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Citation

Published Version
doi:10.1021/jacs.6b08200

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A >200 meV Uphill Thermodynamic Landscape for Radical Transport in *Escherichia coli* Ribonucleotide Reductase Determined Using Fluorotyrosine-Substituted Enzymes

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Supporting Information

ABSTRACT: *Escherichia coli* class Ia ribonucleotide reductase (RNR) converts ribonucleotides to deoxynucleotides. A diferric-tyrosyl radical (Y122•) in one subunit (β2) generates a transient thyl radical in another subunit (α2) via long-range radical transport (RT) through aromatic amino acid residues (Y122⇌[W48]⇌Y356 in β2 to Y751⇌Y730⇌C439 in α2). Equilibration of Y356•, Y731•, and Y730• was recently observed using site specifically incorporated unnatural tyrosine analogs; however, equilibration between Y122• and Y730• has not been detected. Our recent report of Y356• formation in a kinetically and chemically competent fashion in the reaction of β2 containing 2,3,5-trifluorotyrosine at Y122 (F3Y122•/β2) with α2, CDP (substrate), and ATP (effectors) has now afforded the opportunity to investigate equilibration of F3Y122• and Y356•. Incubation of F3Y122•/β2, Y356F-α2 (or Y731F-α2), CDP, and ATP at different temperatures (2–37 °C) provides evidence for equilibration of Y356• with Y730• and Y731• equilibrated with C439 at 25 °C. The pH dependence of the F3Y122•⇌Y356• interconversion (pH 6.8–8.0) reveals that the proton from Y356 is in rapid exchange with solvent, in contrast to the proton from Y122. Insertion of 3,5-difluorotyrosine (F2IY) at Y356 and rapid freeze-quench EPR analysis of its reaction with Y731F-α2, CDP, and ATP at pH 8.2 and 25 °C shows F3Y1356• generation by the native Y122•, F3Y-RNRs (n = 2 and 3) together provide a model for the thermodynamic landscape of the RT pathway in which the reaction between Y122 and C439 is ~200 meV uphill.

INTRODUCTION

The *E. coli* class Ia ribonucleotide reductase (RNR) contains two homodimeric subunits, α2 and β2, and functions as an α2β2 complex. Its active cofactor is a diferric-tyrosyl radical (Y122•) unit buried within β2. This cofactor generates a transient thyl radical (Cα•) in α2, which initiates reduction of the four nucleotides (CDP, GDP, ADP, and UDP) to their corresponding 2′-deoxynucleotides (dNDP), with the specificity of reduction dictated by the appropriate allosteric effector (ATP, TTP, dGTP, and dATP). During each turnover, Y122• reversibly oxidizes Cα• via multiple proton-coupled electron transfer (PCET) steps through a pathway involving aromatic amino acid residues Y122⇌[W48]⇌Y356 in β2 to Y751⇌Y730⇌C439 in α2. Currently, there is no direct evidence for the involvement of W48 in RT. In the wild-type (wt) RNR, only Y122• is observed in the presence of substrates (S) and effectors (E); there has been no detectable electron delocalization over the other pathway tyrosines. In this paper, we present the first insight into the thermodynamic landscape of the RT pathway within β2. Site-specific replacement of either Y122 or Y356 with fluorotyrosines (F3Y, n = 2 and 3) in combination with pathway-blocked α2 mutants (Y731F-α2 or Y730F-α2)/CDP/ATP and X-band electron paramagnetic resonance (EPR) spectroscopy provides evidence for equilibration of α2 between Y356• with Y730• as a function of temperature and pH. These studies have allowed estimation of ΔE°(Y356•⇌Y730•) of ~100 mV.

Detection of low concentrations of any pathway radical in the wt RNR system is challenging due to rate-limiting conformational changes and the substantial overlap in the EPR spectra of the Y•s. Initial attempts to address if Y122• equilibrated with the pathway tyrosines (Y356, Y731, and Y730) utilized the ability to collapse the Y• doublet EPR spectrum into a singlet with β-methylene-deuterated ([β-H2]Y) Y•'s. β2 containing globally incorporated [β-H2]Y's was reacted with α2 containing protonated Y's, dCDP, and TTP. These conditions promote α2β2 complex formation but prevent turnover, thus potentially allowing equilibration of the pathway Y•'s. Unfortunately, no
unlabeled Y• signal could be detected; the EPR spectrum of Y• in the α2β2 complex was identical to that in free β2.12

Recently, we showed that the reaction of NO2Y122•/β2 (3-nitrotyrosine at position 122), which is predicted to be 200 mV more difficult to oxidize than Y at pH 7.0,15,16 with wt-α2, CDP, and ATP generates a new Y•, localized to Y356. Using 3,5-difluorotyrosine (F3Y) at Y731 (or Y736) we demonstrated that Y356• equilibrated with F3Y731• or F3Y730•.14 The analysis was facilitated by the unique F3Y• features arising from 19F and 1H-β hyperfine interactions that are observed in both the low- and high-field regions of the EPR spectrum.11,13 This spectroscopic handle gave us the first opportunity to investigate the effect of the protein environment on the reduction potentials of the pathway Y•s. Quantitation of Y356• in β2 and F3Y731• (or F3Y730•) in α2 by EPR spectroscopy allowed estimation of a ΔE°(Y356/Y731) of ~100 mV.14 The thermodynamic landscape of the RT pathway constructed from these studies is shown in Figure 1. We proposed that the overall

equilibrate F3Y122• and Y356• with Y731-F-α2 also provided the opportunity to investigate the fate of the Y356• proton upon oxidation of this pathway Y. A plot of the log([Y356•]/[F3Y122•]) versus pH provides a slope of 1.2 ± 0.2 at 25 °C, consistent with rapid release of the Y356• proton to solvent. With a knowledge of the pH dependence of the F3Y122•/Y356• equilibration, we have implemented an experimental design to determine the thermodynamic difference between Y122 and Y356. Increasing amounts of Y356• are observed with increasing pH. Additionally, by choosing an appropriate pH the reduction potential of F2Y can be tuned to be essentially equal to that of Y122,15–21 but oxidized F3Y• has the potential to be spectroscopically observable because of the 19F hyperfine features.12 Thus, the ability of Y122• to oxidize F2Y incorporated in place of Y356 (F2Y356/F2) was tested. Rapid freeze-quench (RFQ)-EPR spectroscopy of the reaction between F3Y356/F2, Y731-α2, CDP, and ATP at pH 8.2 and 25 °C revealed F3Y356• at 3 ± 1% of the total radical concentration. This observation provided a ΔE°(F3Y122•-/Y356•) of 0.7 ± 0.6 mV, which along with our recent measurement of the reduction potential of F2Y in a protein environment15–21 gives an estimate of ΔE°(F3Y122•-/Y356•) of ~100 mV at pH 7.6. The results of the site specifically incorporated unnatural amino acids described herein together with our previous studies allow us to propose a thermodynamic landscape for the RT pathway in the E. coli class Ia RNR that is ~200 mV uphill between Y122 and C459•.

Figure 1. Proposed thermodynamic landscape of the PCET pathway at 25 °C and pH 7.6. The overall reaction is proposed to be thermodynamically uphill and driven forward by the rapid irreversible loss of water from NDP substrate in the active site of α2. No direct evidence is available for the presence of a discrete Wα radical intermediate. Studies performed on NO2Y122•/β2 determined the relative reduction potentials of Y356 Y731, and Y356•.

RT pathway in wt RNR is thermodynamically uphill and driven forward by the nucleotide reduction process, specifically the rapid irreversible cleavage of the C2–OH bond18 of the substrate and loss of water (10−6–10−5 s−1)19–21 in the active site of α2. Equilibration of the pathway Y•s could be measured because oxidation of Y356• by NO2Y122• is irreversible. Unfortunately, this same feature prohibited use of NO2Y122•/β2 to monitor equilibration of NO2Y122•/Y736•. To obtain insight over the entire thermodynamic landscape of RNR, ΔE°(Y122•-/Y356•) must be defined. A recently engineered β2 containing 2,3,5-trifluorotyrosine (F3Y) at position 122 provides an avenue to assess the ΔE°(Y122•-/Y356•) energetics.15,22 The reactivity of F3Y122•/β2, α2, CDP, and ATP results in rapid formation of dCDP concomitant with loss of water from NDP substrate in the active site of RNR, and F2Y731• and Y730•.17 Using the thermodynamic landscapes of the RT pathway constructed from these studies is shown in Figure 1. We proposed that the overall

equilibrate F3Y122• and Y356• with Y731-F-α2 also provided the opportunity to investigate the fate of the Y356• proton upon oxidation of this pathway Y. A plot of the log([Y356•]/[F3Y122•]) versus pH provides a slope of 1.2 ± 0.2 at 25 °C, consistent with rapid release of the Y356• proton to solvent. With a knowledge of the pH dependence of the F3Y122•/Y356• equilibration, we have implemented an experimental design to determine the thermodynamic difference between Y122 and Y356. Increasing amounts of Y356• are observed with increasing pH. Additionally, by choosing an appropriate pH the reduction potential of F2Y can be tuned to be essentially equal to that of Y122,15–21 but oxidized F3Y• has the potential to be spectroscopically observable because of the 19F hyperfine features.12 Thus, the ability of Y122• to oxidize F2Y incorporated in place of Y356 (F2Y356/F2) was tested. Rapid freeze-quench (RFQ)-EPR spectroscopy of the reaction between F3Y356/F2, Y731-α2, CDP, and ATP at pH 8.2 and 25 °C revealed F3Y356• at 3 ± 1% of the total radical concentration. This observation provided a ΔE°(F3Y122•-/Y356•) of 0.7 ± 0.6 mV, which along with our recent measurement of the reduction potential of F2Y in a protein environment15–21 gives an estimate of ΔE°(F3Y122•-/Y356•) of ~100 mV at pH 7.6. The results of the site specifically incorporated unnatural amino acids described herein together with our previous studies allow us to propose a thermodynamic landscape for the RT pathway in the E. coli class Ia RNR that is ~200 mV uphill between Y122 and C459•.

Materials

Materials. (His)6-Y731F-α2,26 (His)6-Y356F-α2,26 wt-α2 (specific activity of 2500 nmol/min/mg),26 tyrosine phenol lyase,27 F2Y,28 and F3Y28 were isolated; apo F3Y122•/β2 was expressed, isolated, and reconstituted22 as previously reported. F3Y356/F2 (0.7 Y•/β2) was available from an earlier study.22 CDP and ATP were purchased from Sigma-Aldrich. Assay buffer consists of 50 mM HEPES pH 7.6, 15 mM MgSO4, and 1 mM EDTA unless otherwise specified. In all studies, the temperature was controlled using a Lauda RM6 circulating water bath. The reference spectrum for F3Y122• and its simulation were recently reported.20 The reference spectrum for Y356•, which was obtained as the signal averaged sum of the Y356• difference spectra, is in agreement with the previously reported spectrum.27

Hand-Quench EPR Analysis of Y356• Formation as a Function of Temperature. Assay mixtures containing a final volume of 250 μL with 25 μM Y356F-α2, 1 mM CDP, and 3 mM ATP in assay buffer were incubated in a water bath set between 2 and 37 °C. F3Y122•/β2 (0.8 F3Y•/β2) was added to a final concentration of 25 μM to initiate each of the reactions. The reaction mixtures were then transferred to X-band EPR tubes maintained in the water bath, and the samples were frozen in liquid isopentane (−140 °C) at 20 s (or 1 min) and analyzed by X-band EPR spectroscopy. The EPR parameters were as follows: microwave frequency 9.45 GHz; power 30 μW; modulation amplitude 1.50 G; modulation frequency 100 kHz; time constant 40.96 ms; and conversion time 20.48 ms. Three independent sets of experiments were carried out.

Analysis of EPR Data. Two different methods, A and B, were used for quantitation of the two radicals due to the small changes in the EPR spectra associated with the changes in T and pH (section described subsequently), the complexity of the spectra, and the half-sites reactivity of RNR (that is, 50% of the starting F3Y•/β2 remains unchanged). The data shown in the Results section were analyzed by method A, chosen for visualization purposes. Both methods of analysis provide similar outcomes and are summarized in Tables S1 and S2. The total spin remained unchanged in all the samples throughout the analysis. The ΔE°(F3Y122•-/Y356•) was calculated based on the two quantitation methods described below and using

$$\Delta E^\circ = \frac{RT \ln K_{S\alpha}}{F}$$

(1)
where \( K_{\text{eq}} = \frac{[Y_{356} \beta]}{[F_3 \beta] Y_{356}} \), \( R \) is the ideal gas constant, \( T \) is the temperature (K), and \( F \) is Faraday’s constant.

**Method A: Quantitation of \( F_2 Y_{122} \) and \( Y_{356} \) in \( \beta 2 \) as a Function of Temperature.** Each EPR spectrum was normalized to have the same intensity in the low-field features associated with \( F_2 Y_{122} \). This representation of the spectra, the intensity of \( F_2 Y_{122} \), remains constant, allowing easier visualization of the \( Y_{356} \) signal that grows in with increasing temperature. Using the low-field features in the spectrum of \( F_2 Y_{122} \), \( F_2 Y_{122} \) was subtracted from each composite spectrum. The amount of \( Y_{356} \) remaining was determined by double integration. The \( Y_{356} \) spectrum observed for each sample was identical by this method.

**Method B.** A detailed description of data analysis by method B is presented in the Supporting Information. In the first step, the baseline was removed from each spectrum with a second-order polynomial fit.

In the second step, the 50% signal from \( F_2 Y_{122} \) that remains in the composite spectra due to half sites reactivity was subtracted using the \( F_2 Y_{122} \) reference spectrum (Figure S1A). The resulting composite spectra show the conversion between \( F_2 Y_{122} \) and \( Y_{356} \) as a function of temperature (Figure S1B), free from the complications caused by half sites reactivity. However, this subtraction increases the noise level of the spectra, so the relative amounts of \( F_2 Y_{122} \) and \( Y_{356} \) cannot be determined reliably by eye. Therefore, a script was written in Matlab 2016a to automatically subtract out the remaining \( F_2 Y_{122} \). The amount of remaining \( F_2 Y_{122} \) was determined by adjusting the intensity of the \( F_2 Y_{122} \) reference spectrum (Figure S1C) until the least-squares difference between the reference spectrum and the composite spectra in the g-value interval between 2.0363 and 2.0390 (this defines the highest S/N region of the low-field \( F_2 Y_{122} \) features) was minimized. The amount of \( Y_{356} \) after subtracting out the remaining \( F_2 Y_{122} \) was determined by double integration. The \( Y_{356} \) spectrum determined by this method was the same in each sample (Figures S1D and S2).

**RESULTS**

**Temperature-Dependent Equilibration of \( F_2 Y_{122} \) and \( Y_{356} \) within the Same Sample.** To support equilibration between \( F_2 Y_{122} \) and \( Y_{356} \) in \( \beta 2 \) (at 25 °C) as described above in the 14YR and 15YR-\( \alpha 2 \) reactions, the EPR spectrum of the 20 s sample was first recorded. Each sample was then thawed by submersion into a room-temperature water bath and was then incubated in a 2 °C water bath for 15 s followed by refreezing and reacquisition of the EPR spectra. The samples were thawed again and then placed in a 2 °C water bath for 15 s, refrozen, and the EPR spectrum recorded. Quantitation of \( Y_{356} \) and \( F_2 Y_{122} \) was performed as described above.

**RFQ-EPR Analysis of \( Y_{356} \) Formation as a Function of Temperature.** RFQ experiments were performed on an Update Instruments 1019 syringe ram unit and a model 715 syringe ram controller (ram speed 1.25 cm/s). \( F_2 Y_{122} \) (70 mM, 0.8 \( F_2 Y_{122}/\beta 2 \)) and CDP (2 mM) in assay buffer in one syringe were mixed with \( Y_{356} F-\alpha 2 \) (70 mM) and ATP (6 mM) in a second syringe and incubated at varying temperatures (2–37 °C) for either 4 or 10 s. The reaction mixture was then sprayed into liquid isopentane (31), and the \( 19F \) and \( 13C \) features of the \( F_3 \) \( F_{14} \) hyperfine tensor (54, 52, and 54 MHz) were in Matlab R2015b. The v5.0.1832 in Matlab R2015b. The total number of scans were 700 (10 s sample), 600 (20 s sample), and 560 (40 s sample). The simulations were carried out using EasySpin v5.0.182. The g-values (2.0073, 2.0044, and 2.0022) and \( \beta 2 \) hyperfine tensor (54, 52, and 54 MHz) were fixed in the simulations using previously reported values for \( Y_{356} \) in the reaction of NO\(_2\) and Y731F-\( \alpha 2 \) with Y731F-\( \alpha 2 \) (14) and the \( \beta 2 \) hyperfine values of \( F_2 Y_{122} \) (22).

**Figure 2.** X-band EPR spectra of equimolar concentrations of \( F_3 Y_{122} \) (pink) and \( Y_{356} \) (blue). All spectra presented subsequently are additive and contain the same concentration of \( F_2 Y_{122} \) and increasing amounts of \( Y_{356} \). The dotted lines highlight the regions of the spectrum where the changes that occur upon \( Y_{356} \) formation are most apparent.
with active β2 containing a F3Y122• in each β monomer.22 Furthermore, while the active form of RNR is α2β2, the enzyme exhibits half-sites reactivity where only one of the two Y122•’s (one α/β pair) is active at a time.22 A consequence of these phenomena is the presence of 50% of the total spin as residual F3Y122• in all reaction mixtures. Thus, the data shown in Figures 3, S3, and S4 are presented using method A.

![Figure 3](https://example.com/figure3.png)

**Figure 3.** Composite EPR spectra of the F3Y122•/β2/Y122•F-α2/CDP/ATP reaction as a function of temperature (2–15°C). The composite spectrum at each temperature was acquired on three independently prepared samples. (A and B) Low- and high-field regions of the spectra for trial 1 are shown here. The color code is described in panel A. Trials 2 and 3 are shown in Figure S3. The composite EPR spectra collected between 15 and 37°C are shown in Figure S4. (C and D) Low- and high-field regions of a simulated spectrum of a reaction mixture containing 50% each of F3Y122• and Y356•. The spectrum was generated by adding the individual spectra of F3Y122• and Y356• (Figure 2). The dotted lines identify spectral features that are characteristic of Y356•.

![Figure 4](https://example.com/figure4.png)

**Figure 4.** Temperature dependence (2–37°C) of Y356• formation in the reaction of F3Y122•/β2, CDP, ATP, and Y731F-α2 (pink) or Y731F-α2 (blue). Each data point represents the average of two (blue) or three (pink) independent trials.

Control Experiments to Support F3Y122•/Y356• Equilibration. Two types of experiments were carried out to provide further support for the equilibration of F3Y122• and Y356•. Previous studies on adenosylcobalamin (AdoCbl) class II RNR23 have shown that slow quenching of samples by hand shifts the equilibrium relative to rapid freezing methods. Thus, changing ratios of F3Y122• and Y356• by RFQ would support equilibration of the two radical states. Preliminary experiments revealed no spin loss and minimal changes in the EPR spectra of samples quenched at 4 and 10 s using the RFQ method. The time scale for quenching was chosen based on kinetic experiments performed with F3Y122•/β2 and wt-α2.22 Thus, subsequent RFQ samples were quenched at 10 s. The results of these experiments are shown in Figure S5 and summarized in Table S1. The amount of Y• observed by RFQ is 5–10% higher than that recorded by the HQ method. However, similar trends are observed between the RFQ-EPR and HQ samples. Increasing amounts of Y356• are observed between 2 and 15°C, whereas the spectra collected between 15 and 37°C show minimal changes in the percentage of Y356• (Table S1 and Figure S6). The RFQ and HQ methods together support equilibration of F3Y122• and Y356• and the ability to shift the equilibrium between the two radical states based on the quenching method.

A second experiment to support equilibration between F3Y122• and Y356• was carried out as described in the Materials and Methods section. In this experiment, the EPR spectrum of a single sample that was equilibrated at 25°C was first measured and the sample thawed, equilibrated at 2°C, and reanalyzed by EPR spectroscopy. The sample was then thawed a final time, shifted back to 25°C, and the EPR spectrum was recorded. The composite EPR spectra are shown in Figure S7A,B, and the amounts of Y356• ascertained from these spectra are summarized in Table S3. The total spin changed minimally and the ratio of the two radicals shifted with temperature as predicted by the trend observed in Figure 4. The data together support equilibration of F3Y122• and Y356• with an unusual temperature dependence.

Effect of the F Block at Residue 731 in α2 on the F3Y122•/Y356• Equilibrium. Recent high-field (HF)-EPR spectroscopy experiments indicate that the electrostatic environment of Y356• changes in a reaction containing Y731F-
alpha2 relative to wt-alpha2. Differences in reactivity between wt-alpha2 and Y731F-alpha2 are also recorded for photo-RNR, which contains a [Re(V)] photooxidant appended to the C-terminal tail of beta2 (S355C). We therefore posited that the block at 731 could perturb the reduction potential of Y356 compared to the wt enzyme. The equilibration experiments were repeated with Y730F-alpha2, and as seen in Figure 4 (blue dots), variations can be observed between Y731F-alpha2 and Y730F-alpha2, with the former construct generating slightly higher amounts of Y356.

**Calculation of \( \Delta E^\alpha (F_3Y_{122} - Y_{356}) \) from the Y731F and Y730F-alpha2 Studies.** To calculate the reduction potential difference between F3Y122 and Y356, the ln Kd (\([Y_{356}] / [F_3Y_{122}]\)) observed in the Y731F and Y730F-alpha2 reactions at 25°C by the HQ method were used (eq 1): \( \Delta E^\alpha (F_3Y_{122} - Y_{356}) \) at 25°C is 20 ± 10 and 5 ± 7 mV, respectively. We note again the unusual temperature dependence of the Y356 amounts with a break at 15°C. A similar temperature dependence has been noted for steady-state dNDP formation in a 1976 study by von Dobeln and Reichard. The cause(s) of the break in Figure 4 and in the previous activity studies are unknown but are likely related to RNR conformational changes that rate-limit RT and nucleotide reduction.

**Equilibration of F3Y122- and Y356- as a Function of pH and Rapid Proton Exchange with Solvent during Y356 Oxidation.** The equilibration of F3Y122- and Y356- described above gave us the opportunity to investigate the fate of the proton released upon Y356 oxidation. Two scenarios for this proton transfer (PT) can be envisioned (Scheme 1). In one case, the proton from Y356 is transferred to an amino acid residue (X) and is not solvent-exchangeable. (B) The proton is in fast exchange with solvent. The initial proton acceptor (Y) is either an amino acid residue or water.

(Scheme 1. Proposed Models for the Fate of the Y356 Proton)

\( F_3Y_{122}O^{-}/Y_{356}O^{-} + H^+ \) is accepted by an amino acid residue (X) and is not solvent-exchangeable. (B) The proton is in fast exchange with solvent. The initial proton acceptor (Y) is either an amino acid residue or water.

**Figure 5.** Composite EPR spectra of the F3Y122-/beta2/Y731F-alpha2/CDP/ATP reaction at 25°C as a function of pH. The composite spectrum for each pH was acquired on two independently prepared samples. (A and B) The low- and high-field regions of the spectra for trials 1 are shown here. The colors represent different pH values as described in panel A. Trial 2 is shown in Figure S8. (C and D) Low- and high-field regions of a simulated spectrum of a reaction mixture containing 50% each of F3Y122- and Y356-. The spectrum was generated by adding the individual spectra of F3Y122- and Y356- (Figure 2). The dotted lines identify spectral features that are characteristic of Y356-

**Figure 6.** pH dependence of Y356- formation in the reaction of F3Y122-/beta2/Y731F-alpha2/CDP/ATP at 25°C. (A) Percentage Y356- as a function of pH. (B) log K as a function of pH where K is the ratio of Y356- to F3Y122-. The observed pH dependence of slope 1.2 ± 0.2 supports that the Y356- proton is in fast exchange with solvent.

**Figure 6A** shows the percentage of Y356- for the pH range 6.8–8.0 at 25°C (see Figure S10A for data from pH 6.8–7.8 for 5°C). The percentage of Y356- at pH 6.8 and 7.0 are very low (Table S2), and the percentage of Y356- above pH 8.0 at 25°C and pH 7.8 at 5°C does not change. The maximum amounts of Y356- at 25°C are carried out using method A. As with the temperature dependent studies, no variations in total spin were recorded, and no differences were observed between the spectra of samples incubated for 20 s and 1 min, observations consistent with a reaction at equilibrium. The spectral changes are shown in Figure 5A,B, and the dotted line shows an increase in the

**% Y356**
\( \Delta C \) (43%) and \( \Delta C \) (31%) reflect the equilibrium concentrations of Y356 at each temperature.

The dependence of \( \log([Y_{356}]/[F_{2}Y_{122}]) \) on pH at 25 and 5 \( \circ \)C is measured in Figures 6B and S10B, respectively. A slope of 1.2 \pm 0.2 is measured at 25 \( \circ \)C (1.0 \pm 0.1 at 5 \( \circ \)C) supporting the model in which the proton from Y356 is in fast exchange with solvent at both temperatures. Y356 formation is favored more at 25 \( \circ \)C compared to 5 \( \circ \)C, an observation that is in accordance with our temperature-dependent distribution between the two radicals (Figure 4).

**Equilibrium of Y_{122}** and F_{2}Y_{356} Using F_{2}Y_{356}/\beta2/\alpha2/CDP/ATP. Although the above studies allowed establishment of \( \Delta E^{\circ}(F_{2}Y_{122}-Y_{356}) \) in F_{2}Y_{122}/\beta2, the \( \Delta E^{\circ}(Y_{122}-Y_{356}) \) in wt RNR, which is essential for understanding the thermodynamics of the RT pathway, remains unknown. The pH studies described above show that maximum Y356 is generated with F_{2}Y_{122}/\beta2 at pH 8.0 or greater and 25 \( \circ \)C. Recent studies suggest that the difference in reduction potential between Y and F_{2}Y at position 356 at pH 8.2 is small (<10 mV) and that the activity of F_{2}Y_{356}/\beta2 at this pH is 50% of the wt activity. The pK_{a} of F_{2}Y_{356} is estimated to be 7.6 at position 356, thus, at pH 8.2, >80% of F_{2}Y_{356} is in the deprotonated state. Due to the ability to detect small amounts of F_{2}Y utilizing its unique spectroscopic features in the low- and high-field regions of the EPR spectrum, we carried out the following experiment in the hope of obtaining insight about \( \Delta E^{\circ}(Y_{122}-Y_{356}) \), F_{2}Y_{356}/\beta2, Y_{731}F-\alpha2, CDP, and ATP were reacted at pH 8.2 for 10, 20, or 40 s, and the reaction was quenched using the RFQ instrument and analyzed by EPR. Quenching on the millisecond time scale was used to avoid potential shifting of the equilibrium observed with hand quenching (Table S1 and Figure S6). The RFQ-EPR data for the reaction at 20 s are shown in Figure 7, and the 10 and 40 s data are shown in Figure S11. A view of the entire spectrum is shown in the inset in Figure 7. The results reveal small features on the low- and high-field sides that suggested the presence of F_{2}Y_{356}. The resolved hyperfine splittings were simulated with the "pepper" module of EasySpin as described in the Methods section. From the initial simulations, it was recognized that the \( \beta-^{3}H \) hyperfine parameters matched the doublet splitting on the high-field side of the spectrum, confirming the identity of this radical species as F_{2}Y_{356}. The interdoublet splitting was reproduced with two equivalent \( ^{19}F \) couplings having an \( A_{zz} \) of 147 MHz. The sharpness of the \( 3.5-^{19}F \) features are similar to those previously reported for the other pathway residues F_{2}Y_{122}, F_{2}Y_{731}, and F_{2}Y_{730} reflecting a rigid conformation constrained by the protein environment. The \( A_{zz} \) value for F_{2}Y_{356} is slightly weaker than those reported previously for the other F_{2}Y's (Table S4) and will be of importance when structural insight is obtained.

The amount of F_{2}Y_{356} was similar at all three time points and was approximated from the simulated spectrum by matching the signal intensities of the wing features in the experimental and simulated spectra and comparing the double integral of the two. The greatest source of error in the analysis comes from the intrinsic line broadening factor (17 \pm 4 MHz) used in all simulations. The amount of F_{2}Y_{356} in the 20 s sample was quantitated as 3 \pm 1% of total spin. This amount of radical reflects \( \Delta E^{\circ}(F_{2}Y_{356}-Y_{122}) \) of 70 \pm 5 mV, which in combination with our reduction potential studies allows calculation of \( \Delta E^{\circ}(Y_{356}-Y_{122}) \) of \( \sim100 \) mV at pH 7.6 (Figure 8).

**Discussion**

RNRs are divided into three classes based on the metallocofactor used for thyl radical formation. All classes of RNR initiate nucleotide reduction by thyl radical mediated 3'-H atom abstraction from the substrate. The reducing equivalents for the reaction are provided by oxidation of a pair of cysteines in the active site with a subtype of the class III enzyme which uses formate as the reductant as the sole exception. The class II RNR utilizes adenosylcobalamin as a cofactor, whereas the class III system uses a stable glycyl radical to generate the transient thyl radical. These...
observations raise the issue of why and how a 35 Å oxidation process evolved in the class I RNR instead of a direct H atom abstraction process that is used by the other classes.\textsuperscript{18} The turnover number for deoxynucleotide formation (2−10 s\textsuperscript{−1})\textsuperscript{43} and the large distance between Y₁₂₂ and C₄₃₉ in the class I RNR\textsuperscript{9,44} require intermediates in the oxidation process and raise the question of how the thermodynamic and kinetic landscape of this process has evolved to maintain balanced dNTP pools and avoid self-inactivation. Investigation of this oxidation process has proven challenging primarily due to the slow rate-limiting conformation changes that occur in the αβ/β complex subsequent to S/E binding and prior to RT.\textsuperscript{43} Furthermore, the substantial overlap of the EPR spectra of YF\textsuperscript{−}s would make identification of these species challenging even if the rate-limiting step could be altered.

Thermodynamic Landscape of the RT Pathway within the β Subunit. Recently we have assembled the dimeric NO₂Y₁₅₆• cofactor (t₁/₂ of 40 s at 25 °C) in the β subunit of RNR. NO₂Y₁₅₆• is ~200 mV more oxidizing than Y₁₅₆\textsuperscript{−}\textsuperscript{16} and has provided insight about the thermodynamic landscape for the RT pathway in two ways. When NO₂Y was substituted in place of each Y₇₃₁ in the pathway (Figure 1, where x = 122 and 356 in β and 731 and 730 in α2), the resulting mutants were all catalytically inactive.\textsuperscript{15} Thus, perturbation of the reduction potential by +200 mV is sufficient to shut down the RT pathway. This observation supports previous proposals about the extent to which uphill steps can be accommodated in electron transfer (ET) pathways in general,\textsuperscript{45,46} and in RNR specifically.\textsuperscript{46,47} NO₂Y substitution at each position also allowed assessment of the protein environment perturbation of the pKₐ of the phenol, relative to the pKₐ in solution. Positions 356, 731, and 730 were found to be minimally perturbed (+0.4, 1.0, and 1.2 units) and position 122 was found to be greatly perturbed (greater than +3 units).\textsuperscript{15} We assume that a similar position-dependent perturbation occurs with the F₂Y’s incorporated at 356, 731, and 730. However, given the unique environment of Y₁₂₂ (hydrophobic and adjacent to the d ferric cluster), this assumption cannot be made.

The ability to generate NO₂Y₁₅₆• in β allowed observation of the equilibration of the pathway tyrosyl radicals: Y₁₇₃₁•, F₂Y₁₇₃₀•, or F₃Y₁₇₃₀•. This observation was fortuitous as the equilibration arose from several unanticipated consequences of NO₂Y₁₅₆• substitution. First, this mutant uncoupled the conformational gating masking the wt RT process. DeoxyCDP and Y₁₅₆• formed during reverse RT occurred at 100−300 s\textsuperscript{−1},\textsuperscript{13} much faster than the wt turnover of 5 s\textsuperscript{−1}.\textsuperscript{43} Although Y₁₅₆• was generated rapidly, it was unable to reoxidize the NO₂Y• phenolate formed during forward RT (Scheme 2). Thus, a block in the pathway occurred without additional mutations. We note that in wt RNR there is evidence to suggest that a proton is delivered to Y₁₂₂• from the water on Fe1 in the cluster during forward RT (Scheme 2).\textsuperscript{28} In the case of NO₂Y, this does not occur, and the phenolate is formed. It is likely that the water on Fe1 remains protonated providing insight into the relative pKₐ of Y₁₂₂ and Fe1−H₂O. Since the NO₂Y phenol has a pKₐ of 7.1, this raises issues about the protonation state of F₃Y₁₅₆• (pKₐ of phenol is 6.4) on reduction during forward RT (Scheme 2).

Due to the inability to investigate equilibration of Y₁₅₆• with Y₇₃₁• and Y₇₃₀• in wt RNR, F₂Y was inserted in place of either Y₇₃₁ or Y₇₃₀ providing access to the unique EPR spectroscopic features of F₂Y\textsuperscript{−}.\textsuperscript{14} These experiments showed the presence of 10−15% F₂Y₇₃₁• (or F₂Y₇₃₀•). A knowledge of the pKₐ perturbation of ~1 unit at these positions\textsuperscript{15} in conjunction with differential pulse voltammetry (DPV) studies on the N-acetyl-3,5-difluoro-L-tyrosinamide\textsuperscript{24} provided an estimate of 85−95 mV for the reduction potential difference between Y₇₃₁• (or Y₇₃₀•) and Y₁₅₆•. This calculation agreed with the results from a second experiment where NO₂Y₁₂₂•/β2 was reacted with [β₂H₂]Y-α2 and probed for variations in the EPR spectrum. Temperature dependent studies provided the ∆E°(β₂H₂[Y−Y₁₂₂•]−Y₁₅₆•) of ~100 mV (Figures 1 and 8). These studies together showed that the RNR protein environment perturbs F₂Y and Y in a similar fashion and that F₂Y is a good probe for the reduction potential of both Y₇₃₁ and Y₇₃₀.

More recently, we have reported the detailed kinetic analysis of the Y₇₃₁•/β2/α2/CDP/ATP reaction.\textsuperscript{22} This reaction generates a kinetically and chemically competent Y₇₃₁• at 20−30 s\textsuperscript{−1}, which in contrast to Y₁₅₆• generated by NO₂Y₁₂₂•/β2 is capable of reoxidizing F₃Y₁₂₂. The reoxidation process is conformationally gated and rate-limiting for subsequent dCDP formation and only observed after several turnovers upon exhaustion of the reducing equivalents. The observation of both radicals (F₃Y₁₂₂• and Y₁₅₆•) and activity required that we utilize a pathway block in order to monitor equilibration. Y₇₃₁•F₂α2 and Y₇₃₀•/F−α2 served that purpose as our previous studies showed that these mutants still allow Y₁₅₆• generation.\textsuperscript{13} To quantitate the reduction potential increase that occurs upon replacement of Y₁₂₂ with F₃Y₁₂₂, it is important to determine whether the latter is reduced to the phenol or phenolate (F₃Y₁₂₂ vs F₃Y₁₂₂•) upon replacement of Y₁₂₂ with F₃Y₁₂₂, it is important to determine whether the latter is reduced to the phenol or phenolate (F₃Y₁₂₂ vs F₃Y₁₂₂•) upon replacement of Y₁₂₂ with F₃Y₁₂₂, it is important to determine whether the latter is reduced to the phenol or phenolate (F₃Y₁₂₂ vs F₃Y₁₂₂•) and activity required that we utilize a pathway block in order to monitor equilibration. Y₇₃₁•F₂α2 and Y₇₃₀•/F−α2 served that purpose as our previous studies showed that these mutants still allow Y₁₅₆• generation.\textsuperscript{13}
protonation state of $F_3Y_{122}$ while favored to be deprotonated, is unknown and is under investigation.

The potential difference of $\sim 20 \text{ mV}$ calculated between $F_2Y_{356}$ and $Y_{356}$ (Figure 4) makes generation of $F_2Y_{122}$ an appealing model. We predict that $\Delta E^\text{O氧化}/(NO_2Y_{122}/NOY_{122}^-)$ and $\Delta E^\text{O消極}/(NOY_{122}/NO_2Y_{122}^-)$ is $\geq 200 \text{ mV}$, owing to the inability of $Y_{356}$ to reoxidize NOY$^-$. With these two values, we can estimate $\Delta E^\text{O氧化}/(NO_2Y_{356}/NOY_{356}^-) = \Delta E^\text{O消極}/(NOY_{356}/NO_2Y_{356}^-) = \Delta E^\text{O氧化}/(NO_2Y_{356}/NOY_{356}^-)$ as greater than or equal to $\sim 184 \text{ mV}$. This calculation agrees with the predicted potential difference between these two analogs based on the solution DPV data collected on the protected amino acids ($\sim 180 \text{ mV}$). Unfortunately, we cannot at present directly extrapolate the potential difference calculated between $NO_2Y_{122}/NOY_{122}^-(or F_2Y_{122}/F_3Y_{122}) and Y_{356}/NOY_{356}$ to $Y_{122}/NO_2Y_{122}$. This is primarily due to the unique nature of residue 122’s environment compared to that of the other pathway’s Y’s. The $Y_{122}$ site is not in equilibrium with solvent $^{46}$ over the time course of our experiments ($<20 \text{ s}$); its reduction potential is pH-independent and is directly determined by the dielectric constant of the protein environment. Due to these reasons, we turned our attention to an alternate way to monitor equilibration of $Y_{122}$ and $Y_{356}$ where the native $Y_{122}$ remains intact but $Y_{356}$ is replaced with $F_3Y_{356}$.

Our observations with $NO_2Y_{122}/F_3Y_{122}$ $^{24,25}$ and the pH-dependent studies reported herein suggest that $\Delta E^\text{O氧化}/(Y_{122}/Y_{122}) = \Delta E^\text{O消極}/(F_2Y_{356}/F_2Y_{356})$ can be easily extrapolated from $\Delta E^\text{O氧化}/(F_2Y_{356}/F_3Y_{122}) = \Delta E^\text{O消極}/(F_3Y_{356}/F_3Y_{122})$. The proton from $F_2Y_{356}$ is in rapid exchange with solvent (Figures 6B and S10B), and at an appropriate pH, we predict that its reduction potential is a good approximation of $Y_{356}$. The reaction of $F_2Y_{356}/F_3Y_{122}$ and $Y_{356}/F_3Y_{122}$ is expected to be roughly the same. $\Delta E^\text{O氧化}/(F_3Y_{122}/F_3Y_{122})$ at $10, 20, and 40 \text{ s}$, supporting equilibration. The observed percentage of $F_2Y_{356}/F_3Y_{122}$ (3%) provides an estimation of $\Delta E^\text{O氧化}/(F_2Y_{356}/F_3Y_{122}) = \Delta E^\text{O消極}/(F_3Y_{122}/F_3Y_{122})$ of $\sim 70 \text{ mV}$. At pH 8.2, the reduction potentials of the $F_3Y_{122}/F_3Y_{122}$ and $Y_{356}/Y_{356}$ couples are predicted to be $\sim 100 \text{ mV}$ (Figure 8B). Finally, we note that our data taken together propose that at $25 \text{ °C}$ and pH 7.6 $F_2Y_{122}$ is $\sim 120 \text{ mV}$ more oxidizing than $Y_{122}$ within the RNR protein environment. This difference is 10 times greater than we had originally predicted based on the solution DPV data collected on the N-acetyl-fluoro-1-tyrosinamide derivatives. $^{11}$ We note that this original prediction assumed that both $F_2Y$ and $Y$ are reduced to the corresponding phenols during turnover.

### Relationship between the Thermodynamic Landscape and Kinetics

It is important to note that the equilibrium studies described in this work were performed under nonturnover conditions (with $Y_{731}$-F-$\alpha$2 or $Y_{730}$-F-$\alpha$2). Thus, a key issue to address is whether the protein environment can alter the thermodynamic landscape to lower $\Delta E^\text{O氧化}/(Y_{356}/Y_{356})$ and facilitate turnover. Although this is a likely possibility, we argue that oxidation of $Y_{356}$ by $Y_{122}$ must be uphill even under turnover conditions. Evidence for this conclusion is provided by our combined studies with wt RNR. $^{43}$ $F_2Y_{122}/F_3Y_{356}$ and $NOY_{122}/Y_{356}$.

In the case of wt RNR, investigation of RT has been hindered by the inability to monitor $Y_{122}$ disappearance and reappearance during turnover. $^{43}$ To account for this observation, we have previously modeled that the reverse RT process in wt RNR in which $Y_{356}$ reoxidizes $Y_{122}$ must be downhill and rapid ($10^3 \text{ s}^{-1}$). $^{43}$ In the case of $F_3Y_{122}/F_3Y_{356}$, we have measured formation of $Y_{356}$ ($\sim 20-30 \text{ s}^{-1}$) and demonstrated that reoxidation of $F_3Y_{122}$ by $Y_{356}$ is slow ($0.4-1.7 \text{ s}^{-1}$) and rate-limiting for multiple turnovers. $^{16,24}$ In the $NOY_{122}/Y_{356}$ system, $Y_{356}$ accumulates ($100-300 \text{ s}^{-1}$) due to the inability of this pathway radical to reoxidize NOY$^-$. $^{16,24}$ In accordance with this prediction, the rate constant for forward RT that generates $Y_{356}$ increases with increasing driving force, whereas the rate constant for reverse RT decreases with driving force, reinforcing our model that oxidation of $Y_{356}$ by the native $Y_{122}$ is uphill. We have previously proposed that the conformational change that triggers RT targets the initial PT step from Fe1–H2O to $Y_{122}$ ($^2$). $^{36}$ Uncoupled PT and ET in NOY$_{122}/Y_{356}$ and potentially F3Y$_{122}/Y_{356}$, suggest that we may have overcome this conformational gating and obtained direct insight into the thermodynamic effect of replacing Y122 with these unnatural analogs. Further support for this model is obtained when the forward RT rate constants in NOY$_{122}/Y_{356}$ and F3Y$_{122}/Y_{356}$ are predicted using the Moser–Dutton equation $^{12}$ (eq 3) for dependence of $k_{\text{ET}}$ on distance ($R$) and driving force ($\Delta G$).

$$\log k_{\text{ET}} = 15 - 0.6R - 3.1(\Delta G + \lambda)^2/\lambda$$

Assuming identical distances and reorganization energies ($\lambda$) for ET in NOY$_{122}/Y_{356}$ and F3Y$_{122}/Y_{356}$, the individual expressions for log $k_{\text{ET}}$ can be combined to assess the effect of the driving force differences ($\Delta G$, 200 mV vs 20 mV, Figure 8A) on $k_{\text{ET}}$. The net equation requires an estimation of $\lambda$; by varying the reorganization energy from 0.7 to 1.4 eV, $k_{\text{ET}}$ in NOY$_{122}/Y_{356}$ was calculated to be 9- to 11-fold faster than $k_{\text{ET}}$ in F3Y$_{122}/Y_{356}$. This approximation is similar to our experimental data (5- to 15-fold) supporting the idea that the driving force dictates the kinetics in these mutant RNAs and further that both NOY$_{122}$ and F3Y$_{122}$ are reduced to the corresponding phenolates during RT.

Based on our static thermodynamic picture constructed from the studies with NOY$_{122}/Y_{356}$ and those reported herein, we propose that the landscape from Y122 to Y730 is $\sim 200 \text{ mV}$ uphill (at $25 \text{ °C}$ and pH 7.6, Figure 8B). The landscape between Y730 and 3’ hydrogen atom abstraction from the nucleotide must further be taken into account to make deoxynucleotides. Electrochemical measurements on the cysteine within glutathione and Y have revealed similar midpoint potentials at pH 7.0, $^{53}$ providing an estimation of $\sim 0.04$% C439$^\bullet$ formation in the $\alpha2/\beta$2 complex. Given the predicted rate constant for H2O loss from the 2’ position (10$^{-10}$ – 10$^{-9}$ s$^{-1}$) $^{19-21}$ of the nucleotide, the rate of this reaction using 0.04% C439$^\bullet$ would be $\sim 10^2$ to 10$^3$-fold faster than conformationally gated nucleotide reduction ($2-10^2$ s$^{-1}$). $^{43}$

The above calculation assumes that the reaction landscape is isoe nergetic subsequent to generation of Y$^\bullet$. However, DFT calculations performed on the individual crystal structure of $\alpha2$ and on model systems have provided an estimate of $\sim 120 \text{ mV}$ for $\Delta E^\text{O氧化}/(C439\bullet/Y_{750})$ $^{54,55}$ and $\sim 90-260 \text{ mV}$ for 3’ H atom abstraction by C439$^\bullet$. $^{56-58}$ If the measured $\Delta E^\text{O氧化}/(Y_{750}/Y_{122})$ of $200 \text{ mV}$ is reflective of the thermodynamic landscape under turnover conditions, then we estimate that the combined
steps of C439 oxidation and 3’ H atom abstraction must be <200 meV uphill to maintain a turnover number of >10 s⁻¹.

The DFT calculations were based on a structure of α2 alone with poor electron density for the substrate and in the absence of allosteric effector. It is likely that the RT pathway and the active site in α2 will be conformationally altered in the active α2/β2/S/E complex. Furthermore, uphill reactions can be partially compensated for by decreasing the ET distance between donor and acceptor 5,6,46 and in the case of PCET reactions by controlling the positioning of the proton acceptor. The distances between Y122, Y356, and Y731 remain unknown because of the disordered C-terminal tail of β2. Thus, structures of the α2/β2 subunit interface and knowledge of how these structures are altered in the presence of S and E binding to α2 are crucial to understanding the overall landscape of the reaction and the tuning of the individual steps in the RT process. Nonetheless, we believe from the studies described herein, that the overall reaction from Y122• reduction to 3’-hydrogen atom abstraction of NDP is uphill and driven forward by rapid and irreversible loss of H₂O from the NDP (Figure 8). 19–21

PCET across the βα Interface Involves Fast Proton Exchange between Y356 and Solvent. The equilibrium between F₁Y₁₂₂• and Y₃₅₆• as a function of pH has further provided important insight about the fate of the Y₃₅₆ proton upon its oxidation. It was originally proposed that a specific sequestered amino acid residue within β2 functioned as the proton acceptor. However, the slope of 1 associated with a plot of log([Y₃₅₆•]/[F₁Y₁₂₂•]) versus pH (Figure 6B) is parallel to the rapid exchange of the Y₃₅₆ proton with solvent at the subunit interface either through an amino acid residue or a water cluster functioning as the initial proton acceptor (Scheme 1). Three distinct types of experiments are currently the basis for favoring the latter possibility. 29,35,37,59,60

The most compelling support for this model has been the work of Bennati and co-workers using multifrequency EPR and [3H]-electron–nuclear double resonance (ENDOR) spectroscopic methods on mutant RNRs containing the radical trap, 3-amino-tirosine (NH₂Y). This unnatural amino acid has site specifically replaced Y₁₅₆, Y₇₃₁, or Y₇₃₀ leading to accumulation of NH₂Y in each case upon incubation with the second subunit, S, and E. 26,61 HF-EPR studies on NH₂Y•₅ and NH₂Y•₇₃₀• specifically the gₛ component of their g tensors, revealed that the electrostatic environment of all three NH₂Y•’s are perturbed, but that of NH₂Y₃₅₆• is perturbed to a greater extent than either NH₂Y₇₃₁• or NH₂Y₇₃₀•. In contrast with NH₂Y₇₃₁• or NH₂Y₇₃₀•, no moderate hydrogen bonding interactions were observed with NH₂Y₃₅₆• by HF-[3H] ENDOR spectroscopy. 59 The studies together led to the proposed importance of water clusters in proton removal at the subunit interface. 59

Using a very different approach, recent studies have been carried out with photo-RNRs in which a photooxidant is attached site specifically to residue 35S in β2 and F₁Y (n = 2 or 3) or W replaces Y₃₅₆. In the presence of α2, S, and E and with light initiation, these constructs exert significant control in facilitating PT during oxidation of residue 356, shuttling reactive intermediates between the subunits and in the case of W, rapid PT out of the αβ interface. 55,60

Finally, prior to the studies reported herein, the conserved residue E₃₅₀ located on the flexible C-terminal tail of β2 near Y₃₅₆ in sequence space, was considered to be the most likely amino acid candidate that could function as a proton acceptor for Y₃₅₆. Mutation of E₃₅₀ to A abolished RNR activity, 57 an observation we have confirmed. 61,62 However, using our ability to incorporate FₘY analogs in place of RNR pathway residues, we have shown that E₃₅₀ is likely not the proton acceptor for Y₃₅₆ but that its essentiality stems from its involvement in subunit interaction and in the protein conformational gate for RT initiation. 59 The experiments presented herein, the E₃₅₀ studies, 59 the EPR and ENDOR results, 59 and the photo-RNR experiments 35,60 together support fast proton exchange between Y₃₅₆ and solvent via water during PCET across the interface.

Summary. Using site specifically incorporated FₘY and FₘY in place of β2 residues 122 and 356, respectively, and taking advantage of the unique EPR features of FₘY relative to Y, we have measured the thermodynamic landscape within β2 in the α2/β2 complex. These results, when combined with similar types of experiments examining the relative reduction potentials of Y₃₅₆, Y₇₃₁, and Y₇₃₀ provide us with the overall thermodynamic landscape that is uphill by >200 meV and is unprecedented in biology. Why would such a design evolve when other classes of RNRs avoid long-range RT by direct hydrogen atom abstraction from the cysteine by their active cofactors? We propose that the enzyme exerts significant kinetic control over radical initiation. RT in class I RNRs plays a very important role in the fidelity of DNA replication and repair by regulating the relative ratios of the dNDP (and hence dNTP) pools and the absolute amounts of these species. This process is largely controlled by binding the appropriate S/E pairs in α2, 40–50 Å removed from the site of RT initiation by the diferri- Y• cofactor. 49 Subtle changes that occur on S/E binding are thus likely to modulate the reduction potential of residues within the wt RT pathway. All of the experiments conducted to determine the thermodynamic landscape summarized in Figure 8 have been performed with different types of pathway blocks, which are likely to have subtle conformational effects on radical initiation. The proposed uphill nature of the pathway would prevent accumulation of reactive pathway radical intermediates and minimize self-inactivation during the radical initiation process. The connection between our current unprecedented and unexpected thermodynamic measurements and conformational gating of RNR activity by S/E binding is the major focus of our efforts.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/jacs.6b08200.

Temperature dependence of Y₃₅₆• formation; temperature-dependent equilibration of F₁Y₁₂₂• and Y₃₅₆• in the reaction of F₁Y₁₂₂•-β2, CDP, ATP, and Y₃₅₀F-α2 or Y₇₃₀F-α2; hyperfine values for β'-H and 19F of FₘY at different positions on pathway; analysis by method B for one trial of the F₁Y₁₂₂•-β2/Y₇₃₁F-α2/CDP/ATP reaction as a function of temperature and one trial of the F₁Y₁₂₂•-β2/Y₇₃₁F-α2/CDP reaction as a function of a hydrogen atom, and one trial of the F₁Y₁₂₂•-β2/Y₇₃₁F-α2/CDP reaction as a function of temperature; and one trial of the F₁Y₁₂₂•-β2/Y₇₃₁F-α2/CDP reaction as a function of temperature (2–15 °C) and the F₁Y₁₂₂•-β2/Y₇₃₁F-α2/CDP reaction as a function of temperature (15–37 °C); temperature dependence of Y₃₅₆• formation monitored by RFQ-EPR spectroscopy and in the reaction of F₁Y₁₂₂•-β2/Y₇₃₁F-α2/CDP/ATP as determined by HQ- and RFQ-EPR.
spectroscopies; temperature-dependent equilibration of F$_{Y122}$• and Y$_{108}$• in the reaction of F$_{Y122}$•/β, CDP, ATP, and Y$_{751}$F-α2 or Y$_{270}$F-α2; composite EPR spectra of the F$_{Y122}$•/β, Y$_{751}$F-α2/CDP/ATP reaction at 25 °C and the F$_{Y122}$•/β, Y$_{751}$F-α2/CDP/ATP reaction at 5 °C as a function of pH; pH dependence of Y$_{108}$• formation in the reaction of F$_{Y122}$•/β, Y$_{751}$F-α2/CDP/ATP at 5 °C; reaction of F$_{Y122}$•/β, Y$_{751}$F-α2, CDP, and ATP monitored by RFQ-EPR spectroscopy (PDF).

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**Notes**

The authors declare no competing financial interest.

**ACKNOWLEDGMENTS**

This work was supported by NIH grants GM29595 (to J.S.), GM47274 (to D.G.N.), and GM079190 (to C.T.). We thank James Mayer for suggesting the pH dependence studies and for helpful discussions regarding the temperature dependence work.

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