50mM DTT and mixed immediately in 10× molar excess with PpsR. Mixture was incubated in the dark for at least 30 min prior to loading on Sephacryl 200 size exclusion column (1.6× 80 cm) connected to ÄKTA FPLC filtration system. Chromatography was performed in the dark in a Tris-HCl buffer pH 8.0, 400 mM NaCl and 5 mM DTT, and eluted complexes were characterized by SDS-PAGE.

RESULTS

Spectroscopic analysis of Q63E and Q63L AppA mutants

We probed the involvement of Gln63 in the photocycle by constructing Glu and Leu substitutions of Gln63 (Q63E and Q63L, respectively) in two different structural constructs, AppA1–126 and AppA17–133. Leu occupies an occluded volume that is similar to that of Gln but is unable to donate or accept hydrogen bonds; Glu, on the other hand, is capable of hydrogen bonding, but introduces an ionizable group in place of the neutral carboxamide functionality. Two AppA BLUF domain constructs were used as they have different hydrogen bonds to Gln63 (25). In AppA1–126 Met106 is hydrogen bonded to Gln63 and in AppA17–133 Trp104 is hydrogen bonded to Gln63 (17, 19, 25). Interestingly, these two BLUF domains exhibit photocycles that are similar to that of full-length AppA with each having an identical dark state spectrum and each showing a similar light induced ~12 nm red-shift of the flavin absorption spectrum and similar decay rates to the ground state (25).

Spectral analysis of the Q63E and Q63L substitution mutants in AppA1–126 and AppA17–133 reveals that each lacks a photocycle. In addition, these mutants exhibit distinct absorbance maxima that are not influenced by the nature of the parent construct. Overall, there is a locked 12.5 nm red-shift in the flavin absorption maximum of the Q63E mutant (λ_{max}=449.5 nm) relative to the Q63L mutant (λ_{max}=437 nm) which also exhibits a locked spectrum (Table 1). This is in comparison to wild type AppA1–126 and AppA17–133 that are characterized by a dark state maximum of 446 nm and a light-excited maximum of 458 nm. Thus, substitution of Q63 with Leu results in a locked flavin spectrum that is blue-shifted 9 nm relative to the dark spectrum of the wild-type AppA. In contrast, substitution of Q63 with Glu which retains the ability to form hydrogen bonds to both N5 and C4=O of the flavin (as well as to other residues), results in flavin absorption spectrum that is permanently shifted to a position between that of the dark- and light-adapted wild type AppA spectra. These spectral studies confirm that Q63 has a major role in the light-induced photocycle red-shift, a finding consistent with models of the photocycle that invoke a change in the hydrogen bonding of the flavin to Gln63.

We next compared the fluorescence emission spectra of wild type, and the Q63E and Q63L mutants, in the AppA1–126 and AppA17–133 BLUF domains upon excitation of Trp at 295 nm. Wild type AppA17–133 and AppA1–126 both exhibit higher flavin fluorescence emission intensity in the dark-adapted state than in the light-adapted state (Figure 2A and 2B). In addition, the intensity of the flavin fluorescence is much greater in wild type AppA17–133 than in wild type AppA1–126. Increased flavin fluorescence by AppA17–133 has been attributed to the fact that Trp104 is closer to the flavin in AppA17–133 and likely transfers more energy non-radiatively to FAD than does AppA1–126 where Trp104 is further away (25). For comparison, the insert in Figure 2A shows fluorescence emission of full-length wild type AppA, which is similar to that of wild type AppA 1–126. It is interesting to note that tryptophan fluorescence maxima are identical for full-length AppA and the separate BLUF domains in a dilute state, which is not the case for more concentrated samples. In dilute state, all samples possess Trp emission maxima at ~ 343 nm. In more concentrated samples, separate BLUF domains have tryptophan maxima blue-shifted to ~ 333–336 nm (25).

Similar analysis of flavin fluorescence was undertaken for the Q63 mutants in the AppA17–133 and AppA1–126 constructs (Figure 2B and 2C). In addition to the absence of a photocycle, these mutants also show no change in their fluorescence spectrum when the samples were kept in the dark versus exposed to light prior to spectral analysis. Consequently, only the fluorescence spectra of dark adapted samples are shown in Figure 2. The Q63E mutant in both AppA17–133 and AppA1–126 reveals low flavin emission

intensity, much like that of light-adapted wild type AppA17–133 and AppA1–126 (Figure 2C and 2D dashed line). In contrast to Q63E, the Q63L mutants exhibit increased flavin emission coupled with a strong red-shift of the flavin emission maximum to ~515 nm as well as a shoulder at ~485 nm (Figure 2C and 2D solid line). Thus, at least two peaks seem to contribute to the Q63L flavin emission with the ratio of these two peaks varying with sample concentration and between different sample preparations (not shown). This is indicative of a non-native heterogeneous pocket surrounding the flavin in the Q63L mutants.

In a previous study, we demonstrated that acrylamide is an effective quencher of Trp fluorescence and can be used to detect light-versus dark-adapted structural changes in AppA1–126 and AppA17–133 (25). As previously observed, wild type AppA1–126 is characterized by partial solvent exposure of Trp104 since it exhibits linear acrylamide quenching in both the dark- and light-adapted states with Stern-Volmer quenching constants of K_{sv}=2.06 M^{-1} and 3.47 M^{-1}, respectively (Figure 3A). This is in contrast to wild type AppA17–133 that exhibits no acrylamide quenching when in its dark state (Ksv close to 0) and only moderate quenching when in the light state (K_{sv}=0.77 M^{-1}) (Figure 3B). Indeed partial light driven Trp movement of wild type AppA17–133 never reaches a degree of exposure of Trp to the quencher as is observed with the dark-adapted AppA1–126. These results, coupled with other techniques (25), led to the conclusion that AppA1–126 contains Trp104 partially solvent exposed in both light and dark states while AppA17–133 has Trp104 buried near the flavin in the dark that only becomes slightly exposed in the light adapted form (25).

A comparative analysis of the Q63E mutant in AppA1–126 and in AppA17–133 reveals that this mutant is characterized by acrylamide quenching curves and K_{sv} values that mimic that of light state wild-type AppA1–126 and AppA17–133 (K_{sv} ~3 M^{-1} and 0.84 M^{-1}, respectively) (Figure 3C and 3D). Acrylamide quenching of these Q63E mutants is also nearly identical when performed at dark or after light illumination indicating that the Q63E mutation locks these proteins in a lit conformation.

The Q63L mutant in AppA1–126 and AppA17–133 exhibits more complex behavior than that of the Q63E mutant. In AppA17–133 the Q63L mutant exhibits no fluorescence quenching under dark or lit conditions indicating that tryptophans are buried under both conditions (Figure 3D). This mutant is also rather unstable with its Fo/Fc values often dropping in the negative range during the quenching experiment. When the Q63L mutation is present in AppA1–126 there is a slight quenching with values of Ksv= 0.61 and 0.56 under both dark and light states, respectively (Figure 3C). These values do not reach the Ksv values of wild type AppA1–126 under dark or light conditions, indicating a non-native conformation of this mutant.

NMR spectral analysis confirms that Q63E in AppA1–126 and AppA17–133 adopt a lit state structure

We acquired ^{1}H-^{15}N HSQC spectra of ^{15}N-labeled wild-type and Q63E AppA1–126 and AppA17–133 to confirm that Q63E substitution locks AppA into a lit state structure in solution. Light- versus dark-state NMR structures of AppA5–125 by Grinstead et al. (14) reveal minor alterations of the overall structure of this domain upon light excitation of the flavin. Specifically, there was a reduction of cross peak intensity for the backbone amide groups of C19-Y21 in the β1 strand, and Q63, W64 and E66 in the β3 strand, as well as chemical shift perturbations for several additional cross peaks, including the side chains of H44 (NHδ1), and W64 (NHε1), and the backbone of F55, E94, R100, F101, G103, H105, Q107, L108 and S109 upon light excitation. ^{1}H-^{15}N HSQC spectra of ^{15}N-labeled wild type versus Q63E mutant forms of AppA1–126 and AppA17–133 in the dark are shown in Figure 4 (panels A and C), with backbone chemical shift perturbation maps also shown for each

AppA construct (Figure 4B, D). As can be seen in Figure 4, perturbation maps observed between the wild type and Q63E ^{1}H-^{15}N HSQC spectra are virtually identical for both the AppA1–126 (Figure 4B) and AppA17–133 (Figure 4D) proteins revealing that the changes in structure imposed by the Q63E substitution is immaterial to the BLUF construct to which it resides. Furthermore the Q63E AppA perturbation map is strikingly similar to that observed for dark versus light-adapted states of wild-type AppA5–125, and also reported for other BLUF domains as studied by NMR (14, 27–29). These regions include elements in and around the flavin binding pocket (C19-Y21 in the β1 strand, G52-L54 on β2, and residues 62–65 in β3), residues linked to E66 in the β3 strand via hydrogen bonding (T51, R100, F101), H44 side chain (NHδ1), W64 side chain (NHε1) and the C-terminal region including E94, G103, H105 and S109 on β5. We can conclude from this analysis that the Q63E substitution mutants mimic the light-excited conformation of wild-type AppA in both AppA constructs.

For comparison, we also recorded the ^{1}H-^{15}N HSQC spectra of ^{15}N-labeled Q63L mutants (Figure 5). Most of cross-peaks exhibit large chemical shifts, and certain peaks disappear, when wild type AppA are compared to Q63L mutant constructs which prevented the assignment of peaks for Q63L (Figure 5A and 5B). When comparing the Q63E and Q63L mutants (Figure 5 C and 5D), it is obvious that Q63L mutants differ largely from the Q63E conformation as well. Therefore we can conclude that Q63L mutation results in the BLUF domain folding in a non-native conformation that is different from dark conformation of the wild type and Q63E BLUF domains.

Complex formation of AppA Q63 full-length mutants with PpsR

The ability of Q63E and Q63L full-length AppA mutant proteins to form a complex with the PpsR repressor was also tested by size-exclusion chromatography. Since light disrupts the interaction between AppA and PpsR (8), analysis of complex formation was undertaken under dark reducing conditions. Ten-fold molar excess of AppA was incubated with PpsR and then subjected to chromatographic seperation. As shown in Figure 6, wild type AppA formed the previously defined 1:2 complex with PpsR eluting at ~ 160 kDa (Figure 6, peak WT1, solid line) while AppA elutes as a monomer at 60 kDa (Figure 6, peak WT2, solid line). When the AppA Q63E mutant was incubated with PpsR no complex was observed and instead PpsR eluted as a tetramer at ~ 200 kDa (Figure 6, peak M1, dashed line). Interestingly, AppA harboring the Q63E mutation elutes in two peaks, M2 at ~95 kDa and M3, at ~50 kDa which likely represent dimer/monomer. This indicates that, unlike wild type AppA, the AppA protein with the Q63E mutation exists as both dimer and monomer in solution and is not able to form a complex with PpsR thereby confirming a lit-state conformation of this mutant.

AppA Q63L was also tested for complex formation with PpsR. If our conclusion about non-native conformation of this mutant is correct, we would expect AppA Q63L to not form a complex with PpsR and perhaps exhibit differences in chromatography profile when compared to AppA Q63E mutant. This was, indeed, the case as AppA containing the Q63L mutation exhibits a similar chromatography profile as observed for Q63E mutant with three major peaks but at slightly different positions (Figure 6, peaks L1, L2 and L3, dotted line). SDS-PAGE shows that no complex was formed with PpsR and that most of the AppA Q63L eluted as dimer and monomer with the monomer peak (L3) containing both full protein and a slightly smaller degradation product that is often observed with AppA full-length preparations. The Q63L protein conformation must be somewhat different than that of the Q63E mutant as the positions of the peaks are not identical. An aberrant chromatography profile, coupled with an aberrant fluorescent emission and quenching profile of Q63L mutants, and finally the NMR ^{1}H-^{15}N HSQC spectra suggest that the Leu substitution at this position results in a non-native conformation of AppA BLUF domain.

DISCUSSION

The AppA1–126 and AppA17–133 BLUF domains are interesting AppA variants in that they possess similar spectral photocycles and yet are characterized by distinctly different hydrogen bonding residues near the flavin-binding pocket (25). Crystallographic and spectroscopic studies have demonstrated that Gln63 is a key residue that in AppA17–133 forms a hydrogen bond to Tyr21, to N5 of the flavin, and to Trp104 (19, 25). However, in AppA1–126 there is a slight conformational change where Trp104 and Met106 swap positions allowing Gln63 to form a hydrogen bond to Tyr21, to N5 of the flavin, and to Met106 (17). Despite these structural differences, these two BLUF domains exhibit nearly identical photocycles, which has led to an early proposal that light excitation of the flavin results in a hydrogen bond rearrangement where Trp104 and Met106 swap positions (18). However, this model is not supported by our recent study which shows that Met106 is close to Gln63 in the ground state and that light excitation of the flavin results in only limited movement of Trp104 (25).

In this study, we have used a variety of spectroscopic and structural approaches to analyze Leu and Glu mutants at position 63 to study their effect on the photocycle and on the structure of the BLUF domain. A Gln to Leu mutation at position 63 in both AppA1–126 and AppA17–133 spectrally locks each BLUF domain in a blue-shifted state. The Q63L mutants also appear to adopt at least two different non-native conformations based on the presence of a heterogeneous flavin fluorescence emission peak that is not seen in the wild type protein or other mutations,. The flavin is thought to be dynamic even in the dark ground state where it apparently samples several different orientations (29). Thus, it is perhaps not surprising that a Q63L substitution which disrupts hydrogen bonds to N5 of FAD and –OH of Tyr21 results in a heterogeneous and non-native microenvironment around the flavin. Indeed the likelihood of a non-native conformation of the Q63L mutants is supported by our observation that full length AppA Q63L does not interact with PpsR *in vitro*, has an aberrant chromatographic profile, and its NMR ^{1}H-^{15}N HSQC spectra are very different from either WT or Q63E proteins. In addition, Masuda et al (30) has also reported that an AppA Q63L mutant is not able to derepress the activity of PpsR *in vivo*.

In contrast to a blue shift of the Q63L mutant, visible spectral analysis of the Q63E mutants shows that this substitution locks AppA in a red-shifted state. Previous NMR and FTIR studies of AppA BLUF domains suggest that light excitation of the flavin results in stronger H-bonds between Tyr21 and Gln63 (29), as well as a stronger hydrogen bond between C4=O of FAD to Gln63 (31). We suspect that the Q63E mutation also establishes stronger H-bonding pattern to both Tyr21 and C4=O of FAD, driving the protein into a rather rigid conformation, closely mimicking the lit state. The red shift observed in the flavin absorption spectrum of Q63E AppA mutants is only 3–3.5 nm instead of the normal 12 nm shift observed upon flavin excitation of wild type AppA. This indicates that the H-bond to N5 of flavin is either missing or significantly weakened in the Q63E mutant. Further characterization of Q63E mutants by steady state fluorescence, acrylamide quenching and by comparative analysis of the ^{1}H-^{15}N HSQC spectra shows clear characteristics of lit spectral and conformational states. Indeed, our results are in agreement with a generally accepted idea that light excitation of the flavin results in numerous small changes in the whole BLUF domain (Figure 7) that represent a complex set of minor structural perturbations extending from residues on the β3 strand (Phe62 through Gly67), to residues on the adjacent β2 strand (Gly52, Ala53, Leu54). We suspect that structural changes caused by light excitation of the flavin propagate from the β2–β3 region to the β4 and β5 strands, the β4–β5 loop, and the downstream C-terminal helical region. Our conclusions seem to be in close agreement with recently reported NMR light –excited changes in BlrP1 from *K. pneumoniae* (15) and its crystal structure (32) and by collection of diffraction data on an

AppA BLUF domain crystal (C20S AppA1–124) in the dark as well as after light excitation of the crystal (17). Light induced changes of the AppA1–124 C20S crystal were assigned to the backbone of the loop before and the end of the β4 sheet (residues 82–86 and 90–95) as well as minor changes in Tyr21, Leu54, Gln63, Asp82, His85, Arg83, Arg84 and Met106. Alterations in Tyr21, Leu54 and Gln63 are observed in our NMR spectra of Q63E, as well as changes in the β4 and β5 sheets.

While our study does not directly address the exact mechanism of the events that occurs at Q63 after light excitation of the flavin, our analysis of Q63 mutants does confirm that this residue is critical the spectral and light-excited properties of BLUF domains. The small structural changes observed here suggest that the BLUF domain can be distinguished as a light sensor different from other blue light absorbing photoreceptors such as LOV domain (33–34) and PYP photoreceptors, which either undergo a covalent reaction with the chromophore or chromophore isomerization during the photocycle, respectively (35).

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Abbreviations

BLUF	*b*lue-*l*ight sensing *u*sing *F*AD
DTT	dithiothreitol

References

1. Gomelsky M, Kaplan S. appA, a novel gene encoding a trans-acting factor involved in the regulation of photosynthesis gene expression in Rhodobacter sphaeroides 2.4.1. J Bacteriol. 1995; 177:4609–4618. [PubMed: 7642486]
2. Masuda S, Hasegawa K, Ishii A, Ono TA. Light-induced structural changes in a putative blue-light receptor with a novel FAD binding fold sensor of blue-light using FAD (BLUF); Slr1694 of synechocystis sp. PCC6803. Biochemistry. 2004; 43:5304–5313. [PubMed: 15122896]
3. Hasegawa K, Masuda S, Ono TA. Structural intermediate in the photocycle of a BLUF (sensor of blue light using FAD) protein Slr1694 in a Cyanobacterium Synechocystis sp. PCC6803. Biochemistry. 2004; 43:14979–14986. [PubMed: 15554705]
4. Kita A, Okajima K, Morimoto Y, Ikeuchi M, Miki K. Structure of a cyanobacterial BLUF protein, Tll0078, containing a novel FAD-binding blue light sensor domain. J Mol Biol. 2005; 349:1–9. [PubMed: 15876364]
5. Rajagopal S, Key JM, Purcell EB, Boerema DJ, Moffat K. Purification and initial characterization of a putative blue light-regulated phosphodiesterase from Escherichia coli. Photochem Photobiol. 2004; 80:542–547. [PubMed: 15453820]
6. Iseki M, Matsunaga S, Murakami A, Ohno K, Shiga K, Yoshida K, Sugai M, Takahashi T, Hori T, Watanabe M. A blue-light-activated adenylyl cyclase mediates photoavoidance in Euglena gracilis. Nature. 2002; 415:1047–1051. [PubMed: 11875575]
7. Gomelsky M, Kaplan S. AppA, a redox regulator of photosystem formation in Rhodobacter sphaeroides 2.4.1, is a flavoprotein - Identification of a novel FAD binding domain. Journal of Biological Chemistry. 1998; 273:35319–35325. [PubMed: 9857073]
8. Masuda S, Bauer CE. AppA is a blue light photoreceptor that antirepresses photosynthesis gene expression in Rhodobacter sphaeroides. Cell. 2002; 110:613–623. [PubMed: 12230978]

9. Nakasone Y, Ono TA, Ishii A, Masuda S, Terazima M. Temperature-sensitive reaction of a photosensor protein YcgF: possibility of a role of temperature sensor. Biochemistry. 2010; 49:2288–2296. [PubMed: 20141167]
10. Tschowri N, Busse S, Hengge R. The BLUF-EAL protein YcgF acts as a direct anti-repressor in a blue-light response of Escherichia coli. Genes Dev. 2009; 23:522–534. [PubMed: 19240136]
11. Schroeder C, Werner K, Otten H, Kratzig S, Schwalbe H, Essen LO. Influence of a joining helix on the BLUF domain of the YcgF photoreceptor from Escherichia coli. Chembiochem. 2008; 9:2463–2473. [PubMed: 18792053]
12. Nakasone Y, Ono TA, Ishii A, Masuda S, Terazima M. Transient dimerization and conformational change of a BLUF protein: YcgF. J Am Chem Soc. 2007; 129:7028–7035. [PubMed: 17489591]
13. Hasegawa K, Masuda S, Ono TA. Light induced structural changes of a full-length protein and its BLUF domain in YcgF(Blrp), a blue-light sensing protein that uses FAD (BLUF). Biochemistry. 2006; 45:3785–3793. [PubMed: 16533062]
14. Grinstead JS, Hsu ST, Laan W, Bonvin AM, Hellingwerf KJ, Boelens R, Kaptein R. The solution structure of the AppA BLUF domain: insight into the mechanism of light-induced signaling. Chembiochem. 2006; 7:187–193. [PubMed: 16323221]
15. Wu Q, Gardner KH. Structure and Insight into Blue Light-Induced Changes in the BlrP1 BLUF Domain (dagger) (,) (double dagger). Biochemistry. 2009; 48:2620–2629. [PubMed: 19191473]
16. Dragnea V, Waegele M, Balascuta S, Bauer C, Dragnea B. Time-resolved spectroscopic studies of the AppA blue-light receptor BLUF domain from Rhodobacter sphaeroides. Biochemistry. 2005; 44:15978–15985. [PubMed: 16331957]
17. Jung A, Reinstein J, Domratcheva T, Shoeman RL, Schlichting I. Crystal structures of the AppA BLUF domain photoreceptor provide insights into blue light-mediated signal transduction. J Mol Biol. 2006; 362:717–732. [PubMed: 16949615]
18. Yuan H, Anderson S, Masuda S, Dragnea V, Moffat K, Bauer C. Crystal structures of the Synechocystis photoreceptor Slr1694 reveal distinct structural states related to signaling. Biochemistry. 2006; 45:12687–12694. [PubMed: 17042486]
19. Anderson S, Dragnea V, Masuda S, Ybe J, Moffat K, Bauer C. Structure of a novel photoreceptor, the BLUF domain of AppA from Rhodobacter sphaeroides. Biochemistry. 2005; 44:7998–8005. [PubMed: 15924418]
20. Gauden M, van Stokkum IH, Key JM, Luhrs D, van Grondelle R, Hegemann P, Kennis JT. Hydrogen-bond switching through a radical pair mechanism in a flavin-binding photoreceptor. Proc Natl Acad Sci U S A. 2006; 103:10895–10900. [PubMed: 16829579]
21. Zirak P, Penzkofer A, Schiereis T, Hegemann P, Jung A, Schlichting I. Absorption and fluorescence spectroscopic characterization of BLUF domain of AppA from Rhodobacter sphaeroides. Chem Phys. 2005; 315:142–154.
22. Obanayama K, Kobayashi H, Fukushima K, Sakurai M. Structures of the chromophore binding sites in BLUF domains as studied by molecular dynamics and quantum chemical calculations. Photochem Photobiol. 2008; 84:1003–1010. [PubMed: 18435699]
23. Domratcheva T, Grigorenko BL, Schlichting I, Nemukhin AV. Molecular models predict light-induced glutamine tautomerization in BLUF photoreceptors. Biophys J. 2008; 94:3872–3879. [PubMed: 18263659]
24. Sadeghian K, Bocola M, Schutz M. A conclusive mechanism of the photoinduced reaction cascade in blue light using flavin photoreceptors. J Am Chem Soc. 2008; 130:12501–12513. [PubMed: 18722438]
25. Dragnea V, Arunkumar AI, Yuan H, Giedroc DP, Bauer CE. Spectroscopic Studies of the AppA BLUF Domain from Rhodobacter sphaeroides: Addressing Movement of Tryptophan 104 in the Signaling State. Biochemistry. 2009
26. Stern O, Volmer M. On the quenching time of fluorescence. Phys. Z. 1919; 20:183–188.
27. Wu Q, Gardner KH. Structure and insight into blue light-induced changes in the BlrP1 BLUF domain. Biochemistry. 2009; 48:2620–2629. [PubMed: 19191473]
28. Wu Q, Ko WH, Gardner KH. Structural requirements for key residues and auxiliary portions of a BLUF domain. Biochemistry. 2008; 47:10271–10280. [PubMed: 18771279]

29. Grinstead JS, Avila-Perez M, Hellingwerf KJ, Boelens R, Kaptein R. Light-induced flipping of a conserved glutamine sidechain and its orientation in the AppA BLUF domain. J Am Chem Soc. 2006; 128:15066–15067. [PubMed: 17117839]

30. Masuda S, Tomida Y, Ohta H, Takamiya KI. The Critical Role of a Hydrogen Bond between Gln63 and Trp104 in the Blue-Light Sensing BLUF Domain That Controls AppA Activity. J Mol Biol. 2007

31. Masuda S, Hasegawa K, Ono TA. Light-induced structural changes of apoprotein and chromophore in the sensor of blue light using FAD (BLUF) domain of AppA for a signaling state. Biochemistry. 2005; 44:1215–1224. [PubMed: 15667215]

32. Barends TR, Hartmann E, Griese JJ, Beitlich T, Kirienko NV, Ryjenkov DA, Reinstein J, Shoeman RL, Gomelsky M, Schlichting I. Structure and mechanism of a bacterial light-regulated cyclic nucleotide phosphodiesterase. Nature. 2009; 459:1015–1018. [PubMed: 19536266]

33. Crosson S, Moffat K. Photoexcited structure of a plant photoreceptor domain reveals a light-driven molecular switch. Plant Cell. 2002; 14:1067–1075. [PubMed: 12034897]

34. Fedorov R, Schlichting I, Hartmann E, Domratcheva T, Fuhrmann M, Hegemann P. Crystal structures and molecular mechanism of a light-induced signaling switch: The Phot-LOV1 domain from Chlamydomonas reinhardtii. Biophys J. 2003; 84:2474–2482. [PubMed: 12668455]

35. Borgstahl GE, Williams DR, Getzoff ED. 1.4 A structure of photoactive yellow protein, a cytosolic photoreceptor: unusual fold, active site, and chromophore. Biochemistry. 1995; 34:6278–6287. [PubMed: 7756254]

36. Arunkumar AI, Klimovich V, Jiang X, Ott RD, Mizoue L, Fanning E, Chazin WJ. Insights into hRPA32 C-terminal domain--mediated assembly of the simian virus 40 replisome. Nat Struct Mol Biol. 2005; 12:332–339. [PubMed: 15793585]

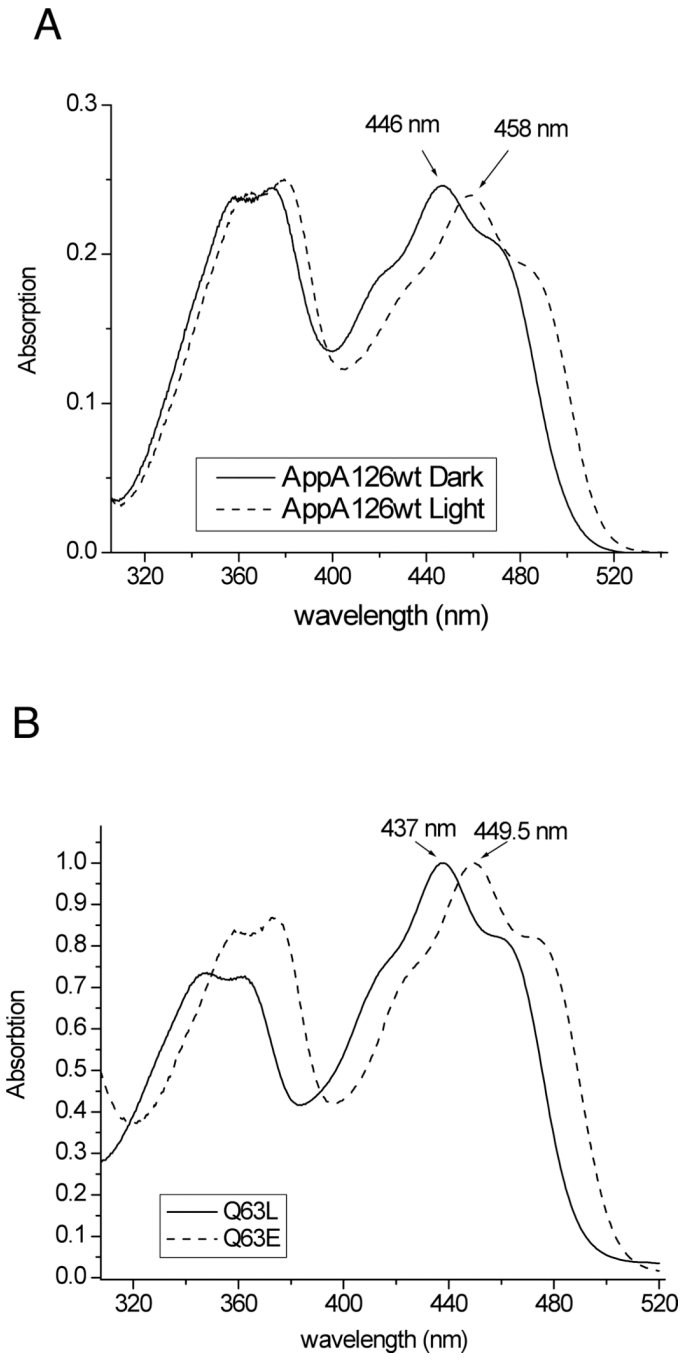

Figure 1.
Absorption spectra of AppA1–126 wt at dark and light (A) and Q63E (B, dash line) and Q63L mutants (B, solid line).

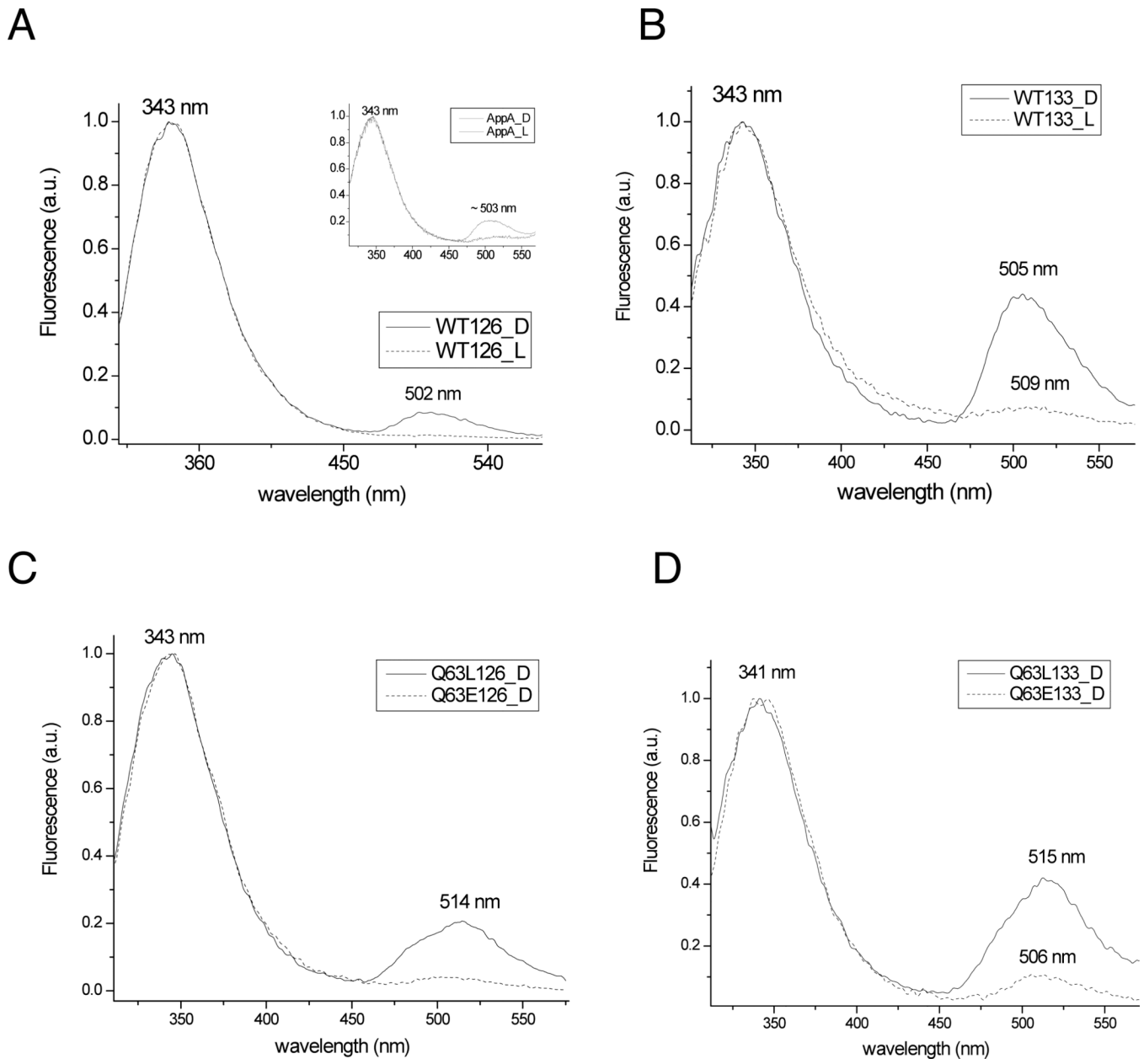

Figure 2.

Normalized fluorescence emission spectra. A) AppA1–126wt (Insert: AppA full-length); B) AppA17–133 WT; C) AppA1–126 Q63E and Q63L; (D), AppA17–133 Q63E and Q63L. All samples were measured at dark (D) and light (L) conditions.

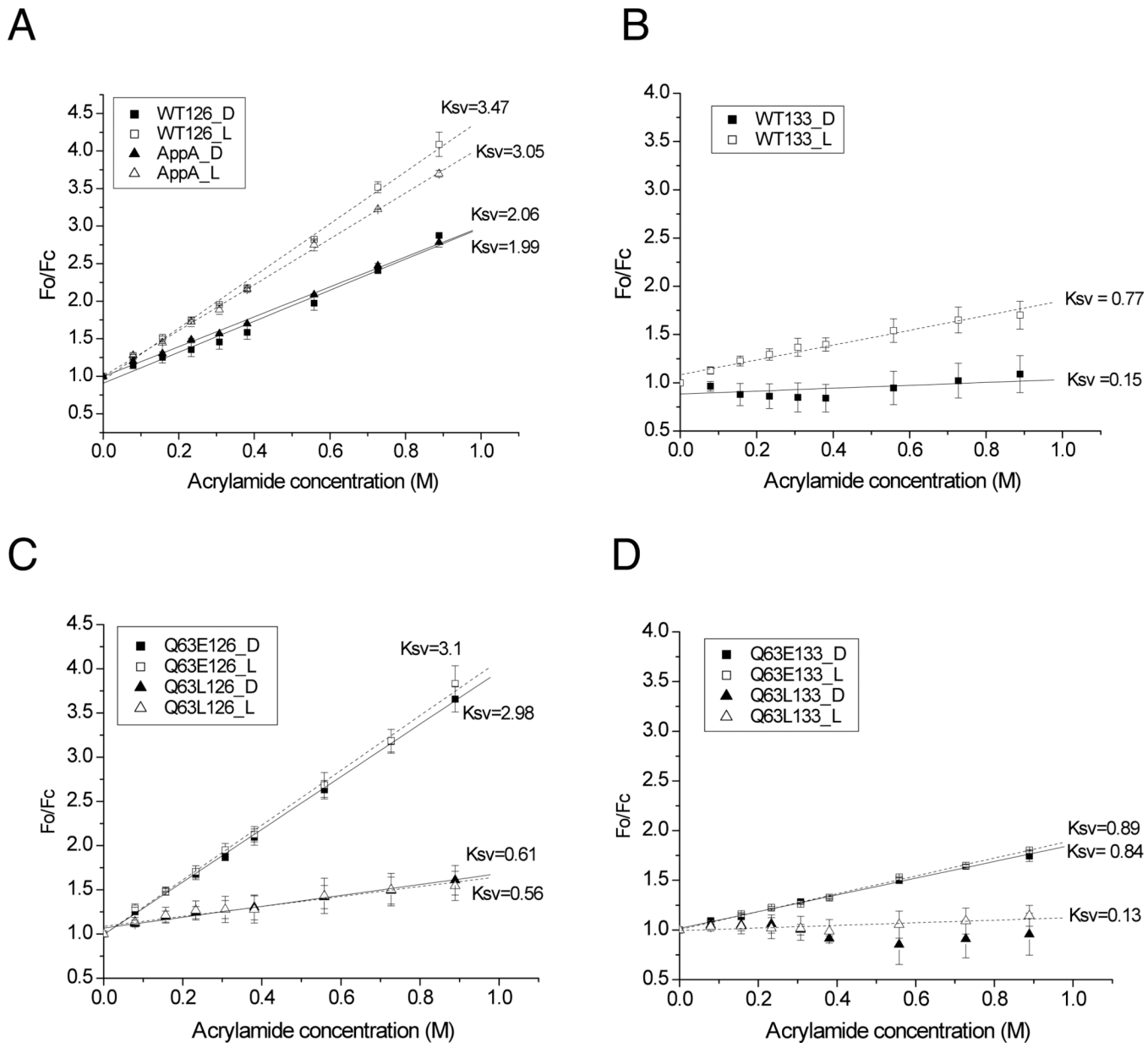

Figure 3.

Quenching of tryptophan fluorescence with acrylamide. Samples are freshly purified and diluted to A_{280}= 0.02 (A) AppA1–126 WT and AppA full-length; (B) AppA17–133 WT; (C) AppA1–126 Q63E and Q63L; (D) AppA17–133 Q63E and Q63L; all samples are measured at dark and light conditions. Ksv values are indicated.

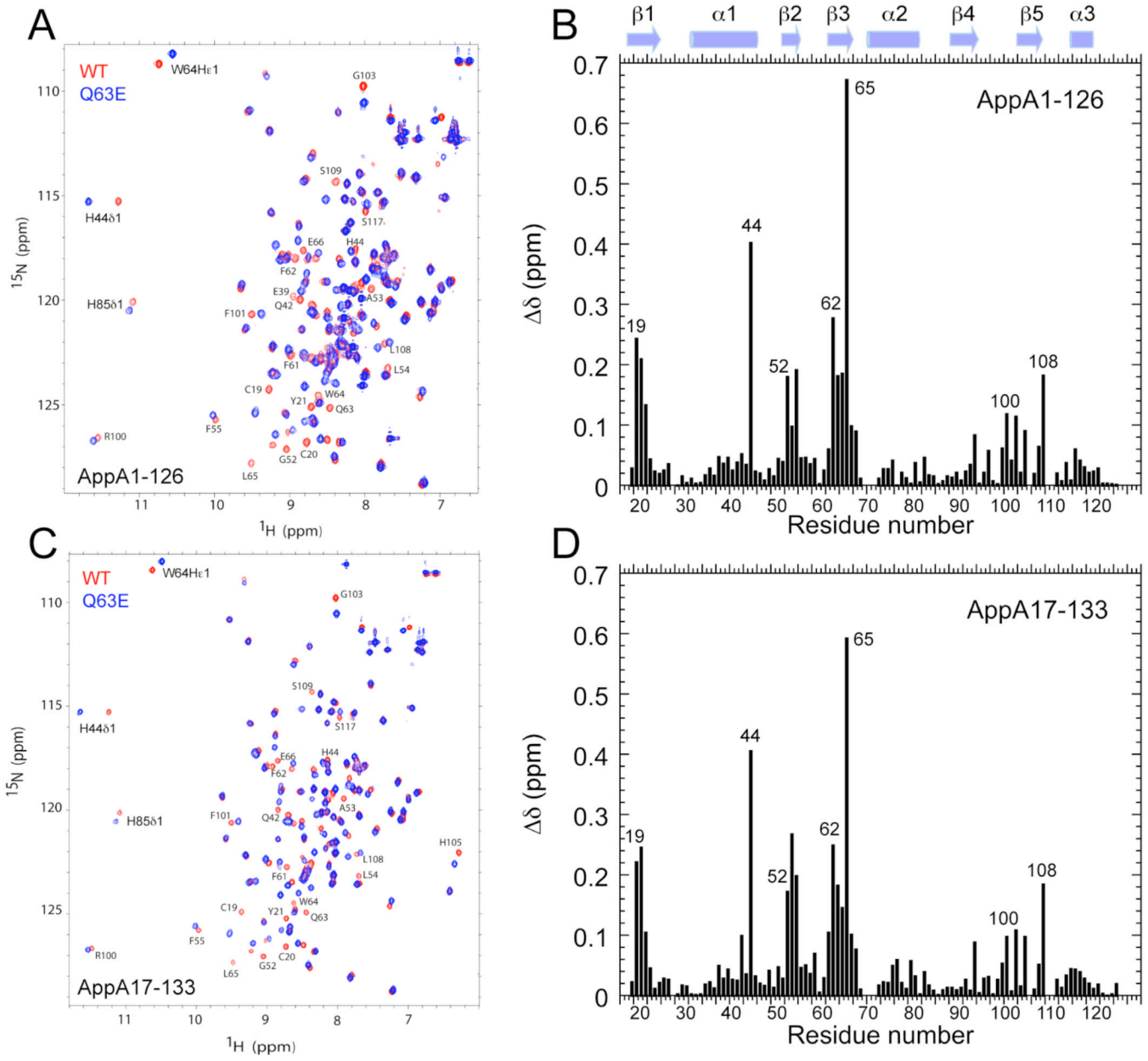

Figure 4.

Superposition of the ^{1}H-^{15}N HSQC spectra of wild-type (*red* crosspeaks) and Q63E (*blue* crosspeaks) AppA1–126 (A) and AppA17–133 (C). The chemical shift perturbation maps of AppA1–126 (B) and AppA1–133 Q63E (D) vs. WT represents the combined ^{1}H and ^{15}N chemical shift, where $\Delta\delta ppm = \sqrt{(\Delta\delta^2_H + (\Delta\delta_N/7)^2)}$ (36).

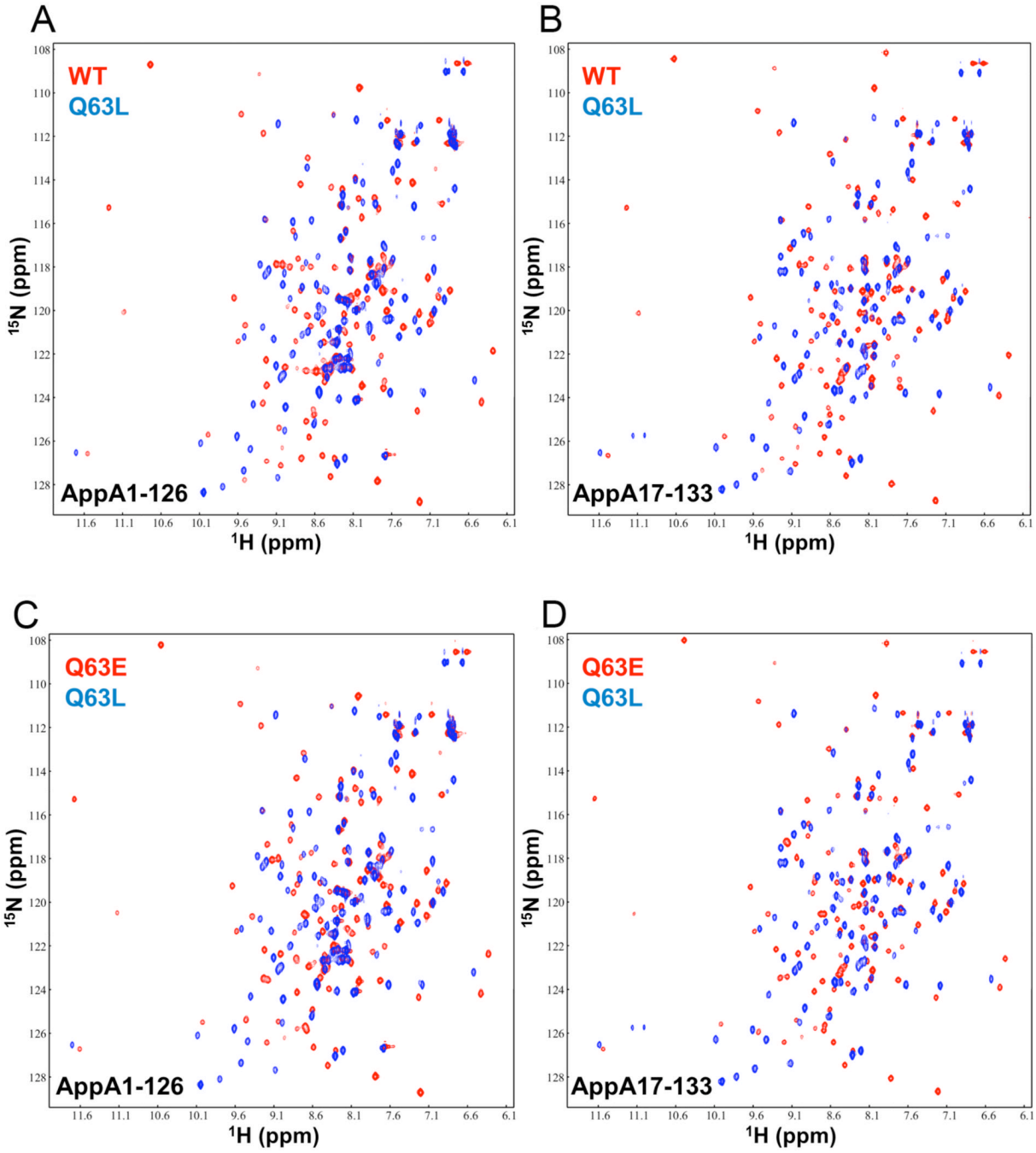

Figure 5.
Superposition of the ^{1}H-^{15}N HSQC spectra of the wild-type (*red* crosspeaks) and Q63L (*blue* crosspeaks) in AppA1–126 (A) and AppA17–133 (B); Q63L (blue) vs. Q63E (red) in AppA1–126 (C) and AppA17–133 (D).

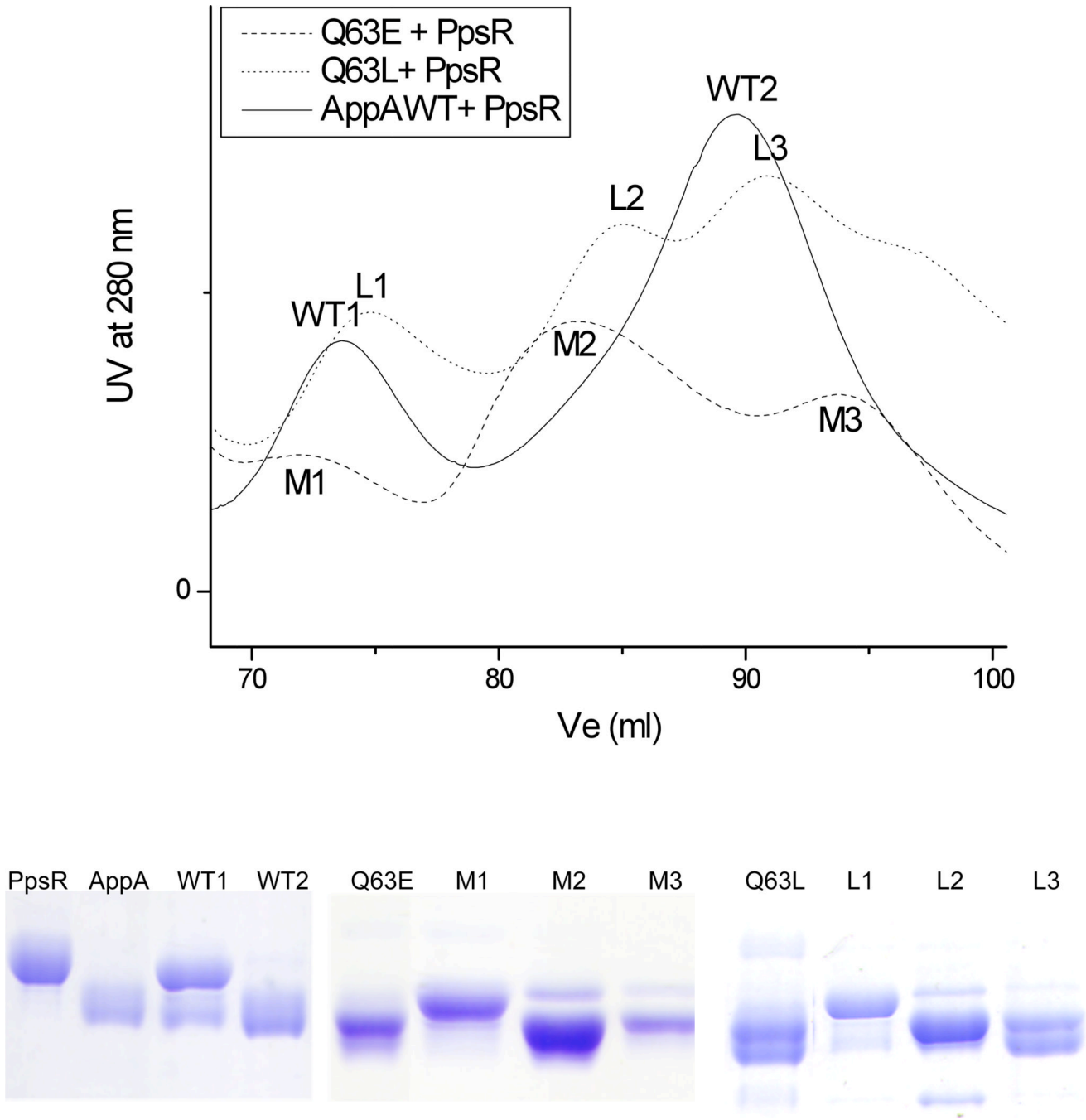

Figure 6.

Size-exclusion chromatography profile (Sephacryl 200) of AppA WT-PpsR, AppA Q63L-PpsR, and AppA Q63E- PpsR, performed at dark and reducing conditions (5 mM DTT), with 10× excess of AppA. Bottom: SDS-PAGE of chromatography peaks (as indicated) including PpsR, AppA WT, Q63L and Q63E purified proteins as controls. AppA full-length protein often contains two bands as the unstable C-terminal (20–30 amino acids) gets easily degraded.

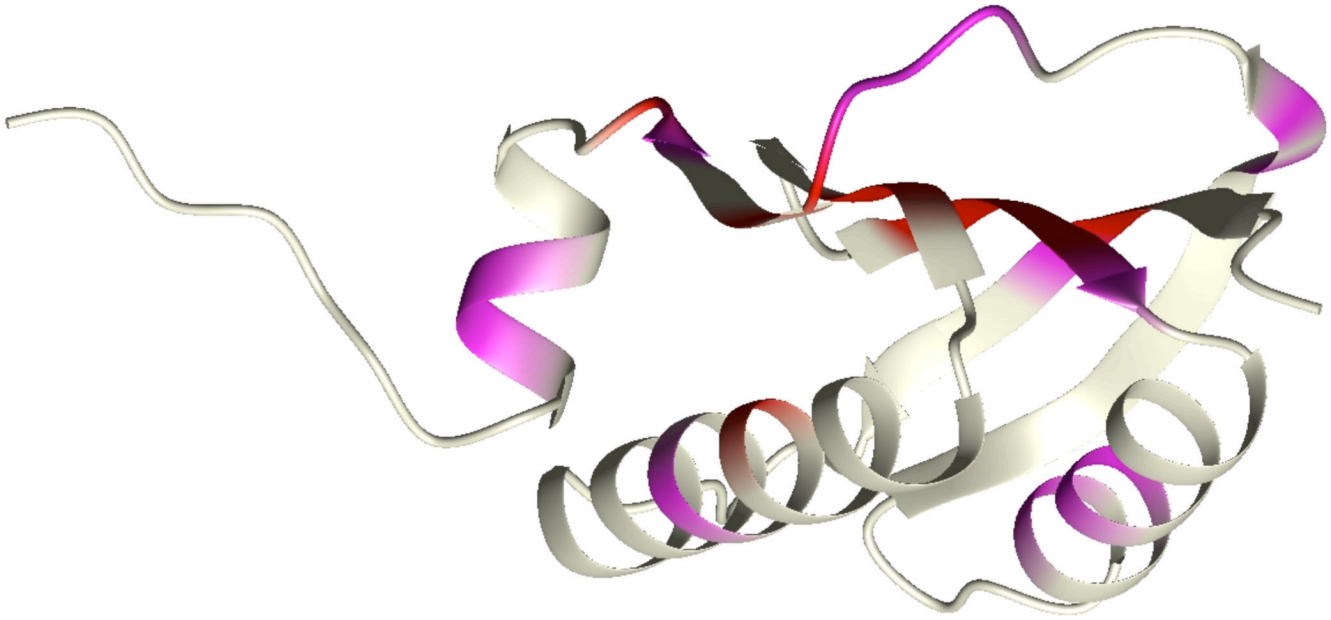

Figure 7.

Ribbon views of the structural differences between wild-type and Q63E AppA17–133 from NMR.chemical shift perturbations. Colors are ramped on a grey ribbon diagram of the structure of AppA17–133 based on the Δδ ppm as follows; *magenta*, $0.05 < \Delta\delta < 0.1$ and *red*, $0.1 < \Delta\delta < 0.60$ (see Figure 4).

Table 1

Absorption maxima and photocycle lifetimes of AppA and its various clones and mutants.

Mutant	Flavin abs. maximum-dark (light) ± 0.5 nm	Photocycle τ (s)
WT 126	446 nm (458 nm)	948.5 ± 6.0 s
17–133	446 nm (458 nm)	690.9 ± 3.1 s
Q63L 126	437 nm -	-
Q63E 126	449.5 nm -	-
Q63L 133	437 nm -	-
Q63E 133	449.5 nm -	-