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Computational and Spectroscopic Characterization of the Photocycle of an Artificial Rhodopsin

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Abstract

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ASSOCIATED CONTENT

Supporting Information

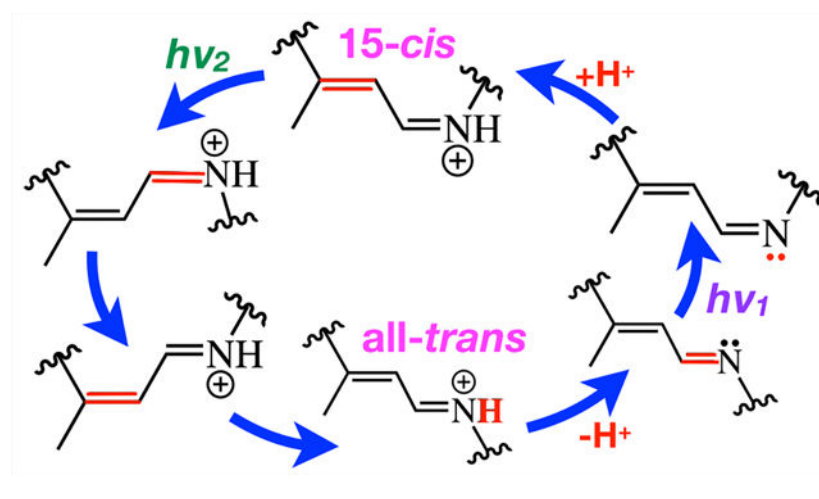
The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acs.jpcllett.0c00751>.

Computational methods, distribution of the absorption energies and computed absorption bands, ASEC protocol diagram, QM/MM setup, schematic of flow of an average cryokinetics experiment, energy profiles, cryokinetic difference spectra, cryokinetic spectra, kinetics, EADS, extracted dynamics, geometric parameters, proton transfer mechanisms, tables of observations and interpretations (PDF)

M215C-PSB isomerization (AVI)

The photocycle of a reversible photoisomerizing rhodopsin mimic (M2) is investigated. This system, based on the cellular retinoic acid binding protein, is structurally different from natural rhodopsin systems, but exhibits a similar isomerization upon light irradiation. More specifically, M2 displays a 15-*cis* to *all-trans* conversion of retinal protonated Schiff base (rPSB) and *all-trans* to 15-*cis* isomerization of unprotonated Schiff base (rUSB). Here we use hybrid quantum mechanics/molecular mechanics (QM/MM) tools coupled with transient absorption and cryokinetic UV–vis spectroscopies to investigate these isomerization processes. The results suggest that primary rPSB photoisomerization of M2 occurs around the C13=C14 double bond within 2 ps following an aborted-bicycle pedal (ABP) isomerization mechanism similar to natural microbial rhodopsins. The rUSB isomerization is much slower and occurs within 48 ps around the C15=N double bond. Our findings reveal the possibility to engineer naturally occurring mechanistic features into artificial rhodopsins and also constitute a step toward understanding the photoisomerization of UV pigments. We conclude by reinforcing the idea that the presence of the retinal chromophore inside a tight protein cavity is not mandatory to exhibit ABP mechanism.

Graphical Abstract



Rhodopsins are a family of photoreceptor proteins found in all domains of life.^{1–3} All members of the rhodopsin family exhibit a similar protein architecture consisting of a retinal chromophore (a retinal unprotonated (rUSB) or protonated Schiff base (rPSB)) located in a tight protein cavity formed by seven interconnected transmembrane α -helices.¹ In the presence of light, rPSB undergoes a selective *cis* \rightarrow *trans* or *trans* \rightarrow *cis* double bond isomerization initiating crucial biological functions such as visual and nonvisual functions in superior animals, ion transport, ion gating, phototaxis, and gene expression in archae and eubacteria.³ The rPSB photoisomerization is one of the fastest and most efficient reactions in nature. For instance, in the dim-light visual pigment rhodopsin the isomerization is complete within 200 fs^{4,5} with a 0.65 quantum yield.⁶ The rPSB isomerization in rhodopsin occurs inside a tight protein cavity through a unique space-saving mechanism called aborted-bicycle pedal (ABP) isomerization where two neighboring double bonds isomerize concertedly in opposite directions and one bond completes the isomerization and reaches the product while the other returns to the original configuration.^{7–11}

Recently, Geiger, Borhan and co-workers engineered the first artificial rhodopsin mimics that can reversibly photoisomerize.¹² A hexamutant (R111 K:Y134F:T54 V:R132Q:P39Y:R59Y) of a cytoplasmic protein called cellular retinoic acid binding protein II (CRABPII) (M2) was prepared by mutating CRABPII such that retinal reacts with a specific lysine residue inside the protein cavity to form a Schiff base linkage and react to light in a way similar to natural rhodopsins.^{12–14} Remarkably, M2 appears to display a photochromic cycle (from now on called photocycle) also observed in certain natural rhodopsins (e.g., in *Anabaena* sensory rhodopsin or in, so-called, bistable rhodopsins such as melanopsin and jumping spider rhodopsin),^{15–17} which has been investigated by using UV spectroscopy and X-ray crystallography. In the thermodynamically favored form of M2 (M2_{AT}-USB), the bound chromophore has the *all-trans* rUSB conformation. When irradiated with UV light (~360 nm), the chromophore isomerizes to the 15-*cis* rPSB conformation, yielding a new protein form (M2_{15C}-PSB). In the presence of green light (~550 nm) or heat, M2_{15C}-PSB is transformed back to M2_{AT}-USB. Such transformations can be repeated continuously, switching the system between the M2_{AT}-USB and M2_{15C}-PSB forms.

The molecular-level elucidation of the intermediate steps driving the M2 photocycle appears to be an important endeavor. This is key in identifying engineering rules allowing for the design and preparation of artificial light-responsive proteins mimicking natural systems. These can provide new molecular devices^{18–21} functioning as sensors and actuators useful in bioimaging and neuromedical science and, more generally, in synthetic biology.²²

Due to the current absence of spectroscopic and theoretical studies, our present knowledge of the steps driving the M2 photocycles are, regrettably, highly incomplete. To date, only a single dynamic study on a triple mutant of CRABP-II has been reported.²³ In the present work we are particularly interested in the direct (*all-trans* to 15-*cis*) and reverse (15-*cis* to *all-trans*) photochemical steps. Indeed, (i) such photochemical steps have not been characterized in several aspects such as isomerization mechanism and time scale and (ii) the following thermal steps, corresponding to successive conformational changes and connecting M2_{AT}-USB to M2_{15C}-PSB and *vice versa* has also not been resolved.

The current information on M2 reveals several biomimetic features. In fact, (i) while the CRABPII is very different from opsin, the retinal chromophore isomerizes upon irradiation and it is somehow coupled with proton translocation as in certain microbial rhodopsins;³ however, (ii) the isomerization takes place around C15=N rather than the C11=C12 or C13=C14 bonds of natural rhodopsins. Thus, the investigation of the M2 photocycle will not only allow us to uncover the missing information mentioned above, but will also provide a model for studying how the protein/chromophore interactions affect the rhodopsin photoisomerization regioselectivity in general.

To address the issues above, we have used a combined computational and experimental approach. More specifically, we use a subpopulation of 20 initial conditions to simulate the light induced dynamics of M2_{15C}-PSB and M2_{AT}-USB for up to 0.8 ps via Tully's semiclassical trajectory computations at the state average CASSCF/6-31G*/AMBER level of theory (see section S11).²⁴ The construction of QM/MM models of both M2_{15C}-PSB and M2_{AT}-USB is performed by using recently reported ASEC-FEG protocol²⁵

that involves geometry optimization on a free energy, rather than potential energy, surface. Such models are subsequently used to study the reaction time scales using semiclassical trajectories. In addition to the trajectories, the possible reaction paths for M2_{AT}-USB photoisomerization around C11=C12, C13=C14, and C15=N bonds are mapped by using relaxed scans. The results of simulations are compared against time-resolved and temperature resolved dynamics. The sample preparation and experimental protocols are outlined in section S2. Ultrafast transient broadband absorption spectroscopy was performed at room temperature as previously described²⁶ to ascertain the efficiency of these photoreactions. The M2_{15C}-PSB and M2_{15C}-PSB photodynamics were initiated with 565 and 400 nm, respectively. Temperature and time-resolved dynamics were measured by using cryokinetic UV-vis absorption spectroscopy as previously reported and outlined in the Supporting Information.²⁷ LEDs resonant with absorption bands of the starting populations were used to initiate the photoreaction, and the cryogenic temperatures trap the resulting photointermediates. As the temperature of the sample is raised, the photointermediates evolve, allowing for the mapping of the photomechanism.

M2_{15C}-PSB and M2_{AT}-USB QM/MM Models.

The wavelength of the absorption maximum (λ_{\max}) of M2_{15C}-PSB and M2_{AT}-USB computed by using the constructed QM/MM models were 499 nm (57.3 kcal/mol or 2.48 eV) and 345 nm (83.0 kcal/mol or 3.60 eV) respectively. These values are blue-shifted by ca. 7 and 5 kcal/mol (0.30 and 0.22 eV), respectively, relative to the observed values (see Figure 1) and, consistently, the values reported by Borhan, Geiger, and co-workers.¹² These values lie within the reported systematic error (7.5 kcal/mol or 0.33 eV) of the ASEC-FEG protocol which is expected to correctly reproduce trends in λ_{\max} rather than in absolute values.²⁵ Furthermore, the visual comparison of computed model against the crystallographic structure indicated that the modeled and observed backbone are substantially consistent with the exception of residues 55–60. As detailed in the Supporting Information, such backbone deviation appears to remove a potentially important π -stacking interaction between a tyrosine residue (TYR59) and the β -ionone region of the chromophore. The impact of such removal in our model has been directly tested and found not to significantly modify the vertical excitation energy nor the results of an excited state scan. Accordingly, the constructed models are assumed to be reliable enough for qualitative (i.e., mechanistic) studies reported in the following sections, mainly based on the comparison between experimental and computationally estimated λ_{\max} and excited state lifetimes.

M2_{15C}-PSB to M2_{AT}-USB Conversion.

The 15-*cis* to *all-trans* reaction of M2_{15C}-PSB was characterized by using ultrafast transient broadband absorption and cryokinetic spectroscopies. First, the ultrafast pump probe experiment conducted for M2_{15C}-PSB revealed that the decay of the excited state exhibited biphasic decay kinetics with two rate constants (400 fs and 5 ps; see Figure 2A). In the transient absorption spectra (Figure 2B) there is a negative signal between 575 and 625 nm that was ascribed to a ground state bleach given the overlap with the ground state absorption (GSA) and positive excited state absorption (ESA) at 475 nm. There also appears to be a

longer-lived negative signal observed (compared to neighboring wavelength such as 650 nm) at 710 nm (Figure S9) and attributed to stimulated emission since it did not follow the GSA band (Figure 2B). The excited state decayed on two different time scales, where the majority (70%) of the excited state population decayed on a 400 fs time scale and a minority (30%) decayed on a 5 ps time scale (Figure 2C,D). The ES population appears to relax back to the ground state, with no measurable long-lived photoproduct, which points to a low quantum efficiency of the reaction.

The ultrafast studies were complemented with cryokinetic UV-vis spectroscopy as described by Mix et al.,²⁷ which resolved four distinct positive bands (Figure 3, Figures S6–S8, Table S1). The first cryotrapped intermediate ($M2_{13C-15C}$ -PSB) was characterized by a red-shifted absorption compared to the parental $M2_{15C}$ -PSB absorption at 560 nm. It was stable to ~180 K whereby it evolves into a second intermediate ($M2_{13C-15T}$ -PSB), which peaks at ~550 nm. This intermediate is stable to ~220 K whereby it then evolves into the next intermediate ($M2_{AT}$ -PSB), which absorbed at an even lower energy of 574 nm. $M2_{AT}$ -PSB persists to ~240 K before evolving into the terminal state peaking at 340 nm, which strongly resembles the ground state $M2_{AT}$ -USB state (Figure S6). This final evolution step is ascribed to a proton transfer event that deprotonates the Schiff base of the chromophore and is responsible for the strong shift in the absorption spectrum from 574 to 340 nm. For these three intermediates, the ground state bleach was added to the difference spectra to produce species associated spectra (SAS) of the photointermediates (Figure 3).

The simulation of the photoinduced dynamics of $M2_{15C}$ -PSB at room temperature as the first step of the $M2_{15C}$ -PSB to $M2_{AT}$ -USB branch of the M2 photocycle is performed by randomly selected 20 initial conditions out of the generated 100 used to simulate the absorption band (see Figure 1 and Figure S1B). Such initial conditions (see Figure S1A) were employed to propagate 20 trajectories starting from S_1 or S_2 (depending from the state displaying the larger initial oscillator strength and therefore transition probability). Within 0.8 ps, seven $M2_{15C}$ -PSB trajectories displayed isomerization and hopped to S_0 while the remaining trajectories remained significantly untwisted. Remarkably, none of the hopped trajectories isomerized around C15=N bond but instead five of them displayed C13=C14 twisting while the remaining two displayed C11=C12 twisting. Both trajectories that exhibited C11=C12 twisting formed, upon S_0 relaxation, the $M2_{15C}$ -PSB reactant and were therefore unproductive. However, the majority of trajectories that isomerized at C13=C14 formed 13-*cis*, 15-*cis* photoproduct. This is assigned to the first cryogenically trapped $M2_{13C-15C}$ -PSB and is thus called by the same acronym.

All isomerizing trajectories followed the ABP isomerization mechanism similar to that of a natural microbial rhodopsin such as bacteriorhodopsin. In fact, the isomerization around C12—C13=C14—C15 and C14—C15=N—C ϵ dihedrals takes place concertedly in opposite directions. As illustrated in Figure 4, the twisting of C13=C14 and C15=N increases along the trajectories until the molecule hops to the ground state. Once the hop takes place, the C13=C14 twisting continues while the C14—C15=N—C ϵ dihedral reverts, yielding a net C13=C14 isomerization and, therefore, the above-mentioned $M2_{13C-15C}$ -PSB intermediate (also see Supporting Information for a movie of a representative reactive trajectory).

Since the above trajectory simulations indicate that M2_{15C}-PSB isomerizes around the C13=C14 double bond leading to the 13-*cis*,15-*cis* photoproduct we hypothesize, on the basis of the cryogenic data discussed above, that M2_{15C}-PSB to M2_{AT}-USB conversion takes place through at least two extra intermediates associated with a single chromophore change each. The second intermediate is predicted to be the 13-*cis*,15-*trans* chromophore isomer and is therefore called M2_{13C-15T}-PSB for consistency with the cryogenic assignment. The third intermediate would feature a 13-*trans*,15-*trans* chromophore and it is called M2_{AT}-PSB being assigned to the third cryogenic intermediate. QM/MM models for each intermediate were constructed by using the ASEC-FEG protocol,²⁵ leading to a prediction of their λ_{\max} values. When looking at these values, we concluded that the increased discrepancy from the experimental value of the corresponding cryogenically trapped intermediate reflects the “distance” of the model from the initial X-ray crystallographic structure of M2_{15C}-PSB (the only available template). In particular, while the primary photoproduct M2_{13C-15C}-PSB displays a value close to the experiment, the more distant M2_{13C-15C}-PSB and M2_{AT}-PSB models deviate significantly, suggesting a shortcoming with the modeling. This decrease in model accuracy can be tentatively attributed to the distant template structure. In fact, while the model of the first intermediate is constructed starting from a model constructed on the basis of an X-ray crystallographic structure, the model of the second intermediate is constructed by taking as a template the model of the first intermediate and it is thus not directly related to an experimental structure. Since the model of the third intermediate is constructed from the model of the second, the accuracy issue is further amplified. For this reason, the M2_{13C-15C}-PSB and M2_{AT}-PSB models are not considered in the following discussion.

Given the results of the cryokinetics and of the computation, we propose the scheme reported in Figure 5 for the M2_{15C}-PSB to M2_{AT}-USB part of the M2 photocycle. The structure of the chromophore in M2_{13C-15C}-PSB and M2_{AT}-PSB is hypothetical and just follows the shortest possible sequential isomerization path from M2_{13C-15C}-PSB to M2_{AT}-PSB, again considering sequential single chemical changes in the chromophore.

Comparison of computed and observed excited state lifetimes (400 ps from ultrafast measurements and theory; Figures 2 and 4) and the λ_{\max} values (Figures 3 and 5) suggests that our description of the primary event is qualitatively correct. More specifically, the red shifting of the computationally predicted first intermediate agrees with the experimentally observed spectral trend, where the initial photointermediate absorption is red-shifted with respect to the reactant absorption. The cryogenic data are then consistent with a blue-shifted secondary intermediate and a red-shifted tertiary intermediate, before blue-shifting to the M2_{AT}-USB dark state.

M2_{AT}-USB to M2_{15C}-PSB Conversion.

As with M2_{15C}-PSB dynamics, the dynamics of M2_{AT}-USB was characterized by ultrafast and cryokinetics experiments. The ultrafast transient absorption spectra and kinetics of M2_{AT}-USB are displayed in Figure 6, where the primary observation is the decay of the excited state back to the ground state over 750 ps. In addition to the decay of the excited state, an evolution of a negative signal in the 575–642 nm (Figure 6A) region over ~300

ps is observed, but due to the location and broadness of the signal this is attributed to PSB contamination. In addition to the appearance of the negative signal for the 642 nm trace (Figure 6A, red curve), there is also a short-lived (c.a. < 200 fs) positive peak that spans from ~625 to 650 nm and is attributed to an early time artifact. The ultrafast data set was fit with a parallel model, and the resulting concentration profile and EADS are depicted in Figure 6C,D, where the red and blue curves represent excited state absorption decay back to the ground state.

The cryokinetics resolved a population red shifted of M2_{AT}-USB and was attributed to M2_{15C}-PSB (Figures 7, S10–S12, and Table S2). M2_{15C}-USB decays back into M2_{AT}-USB at 180 and 190 K, suggesting the presence of a shunt back to M2_{AT}-USB (Figure S10E, H) and directly evolves into the M2_{15C}-PSB photoproduct between 210 and 230 K (Figure S11G–I). When a high enough temperature (240 K) was reached, a decay of the green absorbing band and a filling of the GSB was observed, suggesting dark conversion back to M2_{AT}-USB (Figures S11 and S12). This shows that M2_{AT}-USB evolves to M2_{15C}-PSB through a single intermediate that is followed by a protonation to the photoproduct. The M2_{15C}-USB photointermediate was not observed in the room temperature dynamics due to the low quantum efficiency of its formation. The M2_{15C}-PSB photoproduct is thermally stable up to 240 K where it thermally reconverts back to the deprotonated M2_{AT}-USB.

In addition to the experimental results, the photoinduced dynamics of the M2_{AT}-USB to M2_{15C}-PSB branch of the M2 photocycle were studied by initiating M2_{AT}-USB trajectories on S₃ or S₄ at the 5-root-state-average CASSCF level due to their high oscillator strength. During the 0.8 ps simulation time, the majority of the trajectories hopped to S₃ or S₂ states but displayed no sign of isomerization possibly due to an encountered small barrier. For this reason, we then mapped the excited state isomerization path driven by the C15=N twist by computing a relaxed scan starting from the M2_{AT}-USB.

At this point, it is important to recall information on two important CIs related to the photoisomerization of conjugated polyene systems.^{28–30} The first is a crossing between two states having 1A_g and 1B_u electronic structures (1B_u/1A_g crossing featuring a single 90° twisted C=C bond) and is found in cationic conjugated systems such as rPSB. The second, a crossing between 2A_g and 1A_g like states (2A_g/1A_g crossing, also called a (CH)₃-kinked CI) is found in nonpolar systems.³⁰

Since rUSB is not a highly polar chromophore, we first assumed that a 2A_g/1A_g kinked CI, is more stable in comparison to 1B_u/1A_g CI and thus more accessible from the Franck–Condon (FC) point. Hence, we mapped the reaction path starting from the FC point and connecting it to a previously optimized 2A_g/1A_g CI. The computed path shows the existence of an S₁ minimum, but it also shows that reaching the CI from the minimum is impossible as this lies ~37 kcal/mol higher (see Figure S13). We then computed similar reaction paths for the isomerization around C11=C12 and C13=C14 double bonds. The results are reported in Figure S14. We then hypothesized that rUSB isomerizes around C15=N and that the reaction proceeds through a 1B_u/1A_g CI that was previously optimized. The computed reaction path is reported in Figure 8. The electronic states are labeled from S₀ to S₅ based on the order of the CASSCF energy at the FC region.

At the FC point, the computed oscillator strength maximum (2.3) corresponds to the $S_0 \rightarrow S_5$ transition at the CASSCF level. With the correction for dynamic electron correlation energy, the S_5 state becomes the lowest excited state at the CASPT2 level. The geometry optimization on S_5 resulted in a minimum whose S_1 and S_5 CASPT2 energy order is switched. This indicates a crossing between the first two lowest excited states at the CASPT2 level. We then proceeded with a S_1 geometry optimization that resulted in a S_1 minimum located ca. 59 kcal/mol. This is assigned to the primary excited state photoproduct intermediate generated after photon absorption.

At this stage, it is important to mention that the above findings on rUSB isomerization display similarities to the information uncovered from the Siberian hamster cone pigments.³¹ The calculations carried out at the CASPT2//CASSCF/6-31G* level in both studies indicate the following. First, at the FC point, the lowest energy $1B_u$ -like state turns out to be the spectroscopically most favorable state at the CASPT2 level. Second, there is a crossing between the lowest two excited states ($2A_g/1B_u$ crossing) immediately after relaxation from the FC point. Third, once the molecule passes such a crossing, it may reach a minimum on the lowest excited state; but the molecular structure of such a minimum does not exhibit inverted bond length alternation (BLA), which is essential for the double bond photoisomerization. However, we observe an expansion in the double bonds and a contraction in the single bonds when going from S_0 optimized to S_1 optimized structures (see Figure S15 for geometric parameters). This suggests that there is a barrier along the BLA coordinate. We computed the rest of the reaction path by constraining C14—C15=N—C ϵ and computing a relaxed scan. The path shows a small ca. 5.4 kcal/mol energy barrier between S_1 minimum and the S_0/S_1 crossing which has a $1B_u/2A_g$ CI structure.

On the basis of the above information, we propose the mechanistic scheme of Figure 9 for the $M2_{AT}$ -USB to $M2_{15C}$ -PSB conversion. Note that the calculated excited state barrier (the 5.4 kcal/mol seen in Figure 8; 1.6 ps excited state lifetime from Eyring equation), is consistent with the observed lifetime 8.5 ps (6.4 kcal/mol barrier from Eyring equation; 50% excited state population) excited state lifetime in $M2_{AT}$ -USB ultrafast experiments.

Proposed M2 Photocycle Mechanism.

According to the above results and to the assumed shortest possible, single chemical event, sequential isomerization hypothesis mentioned above, the molecular-level motion driving the M2 photocycle changes are proposed as follows (see Figure 10). The $M2_{15C}$ -PSB to $M2_{13C-15C}$ -PSB photoisomerization takes place via an ABP mechanism involving the C13=C14 and C15=N bonds. If we consider plane β , which is defined by C14, C15, and H15 atoms and looking through the C14—C15 single bond in the direction of the β -ionone ring, the plane rotates in the clockwise direction. This suggests that C13=C14 and C15=N double bonds twist in clockwise and counterclockwise directions, respectively. After the isomerization, a $M2_{AT}$ -PSB intermediate is produced after two thermal steps (see Figure 5) indicated by the experimental investigations. At this stage, the deprotonation of the rPSB takes place. We examined the molecular structures that constitute the $M2_{AT}$ -PSB ASEC configuration and noted a hydrogen bond network connecting the iminium hydrogen and a glutamate (GLU73 residue) located ca. 9 Å away from it. This network is also

observed in the structure closest to the average (see Figure S16A). We propose that the proton translocation from rPSB to GLU73 takes place through such a network involving, according to our model, at least three water molecules during the $M2_{AT}$ -PSB to $M2_{AT}$ -USB conversion.

As discussed above, $M2_{AT}$ -USB then undergoes an isomerization around the C15=N bond in the presence of UV light and produces $M2_{15C}$ -USB directly. The corresponding atomic motion can be described similar to the $M2_{15C}$ -PSB case by considering a plane γ defined by C ϵ , N15, and the nitrogen lone pair. During $M2_{AT}$ -USB isomerization, the C15=N bond continues to twist in the counterclockwise direction while the C13=C14 bond undergoes a slight twist in the clockwise direction. The corresponding photoproduct regenerates the $M2_{15C}$ -PSB by obtaining a proton from the environment. We propose that a proton residing on the nearby glutamic acid residue (GLH73) is transferred to the Schiff base in this process. Moreover, we propose that such a transfer occurs through a H bond network that involves at least one water molecule (see Figure S16B).

Is M2 a Good Model System To Study the Factors Effecting Rhodopsin Photoisomerization?

The features of M2 that we have discussed above, especially in its rPSB bound form, are not too far from the isomerization of certain microbial rhodopsins. These include (1) the primary photoisomerization of the rPSB occurring at the C13=C14 double bond, (2) the isomerization intermediates bearing similarities to the ones proposed and documented for *Anabaena* sensory rhodopsin,^{32,33} (3) the presence on an ABP photoisomerization mechanism which has been shown in bacteriorhodopsin.^{11,34} We have also uncovered a fourth feature of this system, namely, electronic state mixing, that we have previously documented for animal and microbial rhodopsin and rPSB in solution (see section S9).²⁹ The fact that $M2_{15C}$ -PSB photoisomerization is similar to natural rhodopsins is, in many ways, an indication that it may be used as a model system to study the chromophore/protein interaction governing rhodopsin photocycles.

In conclusion, above we have studied the photocycle of a man-made rhodopsin, M2, that can undergo reversible photoisomerization. The study has been carried out with a combination of theory and experiments. The results suggest that the photocycle involves several intermediates and two separate photoisomerization events that are initiated by the absorption of photons with very different wavelengths. More specifically, green light excites $M2_{15C}$ -PSB, which produces 13-*cis*,15-*cis* photoproduct which then isomerizes into 13-*cis*,15-*trans* and, finally, an *all-trans* form. This process is associated with the ABP photoisomerization mechanism, which has never been documented in an artificial rhodopsin before. Our results also reinforce the idea that the bicycle-pedal isomerization mechanism does not necessarily occur inside a space confining environment and can be rather an intrinsic property of the chromophore.^{35,36}

The photoisomerization of rUSB takes place directly around the C15=N double bond from 15-*trans* into 15-*cis* form. The consistency between our findings related to rUSB isomerization and Siberian hamster cone pigments suggests that the information we have

documented above may be valid for other rhodopsins hosting rUSB chromophores. For instance, such information may be useful to investigate the UV pigments found in birds and fish.³⁷

The observation that while a PSB gives a 13-*cis* photoproduct, the rUSB gives rise to photoisomerization of the C15=N bond is consistent with a recent study of a rhodopsin mimic variant of M2.³⁸ In this study, it was shown that an all-*trans* retinylidene can be photoisomerized to a stable 13-*cis*,15-*cis* product; but only in its PSB state. This illustrates the clear difference in photoproduct outcome between protonated and unprotonated systems, as predicted here. The production of the 13-*cis*,15-*cis* photoproduct suggests a similar ABP photoisomerization mechanism in this rhodopsin mimic as well.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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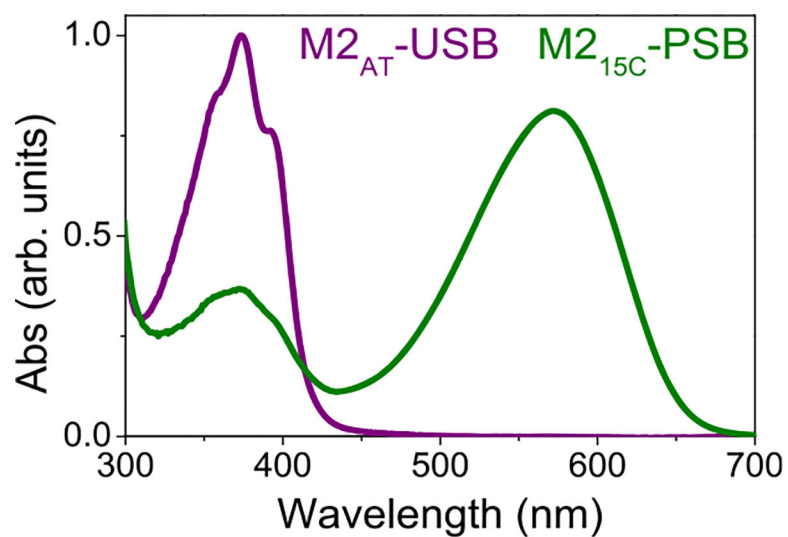


Figure 1. Ground state absorption of the dark adapted M2_{AT}-USB (purple) and light adapted M2_{15C}-PSB (green) states. The M2_{15C}-PSB light state spectrum had contamination of the M2_{AT}-USB dark state as evident by the absorption in the UV region.

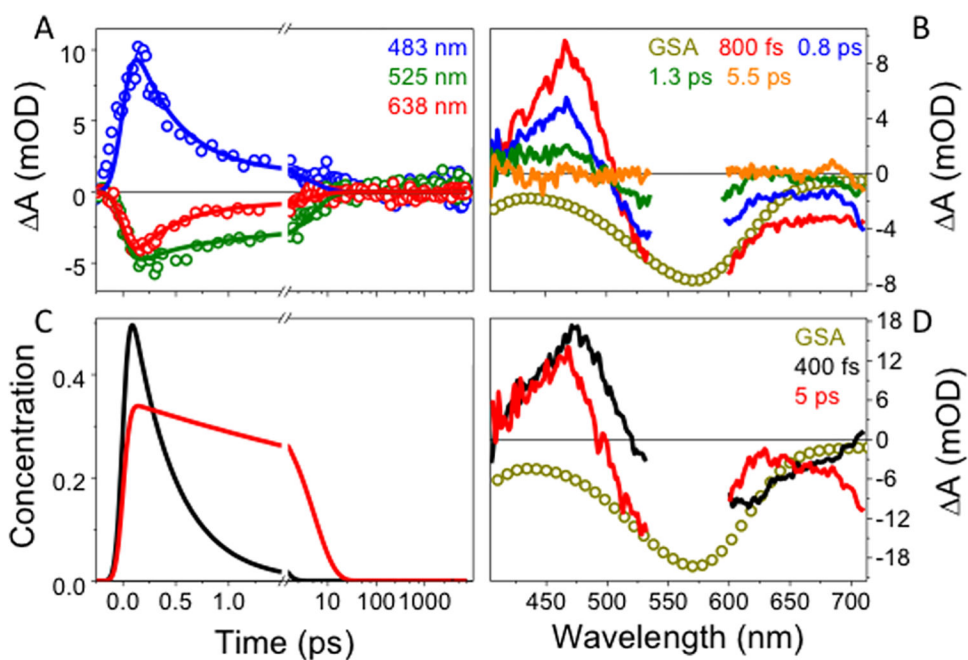


Figure 2. Photodynamics of M215C-PSB after 565 nm excitation (A, B). In the kinetics (A), the data are represented by open circles and the fit is represented by solid lines. Global analysis of the same reaction using a parallel model where 70% of the population is in the faster state (C, D). GSA stands for ground state absorption and are represented by open golden circles. The resulting concentration profiles and EADS are color coded to the legend in (D).

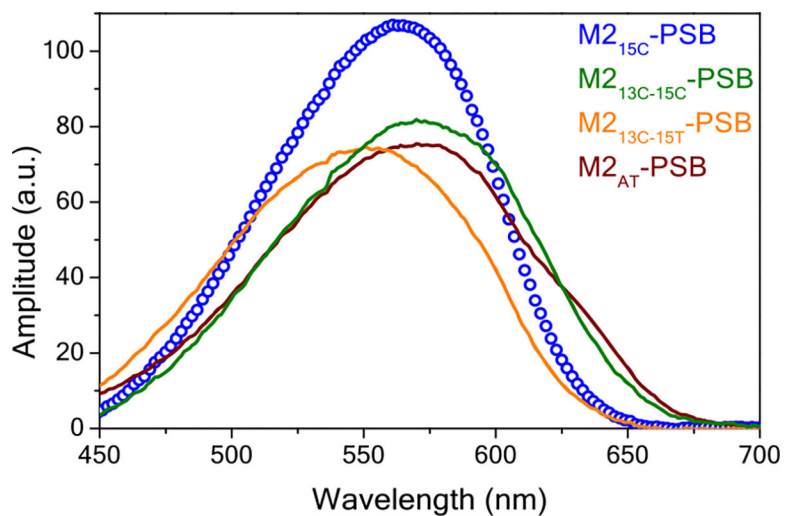


Figure 3. Species associated spectra (SAS) of the PSB intermediates obtained from adding the $M2_{15C}$ -PSB bleach (at the same temperature) to the difference spectra (Figure S6). The $M2_{15C}$ -PSB light state static spectra (blue curve) was taken from the 170 K reference spectra, and $M2_{13C-15C}$ -PSB, $M2_{13C-15T}$ -PSB, and $M2_{AT}$ -PSB photointermediates were isolated at 190, 220, and 240 K, respectively.

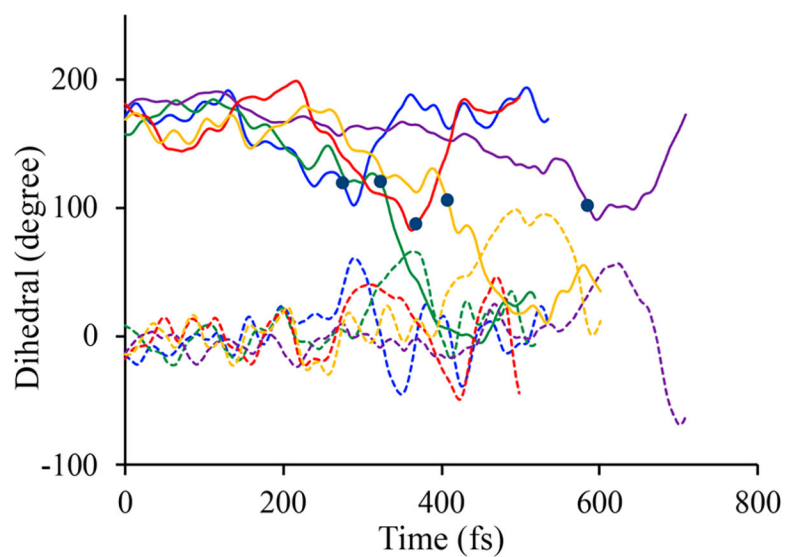


Figure 4. Evolution of C12—C13=C14—C15 (solid) and C14—C15=N—C ϵ (dashed) dihedrals of the trajectories that displayed isomerization around C13=C14 double bond. Black spheres denote the hop times.

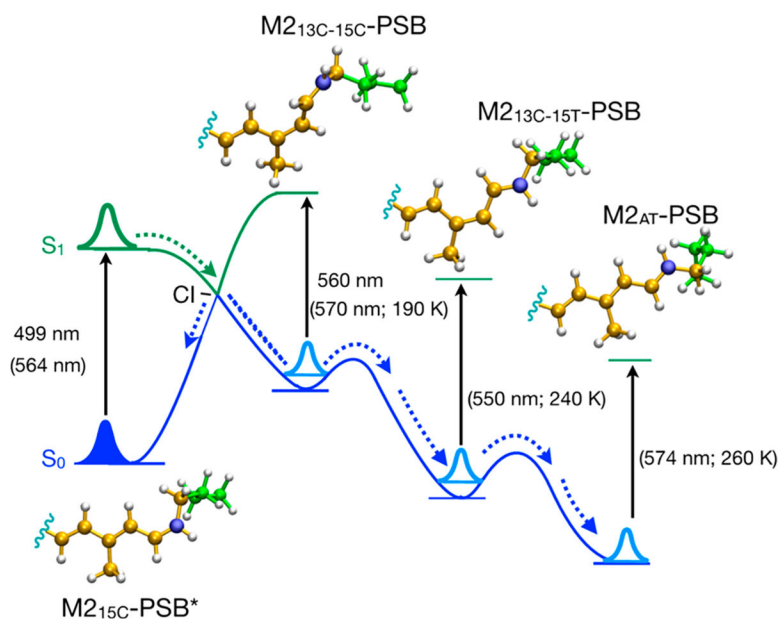


Figure 5. Schematic representation of the PESs driving $M2_{15C}$ -PSB to $M2_{AT}$ -USB conversion. A population of $M2_{15C}$ -PSB molecules absorbing green light is promoted to S_1 . The excited population then relaxes and passes a CI. A fraction of this population reaches the photoproduct form $M2_{13C-15C}$ -PSB. We hypothesize that this subpopulation is further isomerized into $M2_{13C-15T}$ -PSB form and, finally, into $M2_{AT}$ -PSB. The last form undergoes a proton transfer resulting in $M2_{AT}$ -USB. Values in brackets are from the species associated spectra (Figure 3) from the cryokinetics experiments. * denotes a model constructed from crystallographic structure. PDB ID: 4YFP.

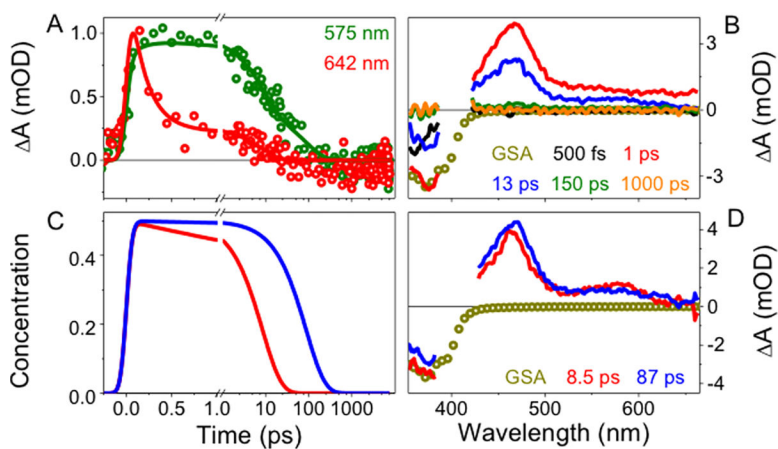


Figure 6. Photodynamics (aof $M2_{AT}$ -USB after 400 nm excitation (A, B). The fits (A, solid lines) are the results of a parallel model consisting of two populations with equal contribution. Concentration and EADS (C, D) from the fit are color coded to the legend in (D). No photoproduct is resolved and only two excited state populations with characteristic double peak features are observed.

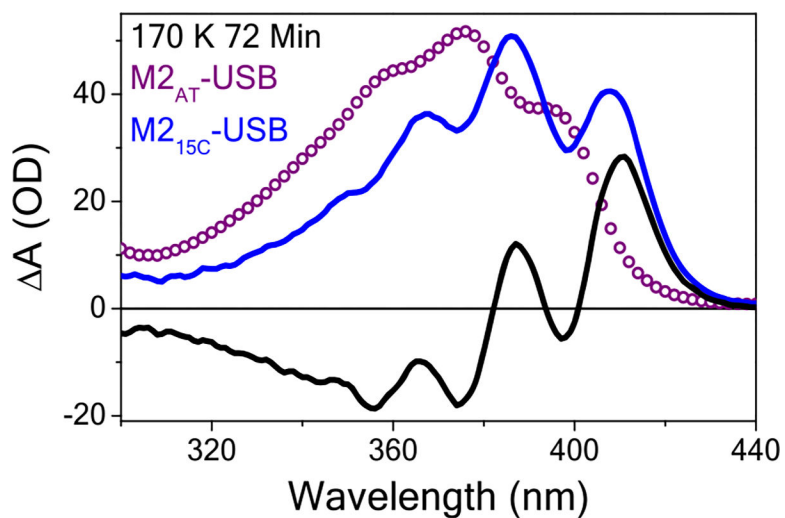


Figure 7. $M2_{AT}$ -USB dark state static spectra (purple open circles curve), difference spectra (black curve), and species associated spectra (SAS; blue curve) of the $M2_{15C}$ -USB intermediate at 170 K. The SAS was obtained from adding the $M2_{AT}$ -USB bleach to the difference spectra.

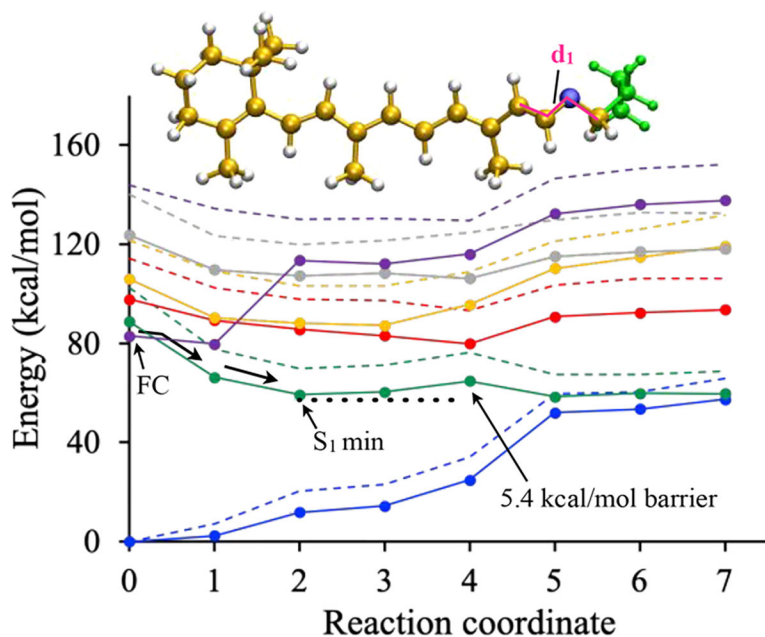


Figure 8. Evolution of CASSCF (dashed) and CASPT2 energies (solid) along the isomerization of $M2_{AT}$ -USB around the $C15=N$ double bond. S_0 to S_5 states are denoted by blue, green, red, yellow, gray, and violet colors, respectively. Points 3–7 of the reaction coordinate were obtained from a series of constraint geometry optimizations. More specifically, the geometry optimizations were carried out while keeping dihedral d_1 (see USB structure on top) constrained at -160 , -140 , -120 , -110 , and -90° , respectively.

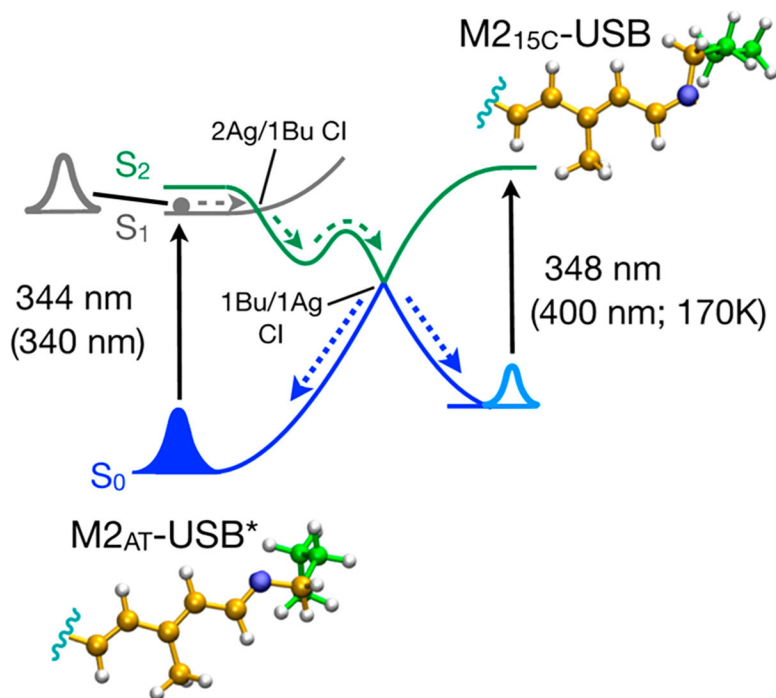


Figure 9.

Proposed isomerization pathway for the $M2_{AT}$ -USB to $M2_{15C}$ -PSB conversion. A population of $M2_{AT}$ -USB absorbing a UV light pulse reaches the lowest excited state at the FC region. It is then relaxed on the same state and crossed to the second excited state which is now lower in energy. The population is further relaxed on this state and reaches a minimum and proceeds toward a second CI and reaches the ground state photoproduct. It then undergoes the proton transfer and reaches the $M2_{15C}$ -PSB state. The wavelengths are in nm, and the values reported in parentheses are experimentally reported values extracted from SAS for the $M2_{15C}$ -USB from the cryokinetics (Figure 7). * denotes a model constructed from the crystallographic structure. PDB ID: 4YFQ.

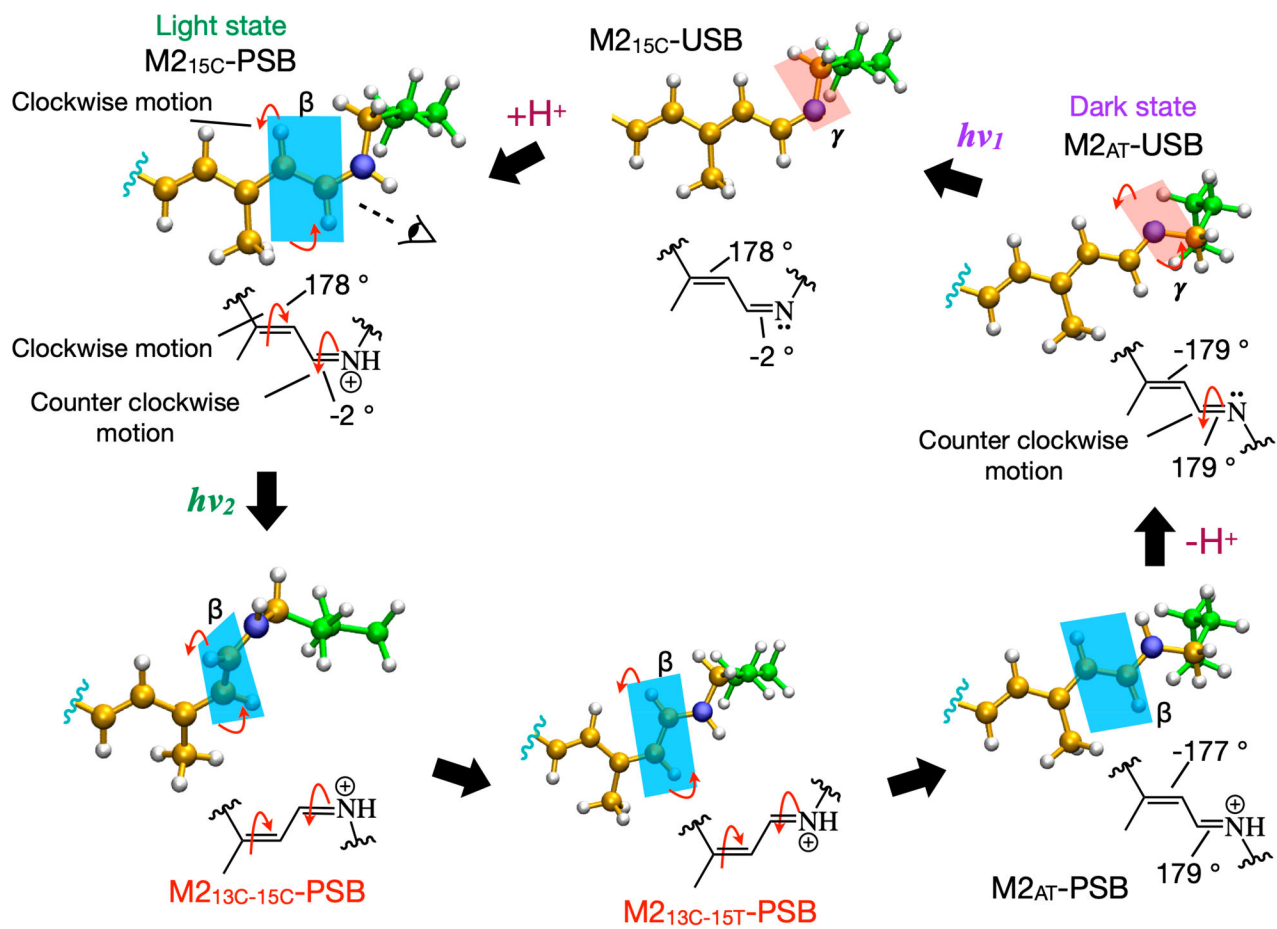


Figure 10. Proposed mechanism for the M2 photocycle. Hypothetical models are labeled in red.