Kinetics of Hydrogen Atom Abstraction from Substrate by an Active Site Thiyl Radical in Ribonucleotide Reductase

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Kinetics of Hydrogen Atom Abstraction from Substrate by an Active Site Thiyl Radical in Ribonucleotide Reductase

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3 Supporting Information

ABSTRACT: Ribonucleotide reductases (RNRs) catalyze the conversion of nucleotides to deoxynucleotides in all organisms. Active E. coli class Ia RNR is an αβ2 complex that undergoes reversible, long-range proton-coupled electron transfer (PCET) over a pathway of redox active amino acids (β-Y122 → [β-W48] → β-Y156 → α-Y731 → α-C439) that spans ~35 Å. To unmask PCET kinetics from rate-limiting conformational changes, we prepared a photochemical RNR containing a [Re] photooxidant site-specifically incorporated at position 355 ([Re]β-Y355), adjacent to PCET pathway residue Y356 in β. [Re]β-Y355 was further modified by replacing Y356 with 2,5,5-trifluorotyrosine to enable photochemical generation and spectroscopic observation of chemically competent tyrosyl radical(s). Using transient absorption spectroscopy, we compare the kinetics of Y· decay in the presence of substrate and wt-α2, Y731F-α2 or C439S-α2, as well as with 3'-[3H]-substrate and wt-α2. We find that only in the presence of wt-α2 and the unlabeled substrate do we observe an enhanced rate of radical decay indicative of forward radical propagation. This observation reveals that cleavage of the 3'-C=H bond of substrate by the transiently formed C439· thyl radical is rate-limiting in forward PCET through α and has allowed calculation of a lower bound for the rate constant associated with this step of (1.4 ± 0.4) × 10^4 s⁻¹. Prompting radical propagation with light has enabled observation of PCET events heretofore inaccessible, revealing active site chemistry at the heart of RNR catalysis.

INTRODUCTION

Managing the coupled translocation of protons and electrons is the keystone to energy storage and conversion.1–5 Biological systems have evolved to capitalize on proton-coupled electron transfer (PCET) to execute energy conversions efficiently and with exquisite control.6,7 E. coli class Ia ribonucleotide reductase (RNR) maintains reversible8,9 PCET over ~35 Å10–13 via a multistep, proton-coupled hopping mechanism and thus serves as a paradigm for the study of PCET in biology.14,15 RNR catalyzes the conversion of nucleotides to deoxynucleotides, the bottleneck in de novo production of monomeric DNA building blocks.16 The active form of E. coli class Ia RNR is composed of two homodimeric subunits, α2 and β2 (Figure 1a).1,13,17 The active site is located in α, while the dfferic-Y122 cofactor required to initiate active site chemistry is buried deep within β (Figure 1a). The rate-determining step in turnover consists of a conformational change triggered by substrate binding.8 This process initiates radical translocation by way of bidirectional PCET to β-Y154, in which a proton is transferred from a specific water molecule ligated to the dfferic cluster,18 while the electron transfer (ET) results in oxidation of β-Y156.19 β-Y156 then oxidizes α-Y731 across the α/β subunit interface which subsequently oxidizes α-Y730 and, in turn, α-C439 in sequential PCET steps (Figure 1b).15,20,21 The C439· thyl radical initiates active site chemistry by abstracting H· from the C3'-position of substrate.22,23 Multistep active site radical chemistry follows,16,24 resulting in reoxidation of C439 and reverse PCET along the same pathway of redox active amino acid residues to restore the radical resting state at β-Y122.16,25 Despite the fact that this multistep radical transport pathway presents RNR as an ideal system in which to examine biological PCET kinetics, rate-determining conformational changes have largely precluded such studies. In order to disentangle conformational gating from PCET kinetics, we have developed photochemical RNRs.25 Bypassing conformationally triggered reduction of the Y122· cofactor, we instead initiate PCET events midway through the RNR mechanism by photooxidation of Y356 (Figure 1b). Synchronization in this way has enabled detailed studies of photoinitiated substrate turnover,26 spectroscopic observation of photogenerated radicals,27 and direct measurement of radical injection rates into α2.28 For initial

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More recently, we have developed a series of unnatural 2,3,5-tri-iodotyrosine (C268S, C305S, and S355C) mutations (C268S, C305S, and S355C) render a single cysteine residue surface-exposed, facilitating site-specific conjugation of a bromomethylpyridyl rhenium(I) tricarbonyl phenanthroline complex to position 355 ([ReI], Figure 1b).29 By measuring the photochemically produced radical, allowing spectroscopic detection of downstream radical propagation kinetics by transient absorption (TA) spectroscopy. We have shown that this construct is competent for photoinitiated enzymatic turnover and present the first direct measure of Y731F-3Y356 fragment (constructed from the [Re]-Br crystal structure)30 is placed in a hypothetical position (dashed green line) intended for illustrative purposes only.

constructs, the β2 subunit was replaced by a short peptide encompassing the 20 C-terminal residues of the β2 protein. More recently, we have developed β2, in which three mutations (C268S, C305S, and S355C) render a single cysteine residue surface-exposed, facilitating site-specific conjugation of a bromomethylpyridyl rhenium(I) tricarbonyl phenanthroline complex to position 355 ([ReI], Figure 1b).29 By measuring the photochemical β2 is capable of reporting on Y356 oxidation.30 However, attempts to measure radical propagation kinetics directly were prevented by fast charge recombination and thus a low yield of photochemically produced radical. We have now achieved direct observation of Y356 oxidation by circumventing the requirement for concomitant proton transfer during the generation of Y356.30.31,32 Using PDB files 1MXR33 and 4R1R,34 we find that only in the presence of wt-α2, and substrate with natural isotopic abundance are radical decay kinetics enhanced. These data support that cleavage of the 3′-C–H bond of substrate by the transiently formed C430 thiol radical is rate-limiting in forward PCET through α. We report a lower limit for the rate constant associated with this step of (1.4 ± 0.4) × 10^{-10} s^{-1}. Unmasking PCET events in the active αβ2 RNR has provided a first direct measure of active site kinetics in the class Ia enzyme, yielding new evidence for a long-standing model and shedding light on the mechanism by which RNR maintains control and specificity during long-range PCET.

Figure 1. (a) Pseudoatomic model of the active E. coli class Ia RNR αβ2 complex.30,31,32 using PDB files 1MXR33 and 4R1R.34 α2 (purple and violet) binds substrate (blue), and effector (state), and crystallizes with the 20-mer peptide corresponding to the C-terminal tail of β2 (forest and light green) contains the β2 subunit was replaced by a short peptide encompassing the 20 C-terminal residues of the β2 protein.

### MATERIALS AND METHODS

**Materials.** Wt-α2 (2000 nmol mmol,min,-1) was expressed from pET28a-nda and purified as previously described.35 Glycerol stocks of Y122F-α2 and C268S-α2 were available from a previous study36 and were expressed and purified as wt-α2. All α2 proteins were prerceded prior to use.21 [5-3H]-cytidine 5′-phosphate sodium salt hydrate ([5-3H]-CDP) was purchased from ViTrax (Placentia, CA). 3′-Deuterated cytidine 5′-phosphate ([3′-2H]-CDP) was available from a previous study,26 in which it was synthesized as reported.22,23 Tricarbonyl(1,10-phenanthroline)(4-bromomethyl-pyridine)rhenium(I) hexafluoropropionate ([ReI]-Br) was available from a previous study.22 E. coli thioredoxin (TR, 40 μmol/min/mg) and thioredoxin reductase (TRR, 1800 μmol/min/mg) were prepared as previously described.37,38 2,3,5-Trifluorotyrosine was synthesized enzymatically from pyruvate, ammonia, and 2,3,6-trifluorophenol with tyrosine phenol lyase as the catalyst.29 Assay buffer consists of 50 mM HEPES, 15 mM MgSO4, and 1 mM EDTA adjusted to the specified pH.

**Preparation of [Re]-F3Y356-β2.** Construction of C268S/C305S/S355C/Y356Z-pBAD-ndaB was achieved by site-directed mutagenesis using pBAD-ndaB as a template, and primers listed in the Supporting Information. E. coli TOP10 cells were cotransformed with the newly constructed ndaB plasmid and pEVOL-F3Yα-aRS obtained from a previous study,37 plated on LB-agar plates supplemented with 100 μg/mL ampicillin and 35 μg/mL chloramphenicol and incubated at 37°C overnight. A 1 mL culture containing the same antibiotics was inoculated with a single colony, incubated at 37°C for 10 h, and then used to inoculate a small culture grown overnight at 37°C. This starter-culture was used to inoculate 4 × 2 L cultures of 2YT at a 100-fold dilution. The cells were grown in the presence of 1.5 mM 2,3,5-F3Y until reaching an OD600 of 0.5, at which point the F3Y-aRS and ndaB genes were induced with arabinose (0.05% w/v). The cells were grown for an additional 4 h to a final OD600 of ~1.5 and then harvested by centrifugation (3000 × g, 10 min, 4°C). Yields of ~2 g/L were obtained. Success of expression was assessed by 10% SDS-PAGE. The protein was purified by anion-exchange chromatography following a previously reported protocol,40 to give 10–15 mg per g of cell paste. Holo-S355C/2,3,5-F3Y356-β2 contained 0.6 Y/Fβ2 and exhibited no enzymatic activity. This variant is inactive due to the presence of a thiol/thiolate in the tricysteine mutant, which may be oxidized by F3Y. This quenching process is not a concern in the photoRNR experiments because conjugation to [ReI] results in a thioether, which is difficult to oxidize. Purified material contained ≤5% ββ' heterodimer resulting from the presence of protein truncated at position 356 (a consequence of the method used for unnatural amino acid incorporation). Treatment with hydroxyurea to quantitatively reduce Y122F, and labeling with [ReI]-Br were achieved as previously and yielded [Re]-F3Y356-β2, exhibiting >95% labeling efficiency.

**steady-state Emission pkc.** Titration. The steady-state emission intensity of 5 μM [Re]-F3Y356 in the presence of 1 mM CDP, 3 mM ATP, and 20 μM wt-α2 was measured in buffer containing 50 mM of either MES (pH 5.2–6.8) or HEPES (pH 7.0–7.6), 15 mM MgSO4, and 1 mM EDTA. Excitation at 315 nm using a 420 nm long-pass cutoff filter allowed spectra to be recorded over 450–650 nm, scanning 3 times per sample at a rate of 0.1 nm/s and detecting in 0.5 nm steps. Samples were held at 25 °C for 2 min prior to scan and
throughout the duration of the measurement. Integrated emission intensity was plotted versus pH and fit to eq 1 (Figure S1). Here, \( I \) corresponds to integrated emission intensity and \( I_{\text{max}} \) and \( I_0 \) correspond to \( I \) at pH 7.6 and 7.2, respectively.

\[
10^{\left( \Delta pK_a \right)} = \frac{I - I_0}{I_{\text{max}} - I_0}
\]  

(1)

**Photochemical Turnover.** Single turnover experiments under photochemical conditions were performed by mixing 10 \( \mu M \) each of met-[Re]-F\(_2\)Y-\( \beta \) with wt-\( \alpha \)-2; 3 mM ATP; and either 1 or 0.5 mM CDP or 1 mM or 0.5 mM CDP or [3'-2H]-CDP. Samples contained 50 \( \mu M \) [Re]-F\(_2\)Y-\( \beta \); 75 \( \mu M \) of wt-\( \alpha \)-2; C\(_{\text{Y356S}}\)-\( \alpha \); or C\(_{\text{Y356F}}\)-\( \alpha \); 3 mM ATP; and either 1 or 0.5 mM CDP or [3'-2H]-CDP.

Laser experiments were performed using a system that has previously been described. LIF and TA spectra were collected at 412.5 nm using slit widths corresponding to 0.7 nm resolution and recorded over 10,000 laser shots for each sample. TA spectra were collected over 500 four-spectrum sequences where two of the four conditions result in exposure to the pump beam.

Lifetimes were obtained by averaging three sets of decay traces from three unique samples of a single protein preparation (both wt-\( \alpha \)-2 and [Re]-F\(_2\)Y-\( \beta \); expression, purification, and [Re]-labeling) (Trial 1 in Table S1), according to eq 2:

\[
y = y_0 - Ae^{-x/t}
\]

Lifetimes from the decay traces for another three sets of unique samples were then obtained using a second protein preparation (Trial 2 in Table S1). Table 1 lists the propagated error for the six measurements across the two trials with weighted averages from error associated with the fit for each data set within a trial, compounded with the standard deviation between the two trials. An exemplary data set, along with fits to eq 2, and associated residuals analysis are included in Figure S3.

**RESULTS**

**pK\(_a\) of 2,3,5-F\(_3\)Y\(_{356}\) within the \( \alpha_2\beta_2 \) Complex.** Photochemical generation of an observable population of F\(_3\)Y\(_{356}\) is enhanced when the amino acid resides in its deprotonated state. This enhanced radical generation is a direct consequence of the ability to generate the radical by removal of only an electron as opposed to removal of an electron and proton (i.e., PCET). To determine the optimum pH for photochemical radical generation, we measured the pK\(_a\) of F\(_3\)Y\(_{356}\) within the \( \alpha_2/\) [Re\(\beta\)\(_2\) complex. This measurement was accomplished by monitoring the steady-state emission from the rhenium complex excited state ([Re\(\beta\)\(_2\)]) which is quenched much more effectively when the adjacent F\(_3\)Y is deprotonated. Plotting emission intensity as a function of pH revealed a pK\(_a\) of 6.2 ± 0.1 (Figure S1). This value is in line with the pK\(_a\) of 6.4 measured for the free amino acid derivative, particularly in light of the fact that a positively charged [Re\(\beta\)] complex is present.

**Observation of Transient Y\(_{\alpha}\).** In order to observe photogenerated Y\(_{\alpha}\)‘s, charge recombination within the initially formed charge-separated state ([Re\(\beta\)\(_2\)]\([\text{Re}\alpha\beta]\)) must be prevented. Therefore, we applied flash-quench methodology by including an excess of Ru(NH\(_3\))\(_6\)Cl\(_3\) in reaction mixtures. Bimolecular quenching of the [Re\(\beta\)]* excited state furnishes the [Re\(\alpha\)] complex via reduction of Ru(NH\(_3\))\(_6\)Cl\(_3\) to Ru(NH\(_3\))\(_5\)Cl\(_2\). This [Re\(\alpha\)] species is capable of driving rapid oxidation of trifluororesinate (Figure 2a). Figure 2b shows the TA spectrum of Y\(_{\alpha}\)-collected 3 \( \mu s \) after excitation, at which point nearly all photochemistry is completed and F\(_3\)Y- and/or Y\(_{\alpha}\) are the only transient species contributing to the absorption feature centered at 412 nm. The overall photochemical yield of Y\(_{\alpha}\) is ~1.9% (calculation included in the Supporting Information).

Experiments were performed at protein concentrations such that >97% of [Re]-F\(_3\)Y\(_{356}\)-\( \beta \) is complexed to \( \alpha \)-2 (based on the previously reported \( K_D \) of 0.7 ± 0.1 \( \mu M \), measured for [Re\(\beta\)] binding to \( \alpha \) under the same conditions). The control experiment performed with [Re]-Y\(_{356}\)-F\(_{25}\) (black, Figure 2b) shows a minor TA signal, which we have previously observed and ascribed to off-pathway generation of Y\(_{356}\). In the absence of an adjacent redox active amino acid, off-pathway radical generation is maximized. Thus, this spectrum (black, Figure 2b) represents a maximum possible contribution to the observed signal and is likely greater than any off-pathway contributions operative when F\(_3\)Y or Y is present.

**Photochemical Competence for Turnover.** To evaluate the relevance of photochemically generated Y\(_{\alpha}\)-in RNR chemistry, we sought to verify chemical competence for enzymatic turnover via photochemical initiation. Steady-state illumination under single turnover conditions in the presence of radiolabeled substrate ([5'-H]-CDP), effector (ATP), Ru(NH\(_3\))\(_6\)Cl\(_3\) and \( \alpha \) allows quantitation and identification of photogenerated products. Of note, the \( \mu\)-O-Fe\(_{\text{II}}\)/Y\(_{122}\) cofactor of [Re]-Y\(_{356}\)-F\(_{25}\) has been reduced with inhibitor hydroxurea to form met-[Re]-F\(_3\)Y\(_{356}\)-\( \beta \) thus the normal mechanism for turnover is not viable with this construct.

<table>
<thead>
<tr>
<th>( \alpha_2 )-variant</th>
<th>substrate</th>
<th>( \tau/\mu s^* )</th>
</tr>
</thead>
<tbody>
<tr>
<td>wt</td>
<td>CDP</td>
<td>18 (1)</td>
</tr>
<tr>
<td>Y(_{356})F</td>
<td>CDP</td>
<td>24 (1)</td>
</tr>
<tr>
<td>C(_{Y356S})</td>
<td>CDP</td>
<td>25 (2)</td>
</tr>
<tr>
<td>wt</td>
<td>[3'-2H]-CDP</td>
<td>26 (1)</td>
</tr>
</tbody>
</table>

*Photogenerated Y\(_{\alpha}\) lifetimes monitored by TA spectroscopy at 412.5 nm and fit to monoexponential decay from 3 to 76.5 \( \mu s \) (Figure S3). Weighted averages represent duplicate sets of three measurements each, on two separate protein preparations of [Re]-F\(_2\)Y-\( \beta \) and wt-\( \alpha \)-2. Samples contain 50 \( \mu M \) met-[Re]-F\(_2\)Y-\( \beta \); 75 \( \mu M \) \( \alpha \)-2 variant, 1 mM or 0.5 mM CDP or [3'-2H]-CDP, 3 mM ATP, 10 mM Ru(NH\(_3\))\(_6\)Cl\(_3\), and assay buffer at pH 8.2.
preparation of both wt-α2 and [Re]-F3Yβ2 data sets from two protein preparations were measured. Accordingly, the data in Table 1 are the propagated error for the six measurements across the two trials. Of note, the initiation process in which F3Y356− is oxidized by [Re2] simply generates the radical on the PCET pathway. All fits to kinetics data begin at 3 μs, after the F3Y- has formed. Thus, by removing the proton dependence of the initiation step, we are able to increase the yield of the radical (by relying only on an ET vs PCET for radical initiation), and we do not alter the PCET mechanism at play during the steps of interest that follow. With the exception of τ measured in the presence of Y731F-α2, the lifetime in each case corresponds to a total signal composed of contributions from F3Y356− in β1, Y731− and Y730− in α2. Similar signal amplitudes were observed at t = 0 within each trial (Table S1), revealing that Y- generation was similar to the different α2 variants and substrates.

We found that the measured lifetime of τ = 18 ± 1 μs for wt-α2 is extended to 24 ± 1 μs for the Y731F-α2 variant, which cannot produce a radical in α2 (Table 1). This observation suggests that the PCET pathway in α introduces an additional route for Y- decay. The significant difference between these two values provides a means of differentiating on- and off-pathway radical decay. The relative kinetics of the productive, on-pathway contribution to the total decay is calculated according to eq 3, where τ0 represents the lifetime measured in the presence of Y731F-α2. The resultant rate constant (kobs) is (1.4 ± 0.4) × 104 s−1.

\[ k_{obs} = \frac{1}{\tau} - \frac{1}{\tau_0} \]  

In order to understand which processes in α limit the rate of radical transport, we next blocked the interior end of the PCET pathway by using C439S-α2. A lifetime identical to that measured in the presence of Y731F-α2 was observed (Table 1), revealing that the rate-determining step operative in the presence of wt-α2 occurs either during or after oxidation of residue C439. We note, however, that this observation does not reveal whether or not radical injection into the α subunit occurs in the presence of this variant. It could be envisioned that the downstream perturbation to the PCET pathway imposed by the C439S amino acid substitution precludes radical injection entirely. Thus, either radical injection followed by rapid reverse PCET and quenching occurs or injection is precluded. Both possibilities provide evidence for strict conformational control over PCET events. Throughout our analysis we have assumed that, in the presence of wt-α2 and CDP, new routes for off-pathway Y- decay have not been introduced. In all cases, τ0 is unrestricted in its definition and simply represents the Y-lifetime via any avenue of nonproductive decay. Thus, in calculating kobs, we apply the same τ0 value for nonproductive decay in the case where the productive pathway (turnover) has also been enabled.

Once C439 is oxidized, the ensuing radical abstracts a hydrogen atom from the 3'-position of substrate (Scheme 1). Subsequent loss of a molecule of water from the 2'-position represents the first irreversible step of turnover. This irreversibility renders any subsequent steps inconsequential to the Y- decay rate. Thus, the rate-determining step with respect to Y- decay in our system (namely, where the native pathway through β is overridden) must be either oxidation of C439 or H-abstraction from C3' of substrate. To differentiate between these two possibilities we next measured τ in the presence of

Figure 2. (a) Scheme describing the photochemistry of F3Y-generation; (b) TA spectra collected 3 μs after 355 nm excitation of 50 μM [Re]-F3Y356β2 (red) or [Re]-Y356Fβ2 (black), and 75 μM α2, 1 mM CDP, 3 mM ATP, and 10 mM Ru(NH3)6Cl3 in assay buffer at pH 8.2.

Photochemical production of dCDP is 9 ± 4% that of wt-β2 under identical conditions (Figures 3 and S2), which produces 1.2 dCDP/α2 out of a theoretical maximum of 4. Dark controls and reactions with Y731F-α2 and C439S-α2 variants produce negligible amounts of product.

Figure 3. Photochemical turnover of met-[Re]-Y356Fβ2 (10 μM), [S-3H]-CDP (0.2 mM), ATP (3 mM), Ru(NH3)6Cl3 (10 mM), and wt, Y731F, or C439S-α2 (10 μM) in assay buffer, pH 7.6 at 25 °C. Numbers are presented as a percentage of product observed with wt-β2. Error bars represent 1 standard deviation for 3–6 independent trials.

Pathway and Isotope Dependence of Y- Lifetime. We set out to explore individual PCET steps by measuring the kinetic behavior of Y- under different conditions. We compared the lifetime of transiently formed Y- (τ) in the presence of CDP, ATP, and wt-α2 with that of τ in the presence of CDP, ATP, and α-variants containing redox-inactive pathway substitutions, as well as in the presence of [3'-H]-CDP, ATP, and wt-α2. Lifetime data were determined from measurements of three unique samples from a single protein preparation of both wt-α2 and [Re]-F3Yβ2. We set out to explore individual PCET steps by measuring the kinetic behavior of Y- under different conditions. We compared the lifetime of transiently formed Y- (τ) in the presence of CDP, ATP, and wt-α2 with that of τ in the presence of CDP, ATP, and α-variants containing redox-inactive pathway substitutions, as well as in the presence of [3'-H]-CDP, ATP, and wt-α2. Lifetime data were determined from measurements of three unique samples from a single protein preparation of both wt-α2 and [Re]-F3Yβ2. We set out to explore individual PCET steps by measuring the kinetic behavior of Y- under different conditions. We compared the lifetime of transiently formed Y- (τ) in the presence of CDP, ATP, and wt-α2 with that of τ in the presence of CDP, ATP, and α-variants containing redox-inactive pathway substitutions, as well as in the presence of [3'-H]-CDP, ATP, and wt-α2. Lifetime data were determined from measurements of three unique samples from a single protein preparation of both wt-α2 and [Re]-F3Yβ2.
Scheme 1. Mechanistic Model Describing Y- Decay

$$\begin{align*}
\text{wt-}Y_{730} & \leftrightarrow \text{wt-}Y_{731} & & \beta-Y_{356} & \rightarrow Q^+ \\
\text{Cys-S} & \rightarrow \text{R}_{3}\text{C} & & \text{H}_2\text{O} & \rightarrow \text{SH}
\end{align*}$$

More than 30 years ago [3′-2H]-NDPs were used to investigate the mechanism of RNR.42,43 Small amounts of RNR-mediated 3H2O release and 3′[V/K] isotope effects provided strong evidence that 3′-C–H bond cleavage occurs during NDP reduction. This study also established that the first irreversible step during a single turnover occurs after hydrogen atom abstraction from substrate and formed the underpinning for the mechanistic model shown in Scheme 1 (intermediates 2–4) and Figure S4.

Stepwise PCET between Tyr-O· → Cys-S· → R3C· akin to the interconversion of 1 → 2 → 3 in Scheme 1 seems contrary to thermodynamic favor (bond dissociation energies of PhO–H, RS–H, and HOCH2–H are ~86, 91, and 94 kcal/mol, respectively).16,44,45 However, a central tenet of the model proposed in Scheme 1 is that enzymatic coupling of endergonic steps to an irreversible reaction can provide a means of overcoming thermodynamic hurdles. The irreversible and entropically favored release of a molecule of water from the 2′-position of substrate (e.g., 3 → 4 in Scheme 1) is postulated to drive the RNR reaction forward as and when small amounts of intermediate 3 are formed from the reversible steps leading up to it. The loss of a rate enhancement for Y- decay in the presence of [3′-2H]-CDP reveals a primary IE on the cleavage of the substrate 3′-C–H bond, providing direct evidence in support of this model.

The steps in the RNR mechanism that are relevant to the current experiment are outlined in Scheme 1. We note that radical translocation in our system is initiated midstream along the PCET pathway; thus steps within the β subunit are inconsequential. Here, 1 accounts for our experimental observable, a composite signal of unknown relative contributions from F3Y356 in β, Y731·, and Y730· in α2. Reoxidation of F3Y356· by Y731· is predicted to be ~110 mV uphill at pH 8.2 based on the relative potentials of these amino acids in solution.42 Yet, experiments in RNR suggests that Y356 is ~100 mV easier to oxidize than Y731 within the subunit interface.46 Similarly, Y731· and Y730· have been predicted,47 and experimentally shown,48 to be isoenergetic within the enzyme complex. Thus, all of these radical species have been drawn as reversibly interconverting and reduction of intermediate 1 by an off-pathway quencher, Q, can potentially occur by way of any of these radical intermediates.

On-pathway Y- decay occurs by oxidation of Cys by Tyr. Oxidation of the Cys thiol by Tyr can potentially occur by way of a pre- or post- ketyl radical intermediate (4). Despite the fact that active site chemical transformations following the formation of 4 ultimately result in the regeneration of the Cys with reverse PCET to reform 1 (Figure S4),48 these processes occur on a much slower time scale (~100 s−1) than under examination here.49 Accordingly, 1 is not expected to reform during the time course of the experiment. Thus, 4 represents a terminal product with respect to Y- decay and the mechanistic steps relevant to our experimental conditions are limited to the interconversion of species 1–4 in Scheme 1.

Our results comparing τ in the presence of [3′-2H]-CDP versus CDP reveal that the rate enhancement for nonlabeled CDP occurs after oxidation of Cys. However, the implications of the reversibility of the oxidation of Cys on the radical lifetimes of 1 must be considered. With little kinetic information regarding the equilibrium between 1 and 2, we turn to small molecule model studies in which the kinetics of bimolecular oxidation of Cys by Tyr were examined by pulse radiolysis.50 These studies report a rate constant of 2 × 107 M−1 s−1 and that the reverse reaction (oxidation of Tyr by Cys) is significantly faster.50 These results suggest that a pre-equilibrium may be established between intermediates 1 and 2 in our system and facilitates an estimate for the magnitude of the corresponding equilibrium constant, K<sub>eq</sub> (k<sub>e</sub>/k<sub>v</sub>), from thermodynamic values. Electrochemical measurements of tyrosine and glutathione reveal that cysteine and tyrosine have approximately equal midpoint potentials at pH 7.0 (0.94 ± 0.04 V and 0.93 ± 0.02 V, respectively).51 However, calculations based on a trapped form of the active RNR complex suggest that oxidation of Cys by Y730· is endergonic by 3–4 kcal/mol, resulting in K<sub>eq</sub> ≈ 10<sup>−2</sup>.47 Taken together, these
The fact that C–H bond cleavage from substrate by the transiently formed C3 was occurs at 10^5 s^-1, along with previous results, reveals that PCET events occur rapidly during radical translocation. Together with recent findings that implicate alignment of the PCET pathway as a target of conformational gating, these results suggest that the reaction profile of the active αβ2 complex remains locked in place as radical translocation and subsequent active site chemical steps transpire. This ability to lock the PCET pathway indicates that RNR capitalizes on the constraints imposed by PT distances in achieving acute control over long-range ET.

A number of studies indicate that the PCET pathway of RNR runs slightly thermodynamically uphill in the forward direction and active site chemistry is driven forward by the rapid and irreversible loss of water from the 2'-position of substrate. This reaction landscape presents a mechanism by which RNR avoids the buildup of reactive amino acid radical intermediates over the course of its ~70 Å round-trip traverse between α and β. Our observation that HAT from C3' of substrate to C439 is rate-limiting in forward PCET through α provides further evidence that an uphill PCET pathway generates the initial substrate radical.

**CONCLUSIONS**

Jump-starting radical propagation with light has enabled the direct observation of PCET events previously inaccessible, revealing active site chemistry at the heart of RNR catalysis. Despite the fact that RNR turnover is rate-limited by conformational changes occurring at ~2–10 s^-1, radial propagation steps are rapid. To unmask PCET events we have constructed a photochemically competent β2 subunit capable of generating observable transient Y'-species within the αβ2 complex. With this construct, we have observed an IE on cleavage of the substrate 3'-C=H bond, revealing that this step is rate-limiting with respect to Y'-propagation through α and allowing us to report a lower bound for the rate constant associated with this step of (1.4 ± 0.4) × 10^5 s^-1. Unmasking PCET events in the active αβ2 RNR has provided a first measure of active site kinetics in the class Ia enzyme, yielding new evidence for a long-standing model and shedding light on the mechanism by which RNR maintains control and specificity during long-range radical transport.

**ASSOCIATED CONTENT**

1. Supporting Information

   Experimental methods and instrumentation; calculation of photochemical Y'-yield; complete table of data including r and Δν amplitudes for two trials; pK₃₄ titration; HPLC analysis of radiolabeled photoproducts; single wavelength kinetics data; fitting, and residuals analysis; scheme depicting the entire model for RNR-mediated substrate turnover. This material is available free of charge via the Internet at http://pubs.acs.org.

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   The authors declare no competing financial interest.
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