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Reversible, long-range radical transfer in *E. coli* class Ia ribonucleotide reductase

Ellen C. Minnihan[†], **Daniel G. Nocera**[¶,*], and **JoAnne Stubbe**[†,‡,*]

[†]Department of Chemistry, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139

[‡]Department of Biology, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139

[¶]Department of Chemistry and Chemical Biology Harvard University, 12 Oxford Street, Cambridge, MA 02138

Introduction

Ribonucleotide reductases (RNRs) catalyze the conversion of nucleotides (NDPs or NTPs where N = C, U, G, or A) to 2′-deoxynucleotides (dNDPs or dNTPs)[1] and are responsible for controlling the relative ratios and absolute concentrations of cellular dNTP pools. For this reason, RNRs play a major role in ensuring the fidelity of DNA replication and repair. RNRs are found in all organisms and are classified based on the metallocofactor used to initiate catalysis,[1] with the class Ia RNRs requiring a diferric-tyrosyl radical (Y•) cofactor.

The prototypical class Ia RNR from *E. coli*, the subject of this account, is composed of two subunits, α2 and β2, and is active as an α2β2 complex, as highlighted in Figure 1. α2 houses the catalytic site for substrate (S) reduction and two allosteric effector (E = ATP, dGTP, TTP, and dATP) binding sites that govern which S is reduced (specificity site) and the overall rate of reduction (activity site). β2 contains the essential diferric-Y• cofactor. This unusually stable Y•, located at position 122, has a $t_{1/2}$ of 4 days at 4 °C in contrast to the μs lifetimes observed for Y•s in solution. Nucleotide reduction occurs by a complex mechanism involving protein- and substrate-derived radicals, some details of which are summarized in Figure 2.[1,3] The stable Y_{122}• transiently oxidizes a cysteine (C_{439}) in the catalytic site to a thiyl radical (S•), which reversibly abstracts a 3′-hydrogen atom (H•) from the NDP. The 3′-nucleotide radical rapidly loses water in the first irreversible step.[1,3] The reducing equivalents are provided by two local cysteines (C_{225} and C_{462}), and the resulting disulfide is re-reduced for subsequent turnovers, ultimately by thioredoxin (TR), thioredoxin reductase (TRR), and NADPH.

Uhlin and Eklund proposed a structure of the active α2β2 complex by *in silico* docking of crystal structures of the individual subunits (Figure 1).[2] An atomic-resolution structure of an active class I RNR is still not available; however, recent experimental evidence supports this model (*vide infra*). The interaction between subunits is governed primarily by the flexible C-terminus of β2 (residues 360-375, Figure 1).[4] The most provocative feature of the docking model was the >35 Å distance between Y_{122}• in β2 and C_{439} in α2. The long distance suggested that direct oxidation of C_{439} by Y_{122}• by a singlestep, electron tunneling mechanism would be too slow (k_{ET} of 10^{-7} to 10^{-9} s^{-1}) to account for the turnover number

*To whom correspondence should be addressed: nocera@fas.harvard.edu, stubbe@mit.edu.

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of the *E. coli* RNR (~10 s^{-1}).[5] Accordingly, Uhlin and Eklund proposed that oxidation occurred by a hopping mechanism utilizing a specific pathway of conserved aromatic amino acids: Y_{122}• ↔[W48?]↔ Y_{356} in β2 to Y_{731} ↔Y_{730} ↔ C_{439} in α2. The necessity of these residues for catalysis was established by site-directed mutagenesis experiments.[6,7]

The thermodynamics of Y or W oxidation require that proton transfer (PT) accompanies electron transfer (ET) at physiological pH. In RNR, these transfers are proposed to occur in a concerted fashion to prevent formation of high-energy, charged intermediates, thereby requiring a proton-coupled electron transfer (PCET) at each step.[8-10] In our model, orthogonal PCET steps are operative in β2, with the proton and electron transferring from the same donor to different acceptors, whereas co-linear PCET steps are operative in α2, with the proton and electron moving between the same donor/acceptor pair (Figure 3a).[7,10,11] Our current model for the thermodynamics of radical transfer (RT) has evolved from studies in which the reduction potentials have been modulated at each Y on the pathway (Figure 3b).[12-14] It holds that the potentials increase from $Y_{122} < Y_{356} < Y_{731} \approx Y_{730} \leq C_{439}$, with the uphill forward oxidation driven by irreversible loss of H^2O during nucleotide reduction. We now give an account of the results that have given rise to our RT mechanism and thermodynamic model.

Tools

Protein engineering

The study of RT is complicated by the fact that the PCET events are masked in the wild-type (wt) RNR by rate-limiting protein conformational changes that occur upon binding of nucleotides to α2β2 prior to RT.[5] To perturb the native RT pathway in a predictable way, we have utilized two methods for site-specific incorporation of eight unnatural amino acids (UAAs) with altered reduction potentials and/or pK_as into RNR (Figure 4a, Table 1). One method involved the semisynthesis of β2 by expressed protein ligation (EPL),[15,16] whereas the second utilized *in vivo* nonsense codon suppression.[13,17] Current research utilizes the latter method, as it may be applied to any residue in either subunit, minimizes mutations to the native enzyme relative to EPL, and has allowed isolation of 100 mg quantities of protein (Figure 4b).

Kinetic techniques and spectroscopic methods

The reactivity of a mutant protein, once isolated, is studied by rapid kinetic techniques to unveil radical intermediates. In a typical experiment, a solution containing a mutant subunit (α2 or β2) and S is rapidly mixed with a solution containing the complementary wt subunit and E, and the reaction monitored with millisecond time resolution for loss of Y_{122}• and formation of a new radical(s) (Figure 5). Changes can be monitored continuously by stopped-flow (SF) UV-vis or fluorescence spectroscopies, or discontinuously using either a rapid freeze quench (RFQ) apparatus and paramagnetic resonance spectroscopy or a rapid chemical quench (RCQ) apparatus and scintillation counting of a radiolabeled product.

Figure 6 shows the spectroscopic signatures of the stable diferric-Y_{122}• in β2. The cofactor gives rise to a UV-vis spectrum with a sharp feature at 411 nm (Figure 6a) and an EPR spectrum (9 GHz) with hyperfine couplings associated with one of its two β-methylene protons and its 3,5 aromatic protons (Figure 6b). The *g* tensors [g_x, g_y, g_z) determined by high-field (HF) EPR (94 or 140 GHz) are particularly informative, as g_x is very sensitive to the electrostatic (i.e., H-bonding) environment of the Y• (Figure 6c). EPR and related methods, including pulsed electron-electron double resonance (PELDOR)[20] and HF [^{2}H]-electron nuclear double resonance (ENDOR)[21] spectroscopies, have allowed characterization of stable and transient radicals observed in engineered RNRs. Together, these methods have provided tools for the study of RT in RNR.

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Complexities in studying E. coli class Ia RNR

Two unresolved issues have complicated our mechanistic studies. The first is the apparent half-sites reactivity of RNR,[5,19] a phenomenon in which radical initiation occurs initially within a single α/β pair and a chemical or conformational step during or subsequent to product formation then triggers RT on the second α/β pair.[5] The second RT event is prevented when a radical is trapped in the first α/β pair by replacing the S with a mechanism-based inhibitor[20] or by modulating the energetics of RT using UAAs.[19,23] The second issue concerns the stoichiometry and distribution of Y_{122}• within β2. The diferric-Y• in β2 is self-assembled from apo-β2 to give ~1.2 Y•/β2 and while the loading of radical in each β monomer is unknown, our *in vitro* biochemical studies suggest it is evenly distributed (0.6 Y•/β).

Evidence for a pathway of redox-active amino acids

Our earliest experiments sought to validate the proposed pathway and the redox reactivity of its constituents (Figure 3a). The role of Y_{356} in the C-terminal tail of β2 was first studied, as its position relative to other residues is unknown (Figure 1). Using EPL, Y_{356} was replaced with 3,4-dihydroxyphenylalanine (DOPA, **2**, Figure 4a), which has a peak potential (E_p) 260 mV lower than Y (pH 7, Table 1) and was utilized as a radical trap. Reaction of Y_{356}DOPA-β2 with wt-α2, S, and E resulted in loss of 50% of the initial Y_{122}• concomitant with formation of an equal amount of $DOPA_{356}$•.[19] No $DOPA_{356}$• was observed in the absence of the second subunit or nucleotides. The kinetics of $DOPA_{356}$• formation involved multiple phases, the majority of which were kinetically competent (i.e., faster than the wt k_{cat}); however, the mutant was unable to make dNDP. These studies demonstrated that nucleotides are required to trigger RT and provided the first evidence for conformation changes associated with RT.

Our attention turned to investigating the roles of Y_{731} and Y_{730} in α2. In collaboration with the Schultz lab, an orthogonal tRNA synthetase (RS) that specifically recognizes 3-aminotyrosine (NH_2Y, **3**, Figure 4a] was evolved and was used to incorporate NH_2Y to positions 730 and 731 of α2 and 356 of β2 (collectively called NH_2Y-RNRs). With an E_p 190 mV lower than Y (pH 7, Table 1], NH_2Y was expected to behave like DOPA, as a radical sink. Indeed, reaction of each of the three NH_2Y-RNRs with the second subunit, S, and E resulted in the generation of an NH_2Y• kinetically coupled to Y_{122}• loss, as measured by SF UV-vis and EPR spectroscopy (Figure 7].[17,24] Radical formation again required the presence of both subunits and nucleotides, was biphasic, and was kinetically competent for all S and E pairs for all three NH_2Y-RNRs. In contrast to DOPA, however, all NH_2Y-RNRs were active in dNDP production. Additional experiments revealed that NH_2Y• was formed only when the other Ys in the wt RT pathway were intact. This result was interpreted as evidence that NH_2Y• formation is pathway-dependent and not the indirect consequence of introducing a thermodynamic trap into the protein.[25] Thus, results obtained with DOPA- and NH_2Y-RNRs support the participation of three Ys acting as redox relays linking Y_{122}• in β2 to C_{439} in α2.

Evidence for an active α2 β2 complex resembling the docking model

The ability to generate moderately stabilized NH_2Y•s ($t_{1/2}$ on min scale) at positions along the pathway coupled with the half-sites reactivity of RNR allowed us to test whether the docking model (Figure 1)[2] is an accurate representation of the active RNR. Specifically, PELDOR spectroscopy, a technique that detects weak dipolar interactions between paramagnetic species separated by 20-80 Å, was utilized to measure diagonal distances between a radical generated on the pathway in one α/β pair and the Y_{122}• on the second α/β pair (Figure 8). The distances measured between Y_{122}• and $DOPA_{356}$• provided the first

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structural constraint on the location of this residue within α2β2. Measurements between Y_{122}• and NH_2Y_{731}•, NH_2Y_{730}•, or an active-site nitrogen-centered radical formed upon reaction with the mechanism-based inhibitor 2′-azido-2′-deoxyuridine 5′-diphosphate (N_3UDP)[1] were all in excellent agreement with the distances predicted by the docking model.[20,23]

We have also observed that generation of an NH_2Y• on the pathway induces a tight, kinetically stable α2/β2 interaction.[26] At low α2 and β2 concentrations in the presence of S and E pairs, the wt α2/β2 interaction is weak (K_d = 50-400 nM) and transient (k_{off} ~50-100 s^{-1}).[4,27] In contrast, under conditions that generate NH_2Y_{730}•, the binding between $Y_{730}NH_2Y$-α2 and wt-β2 is tight (K_d = 7 nM), cooperative, and long-lived (k_{off} ~10^{-3} s^{-1}). The stable complex has been structurally characterized by electron microscopy (30 Å resolution) and was found to be consistent with the docking model, providing the first direct visualization of RNR in a catalytically relevant state.[26]

Mechanism of long-range PCET in *E. coli* RNR

pK_as of pathway residues

UAAs with perturbed pK_as (Figure 4a, **1** and **4**-**8**, and Table 1) provide a means to study the nature of the PT coupled to ET (i.e., orthogonal vs. co-linear PCET, Figure 3a). To interpret the results of such experiments, we initially determined the extent to which the pK_as of the pathway Ys are modulated by their local protein environment using NO_2Y (Figure 4, **1**). The absorbance features of the NO_2Y phenolate (NO_2Y^-, λ_{max} = 430 nm, ε = 4,200 cm^{-1} M^{-1}) allowed titration of a single residue in the 258 kDa complex of α2β2, S and E. When incorporated at position 356 of β2 and 730 and 731 of α2, the pK_a of NO_2Y was increased by ≤1 pH unit compared that of NO_2Y in solution (7.2).[15,28] In contrast, NO_2Y incorporated at position 122 of β2 revealed an increase in pK_a by >2.5 units,[28] suggesting that the hydrophobic pocket surrounding the cofactor confers unique properties on Y_{122} relative to the other pathway Ys. X-ray structures of α2 and β2 mutants containing NO_2Y revealed minimal changes in comparison to structures of the respective wt subunits.[28,29]

Mechanism of RT in β2

Our proposal for orthogonal PCET in β2 (Figure 3a) was first examined by replacing Y_{356} with 2,3-F_2Y (**5**, Figure 4a), which has a pK_a of 7.8.[30] A pH rate profile of dCDP formation with $Y_{356}(2,3)F_2Y$-β2 and wt-α2 revealed that the complex was active from pH 6-9, indicating that ET through position 356 does not require PT and suggesting that an H-bond to Y_{356} is not necessary for RT through that position.[30] Subsequently, a complete series of F_nYs (**4**-**8**, Figure 4a) with pK_as ranging from 5.6-7.8 (Table 1) were incorporated at position 356. In no case was a correlation between enzyme activity and protonation state observed, consistent with an orthogonal PCET mechanism.[16]

An orthogonal PCET mechanism involving 356 suggests the importance of a proton acceptor. This was proposed to be the conserved acid E_{350} in the C-terminus of β2 (Figure 3a)[6] after Sjöberg and colleagues observed that E_{350}A-β2 is catalytically inactive despite maintaining its ability to bind α2 and to assemble cofactor.[6] Furthermore, reactions between $E_{350}A/Y_{356}NH_2Y$-β2 and wt-α2, or E_{350}A-β2 and $Y_{731}NH_2Y$-α2, fail to generate NH_2Y•, indicating that the E_{350} mutation prevents NH_2Y oxidation at positions 356 and 731.[14] While these results highlight the importance of E_{350} in mediating RT through position 356, the inactivity of these and the E_{350}D- and E_{350}Q-β2 mutants prevents drawing strong mechanistic conclusions.

Mechanistic insight into the first step of RT, reduction of Y_{122}•, has been investigated in collaboration with the Bollinger/Krebs lab.[31] The model (Figure 3a) proposes that Y_{122}•

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reduction is coupled to PT from a Fe1-bound water. To test this hypothesis, the Mössbauer spectrum of the resting diferric-Y_{122}• in [^{57}Fe]-loaded wt-β2, wt-α2, and E was compared to that of the Y•-reduced cofactor generated upon reaction of β2, α2 and E with 2′-N_3UDP.[1] The similarities in the isomer shifts and the differences in the quadrupole splitting parameter associated with Fe1 suggest no change in the Fe oxidation state and a change in ligation to Fe1 from a bound water to a bound hydroxide, consistent with PT from this ligand to the reduced Y_{122}.[31]

Mechanism of RT in α2

Experimental evidence for co-linear PCET within α2, suggested by the proximity of pathway residues in the α2 structure, was obtained by studying light-initiated RT in systems in which the β2 subunit is replaced by a photopeptide (Figure 9).[7,10] The peptide corresponds to the C-terminal 19 amino acids (356-375) of β (βC19) with either a Y or F_nY at position 356 and a photooxidant (PO) such as benzophenone (BP), anthraquinone (Anq), or Re(bpy)(CO)$_3$CN ([Re]) appended to the N-terminus.[10,11] Pairing different POs with different Y analogs allows modulation of the driving force of oxidation at position 356 and of radical injection into α2. Upon excitation, the PO generates a transient radical at 356, a small fraction of which migrates into α2 (Figure 9). The time-resolved formation and decay of the 356 radical is monitored by transient absorption spectroscopy.

Photolysis of either [BP]- or [Anq]-Y-βC19 with wt-α2, [^{14}C]-CDP, and ATP under single-turnover conditions generated 0.25 dCDP/α2, demonstrating the chemical competence of the system.[32] The redox-inert Y_{730}F-α2 prevented dCDP formation, supporting co-linear transport of an H^+ and e^-.[32] The light-initiated reaction of [Re]-2,3,6-F_3Y-βC19 with wt-α2 was compared to that with various α2 mutants to investigate whether the photogenerated F_3Y_{356}• could initiate RT into α2. Radical injection occurred with a k_{et} of ~10^5 s^{-1} in both the wt enzyme and C_{439}S mutant, but was not observed in the Y_{731}F and Y_{730}F variants. These results suggest that the intact Y_{731}/Y_{730} dyad and its associated H-bonding network are necessary for RT.[33] Experiments are underway to test this hypothesis with [Re]-C_{355}S-β2, a mutant β2 in which the PO is attached at position 355, in the intact α2β2 complex.[34]

Additional support for co-linear PCET within α2 has been obtained from studies of the NH_2Y_{730}• formed upon reaction of $Y_{730}NH_2$Y-α2 with wt-β2, CDP, and ATP by HF-EPR and ENDOR spectroscopies. Multifrequency EPR analysis of [^{14}N]- and [^{15}N]-NH_2Y_{730}• in H_2O and D_2O allowed for accurate simulations of experimental spectra and revealed an unusually low g_x value of 2.0052, suggesting the importance of a local H-bonding environment.[35] Analysis of ND_2Y_{730}• using HF [^{2}H]-ENDOR spectroscopy (Figure 10), combined with structural information[24] and DFT calculations, allowed assignment of exchangeable protons in the immediate vicinity of the NH_2Y_{730}•.[21] These studies revealed strong intramolecular H bonds from the NH_2 group, two moderate H-bonding interactions (presumably with the adjacent pathway residues, Y_{731} and C_{439}), and a weaker interaction likely associated with an ordered water molecule. These results support a co-linear PCET mechanism within α2 by demonstrating a structured H-bonding network in the active α2β2 complex.[21]

Mapping the thermodynamic landscape of the PCET pathway

A barrier to the RT pathway: NO_2Y or F_nY

UAAs incorporated into RNR alter the thermodynamics from 260 mV easier to oxidize (DOPA) to 190 mV harder to oxidize (NO_2Y) than Y based on E_p measurements near physiological pH (Table 1). When the Y at position 356, 731, or 730 is replaced with NO_2Y, the resulting mutant is inactive indicating that NO_2Y cannot be oxidized by other pathway

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radicals and hence cannot support RT. A series of F_nYs (**4-8**, Figure 4a, Table 1) incorporated at position 356 of β2 by EPL provided access to E_ps that varied from −50 mV to +250 mV relative to Y in the pH 6-9 range in which RNR is active (Figure 11).[18] pH rate profiles of these mutants demonstrated that their activities fell into three regimes based on the difference in E_p (ΔE_ps) between the F_nY (or F_nY^-)/F_nY• and Y/Y• couples. $Y_{356}F_n$Y-β2s had activities resembling wt-β2 at ΔE_ps <80 mV, whereas they were inactive at ΔE_ps <200 mV, consistent with the results of NO_2Y mutants. In the range from 80-200 mV, $Y_{356}F_n$Y-β2s exhibited measurable activities that decreased with increasing ΔE_p.[16]

A sink in the RT pathway: DOPA or NH_2Y

Substitution of pathway residues by DOPA or NH_2Y (**2** and **3**, Figure 4a) has allowed us to explore the consequence of lowering the potential at positions on the pathway by 260 and 190 mV, respectively (Table 1). As noted above, Y_{356}DOPA-β2 is catalytically inactive, presumably due to the inability of $DOPA_{356}$• to oxidize Y_{731}. We expected that NH_2Y-RNRs would also be inactive, however these three mutants possessed 3-12% of the activity of their corresponding wt subunits.[17,24] (*Footnote 1*: This result was unexpected, as the ΔE_p between Y and NH_2Y is near the 200 mV threshold observed to shut down RT. However, the E_ps reported herein (Table 1)[15,17-19] have been measured by various methods by different researchers, and thus significant error could exist in our calculated ΔE_ps. We are collaborating with the Koppenol lab to re-measure the potentials of these UAAs to obtain a single set of reliable values. Further error arises from the fact that E_p values are sensitive to the reaction conditions under which they were measured, and thus the observed E_ps may differ significantly from true reduction potentials (E°s).) The combination of kinetically competent NH_2Y• formation and catalytic dNDP formation in NH_2Y-RNRs present an opportunity to measure solvent isotope effects at individual steps in the RT pathway and during NDP reduction, providing insight on mechanistic details that are kinetically masked in the wt enzyme.[14] In summary, activity measurements of RNRs containing UAAs indicate that the thermodynamics of RT can be modulated by ≤±200 mV relative to the native pathway at positions 356, 731, and 730 while retaining some enzymatic activity.

Increasing the driving force of RT at position 122: NO_2Y and F_nYs

In an effort to characterize the native Y• intermediates, we replaced Y_{122} with NO_2Y and F_nYs (**1** and **4-7**, Figure 4a). We anticipated the ability to generate radicals of NO_2Y and F_nYs at this position given the unique mechanism of diferric-Y_{122}• assembly in the wt enzyme, which utilizes a strongly oxidizing Fe^{3+}/Fe^{4+} intermediate ("X," Figure 12).[7] A three-syringe, double-mixing apparatus was employed for these experiments in which Fe^{II}-loaded $Y_{122}NO_2$Y-β2 was rapidly mixed with O_2-saturated buffer to generate NO_2Y_{122}• (1.2 eq/β2, $t_{1/2}$ ~40 s at 25 °C) on the first syringe drive, followed immediately by reaction of this short-lived NO_2Y_{122}• with wt-α2, S, and E on the second syringe drive (Scheme 1, step 1).[29] The reaction was monitored by SF, RFQ-EPR, RFQ-PELDOR and RCQ methods (Figure 5) and the results are summarized in Scheme 1.[29] After assembly of the active cofactor, NO_2Y_{122}• is rapidly reduced (>100 s^{-1}) in the first step of RT to generate the phenolate ($NO_2Y_{122}^-$) rather than the anticipated phenol, indicating an uncoupling of PT from ET. All subsequent steps, including formation of dCDP and a new Y•(s), occurred with similar rate constants (>100 s^{-1}). The ability to detect dCDP and new Y• formation at rate constants 10- to 50-fold faster than the wt k_{cat} indicated that disruption of the PT/ET coupling in the first step bypassed the conformational change that is rate-determining in the wt enzyme. Only 0.6 eq dCDP/β2 and 0.6 eq Y•/β2 were generated in this process, indicating that the mutant enzyme (1.2 NO_2Y_{122}•/β2) could perform only a single turnover with half-sites reactivity, presumably due to inability to reoxidize the $NO_2Y_{122}^-$ to NO_2Y_{122}• during reverse RT.

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The results of additional studies of NO_2Y-containing β2s with either additional mutations of pathway residues (Y-to-F or Y-to-3,5-F_2Y) or globally labeled β-[2H]-Ys, in conjunction with HF EPR and PELDOR spectroscopies, indicated that the observed Y• is generated during reverse RT and exists as an equilibrium of radicals at positions 356, 731, and 730 in ~10:1:1 ratio.[12,29] These findings provide the basis for the relative positioning of Y_{356}, Y_{731}, and Y_{730} in the proposed thermodynamic landscape of the RT pathway (Figure 3b).[12]

To explore reactivity in the ~200 mV regime separating NO_2Y and Y, a series of F_nYs (**4**-**7**, Figure 4a) were incorporated in place of Y_{122}. Assuming that $Y_{122}F_nY$-β2s experience a pK_a perturbation similar to that of NO_2Y_{122} (>2.5 units),[28] all F_nYs would remain protonated at pH 7.6 and would vary from 50 mV easier to 100 mV harder to oxidize than Y (Figures 3b and 11).[18] Using an evolved, polyspecific F_nY-RS, four $Y_{122}F_nY$-β2s were isolated, and the assembly and stability of their F_nY_{122}•s were spectroscopically characterized.[13,14] Their EPR spectra feature hyperfine couplings of the radical to the fluorine nuclei, giving rise to sharp low- and high-field features that facilitate spectral deconvolution of F_nY_{122}•s from pathway Y•s (Figure 13a).[13] All $Y_{122}F_nY$-β2s are active in the steady-state with 10-100 % the activity of wt-β2.14 When the driving force of RT is raised relative to Y, reaction of $Y_{122}F_nY$-β2s with wt-α2 (or $Y_{731}F$-α2), S, and E resulted in loss of F_nY_{122}• concomitant with the generation of a new radical, hypothesized to be Y_{356}• generated during forward RT (Figure 13b).[13,14] The kinetics of new radical formation and dCDP production have been studied for the reaction of $Y_{122}(2,3,5)F_3Y$-β2 with wt-α2, CDP, and ATP, and indicate that Y_{356}• formation is kinetically competent relative to dCDP formation.[14]

Finally, the ability to monitor oxidation of Y_{356} by NO_2Y_{122}• or F_nY_{122}•s has allowed us to address the function of W_{48} (Figure 3a).[2,7] This residue has been shown to participate during *in vitro* cofactor assembly, but its role in long-range RT has not been established. Preliminary studies of the reactivity of $Y_{122}NO_2Y/Y_{356}F$-β2 or $Y_{122}(2,3,5)F_3Y/Y_{356}F$-β2 double mutants provided no evidence for the formation of a discrete W_{48}•/W_{48}•+ intermediate during in RT, although it is possible that W_{48} plays an important role in conformational gating.[13,14,29]

From the studies conducted to date, a thermodynamic landscape for the RT pathway is emerging (Figure 3b). This model indicates that position 122 is the pathway minimum, however, detection of Y_{356}• in the reaction with $Y_{122}(2,3,5)F_3Y$-β2 as a radical initiator suggests that the thermodynamic difference between position 122 and 356 is small and that the stability of Y_{122}• may be kinetic in origin. W_{48} is colored in gray, as we currently have no evidence in support of its participation as a discrete radical intermediate. The three transiently oxidized Ys are harder to oxidize than Y_{122}, with Y_{731} and Y_{730} 50-100 mV harder to oxidize than Y_{356} and roughly isoenergetic with one another.[12] Finally, C_{439} is placed at a reduction potential quite similar to or slightly elevated above the 730/731 dyad based on the solution reduction potential of glutathione radical at neutral pH.[36] In our model, the forward RT pathway is thus uphill, and C_{439} oxidation is driven by the rapid, irreversible loss of water in the second step of nucleotide reduction (Figure 2),[1,3] and the reverse RT pathway is downhill and rapid.

Conclusions

This account summarizes the results of recent mechanistic studies on mutant *E. coli* class Ia RNRs containing unnatural Y analogs at the proposed sites of stable and transient Y• formation on the RT pathway. Specifically, the results obtained from unnatural DOPA-, NH_2Y-, NO_2Y- and F_nYs-RNRs and light-initiated photo-RNRs, were used to establish: (1) that there exists a specific pathway containing a minimum of four Ys involved in long-range RT over 35 A across a compact, globular α2β2 resembling Uhlin and Eklund's docking

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model; (2) that RT occurs by orthogonal and co-linear PCET transfers in the β2 and α2 subunits, respectively; (3) that the overall thermodynamics of RT are only slightly uphill in the forward direction, with several of the intervening steps being nearly isoenergetic; (4) that the individual RT steps and the chemistry of nucleotide reduction are fast (~10^5 s^{-1} and >100 s^{-1}, respectively), despite being kinetically masked by several conformational changes (10-100 s^{-1}) that occur when nucleotides bind to α2β2; and (5) that the rate-limiting conformational changes likely target the RT pathway and its tightly coupled proton and electron transfers.

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Biography

Ellen C. Minnihan conducted graduate research in the Stubbe lab and earned her PhD in Chemistry from MIT in 2012.

Daniel G. Nocera is the Patterson Rockwood Professor of Energy at Harvard University. His research focuses on the study of PCET as it pertains to the biology of nucleotide metabolism and energy conversion.

JoAnne Stubbe, the Novartis Professor of Chemistry and Professor of Biology at MIT, has dedicated her career to the study of the mechanisms of ribonucleotide reductases and other enzymatic systems.

ABBREVIATIONS

α2	RNR large subunit
β2	RNR small subunit
E	effector
E_p	peak potential
ET	electron transfer
HF	high-field
N_3UDP	2′-azido-2′-deoxyuridine 5′-diphosphate
PCET	proton-coupled electron transfer
PO	photooxidant
PT	proton transfer
RT	radical transfer
S•	cysteine radical
S	substrate
UAA	unnatural amino acid
wt	wild-type
Y•	tyrosyl radical

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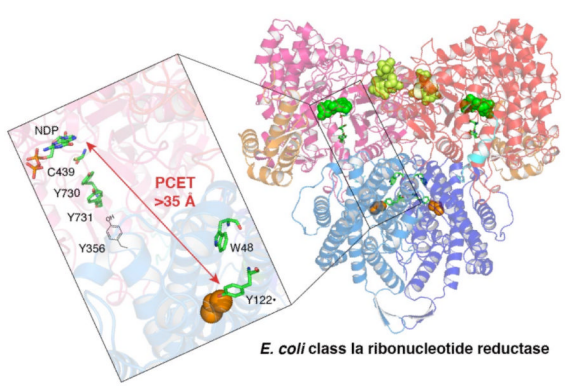
CONSPECTUS

Ribonucleotide reductases (RNRs) catalyze the conversion of nucleotides to 2′-deoxynucleotides and are classified on the basis of the metallo-cofactor used to conduct this chemistry. The class Ia RNRs initiate nucleotide reduction when a stable diferric-tyrosyl radical (Y•, $t_{1/2}$ of 4 days at 4 °C) cofactor in the β2 subunit transiently oxidizes a cysteine to a thiyl radical (S•) in the active site of the α2 subunit. In the active α2β2 complex of the class Ia RNR from *E. coli*, this oxidation has been proposed to occur reversibly over 35 Å by a radical hopping mechanism along a specific pathway comprising redox-active aromatic amino acids: Y_{122}• ↔ [W_{48}?] ↔ Y_{356} in β2 to Y_{731} ↔ Y_{730} C_{439} in α2, with each step necessitating a proton-coupled electron transfer (PCET). Protein conformational changes constitute the rate-limiting step in the overall catalytic scheme, thereby kinetically masking the detailed chemistry of the PCET steps. Technology has evolved to allow the site-selective replacement of the four pathway Ys with unnatural Y analogs. Rapid kinetic techniques combined with multi-frequency electron paramagnetic resonance, pulsed electron-electron double resonance, and electron nuclear double resonance spectroscopies have facilitated analysis of stable and transient radical intermediates in these mutants, thereby beginning to reveal the mechanistic underpinnings of the radical transfer (RT) process.



This account summarizes recent mechanistic studies on mutant *E. coli* RNRs containing the following Y analogs: 3,4-dihydroxyphenylalanine (DOPA) or 3-aminotyrosine (NH_2Y), both thermodynamic radical traps; 3-nitrotyrosine (NO_2Y), a thermodynamic barrier and probe of local environmental perturbations to the phenolic pK_a; and fluorotyrosines (F_nYs, n = 2 or 3), dual reporters on local pK_as and reduction potentials. These studies have established the existence of a specific pathway spanning 35 Å within a globular α2β2 complex that involves one stable (position 122) and three transient (positions 356, 730, and 731) Y•s. Our results also support that RT occurs by an orthogonal PCET mechanism within β2, with Y_{122}• reduction accompanied by proton transfer from an Fe1-bound water in the diferric cluster and Y_{356} oxidation coupled to an off-pathway proton transfer likely involving E_{350}. In α2, RT likely occurs by a co-linear PCET mechanism, as evidenced from studies of light-initiated radical propagation from photopeptides mimicking the β2 subunit to the intact α2 subunit, and by [^{2}H]-ENDOR spectroscopic analysis of the hydrogen-bonding environment surrounding a stablized NH_2Y• formed at position 730. Additionally, studies on the thermodynamics of the RT pathway reveal that the relative reduction potentials decrease according to $Y_{122} < Y_{356} < Y_{731} \approx Y_{730} \leq C_{439}$, and that the pathway in the forward direction is thermodynamically unfavorable, with C_{439} oxidation likely driven by rapid, irreversible loss of water during the nucleotide reduction process. Kinetic studies of radical intermediates reveal that RT is gated by conformational changes occurring on the order of > 100 s^{-1} in addition to the

changes that are rate-limiting in the wt enzyme (~10 s^{-1}). The rate constant of one of the PCET steps is ~10^5 s^{-1}, as measured in photo-initiated experiments.

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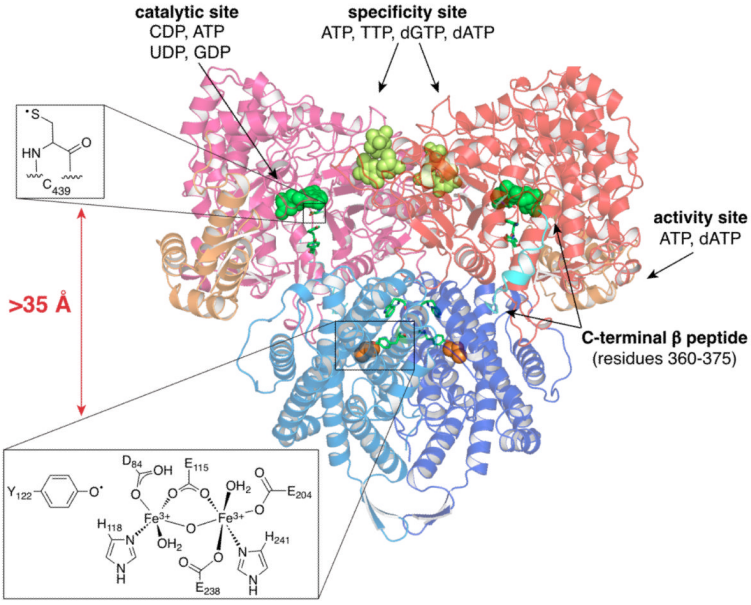

Figure 1.

A docking model of the *E. coli* α2β2 complex.[2] α2 (pink and red) contains three nucleotide binding sites. β2 (light and dark blue) contains the diferric-Y• cofactor; residues 340 to 375 are not resolved in this structure. A peptide corresponding to the C-terminal 20 amino acids of β is bound to each α, a portion of which (residues 360-375) is resolved in the crystal structure (cyan). The "ATP cone" region of α, which contains the effector site that governs activity, is colored orange. This model separates Y_{122}• in β2 from C_{439} in α2 by >35 Å. GDP (green), TTP (yellow) and the Fe_2O core of the diferric cluster (orange) are shown in CPK space-filling models. Residues constituting the RT pathway (green) are shown in sticks.

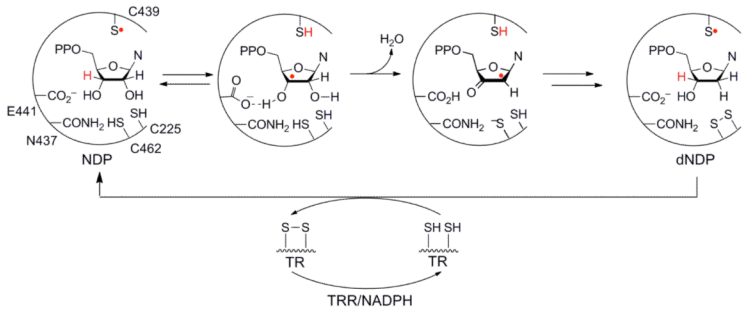

Figure 2.

Mechanism of NDP reduction by RNR. The S• shown on C_{439} of α2 in the first reaction step is reversibly generated by Y_{122}• in β2 by the mechanism shown in Figure 3a.

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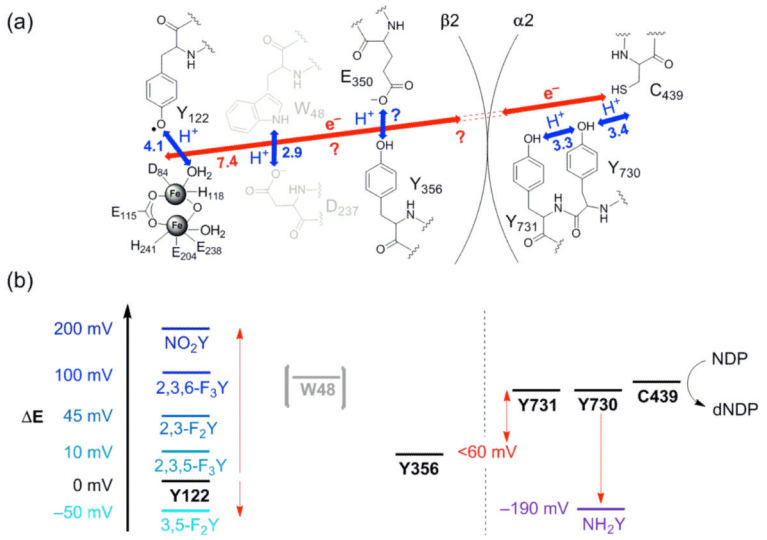

Figure 3.

The Nocera/Stubbe elaboration of the Uhlin/Eklund model for RT in *E. coli* class Ia RNR. (a) The proposed movement of protons (blue arrows) and electrons (red arrows) at each step on the pathway. Distances (Å) are from structures of α2 and β2. E_{350} and Y_{356} are disordered in all β2 structures, and their positions are unknown. There is no direct evidence that W_{48} and D_{237} participate in RT and thus they are shown in gray. The distance between W_{48} and Y_{731} is modeled to be 25 Å. (b) The proposed relative reduction potentials of residues on the RT pathway from experiments using the indicated UAAs site-specifically incorporated in place of each Y. NH_2Y has been incorporated at position 356, 730, or 731. Note that the absolute reduction potentials of these residues, the structures of which are shown in Figure 4, are not known, and the relative reduction potentials indicated are our best estimates given current knowledge (see Table 1 and Footnote 1).

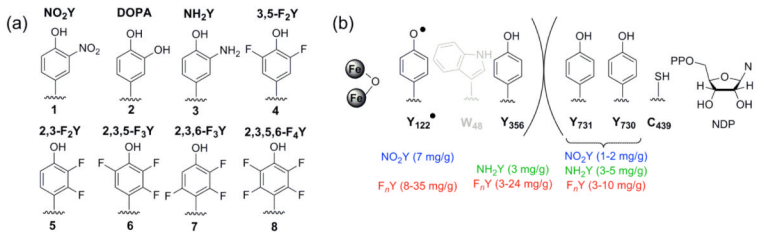

Figure 4.

UAAs incorporated into *E. coli* class Ia RNR. (a) Compounds **1**-**2** and **4**-**8** have been incorporated in position 356 of β2 by EPL, while compounds **1**, **3**-**7** have been incorporated to sites in both α2 and β2 by *in vivo* nonsense suppression. (b) Purified protein yields achieved by *in vivo* nonsense suppression are given in parenthesis for each UAA at each position (in mg protein/g cells).

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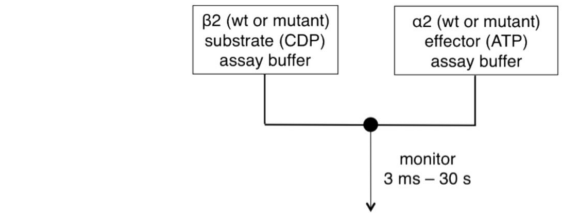

Technique	Quench mode	Detection mode	Observable
Freeze quench	Isopentane/liq. N_2 bath (−140 °C)	EPR spectroscopy	Formation and decay of amino acid radicals
Chemical quench	Acid	Scintillation counting	Formation of radiolabeled dNDP
Stopped-flow	None (continuous)	UV-vis absorption or fluorescence spectroscopy	Changes to amino acid radicals, diferric cluster, protein environment

Figure 5.
Experimental design, kinetic techniques, and detection methods for studying RT.

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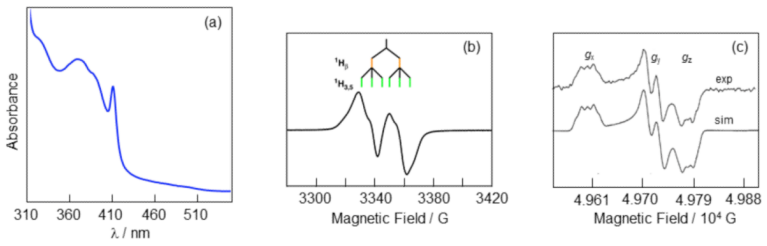

Figure 6.

Spectroscopic characterization of the diferric-Y_{122}• cofactor from *E. coli* class Ia RNR. (a) The UV-vis spectrum has contributions from the diferric cluster at 325 and 365 nm and Y_{122}• at 411 nm. (b) The 9 GHz EPR spectrum of Y_{122}• with the origin of its hyperfine couplings indicated. (c) The 140 GHz EPR spectrum of Y_{122}• resolves three distinct *g* tensors. Adapted from reference 22.

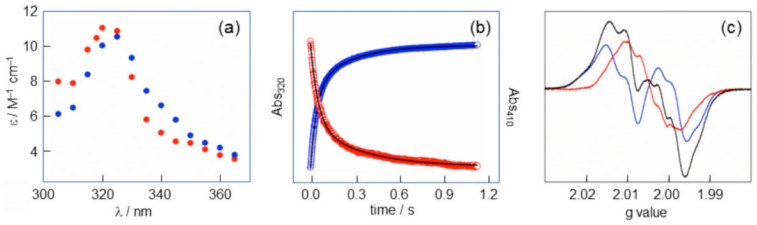

Figure 7.

Spectroscopic characterization of NH_2Y•s. (a) A point-by-point reconstruction of the absorbance spectra of NH_2Y_{730}• (blue) and NH_2Y_{731}• (red) formed 1.5 s after reacting $Y_{731}NH_2Y$-α2 (or $Y_{730}NH_2Y$-α2) with wt-β2, CDP, and ATP. (b) Averaged single-wavelength SF UV-vis traces for the $Y_{731}NH_2Y$-α2 reaction described in (A). Loss of Y_{122}• (red, 410 nm] correlates with the formation of NH_2Y_{731}• (blue, 320 nm]. Biexponential fits to the data are shown as black lines. (c) The 9 GHz EPR spectrum (black) of an identical reaction frozen after 10 s is a ~1:1 composite of residual Y_{122}• (blue) and NH_2Y_{731}• (red). Figure adapted from reference 17.

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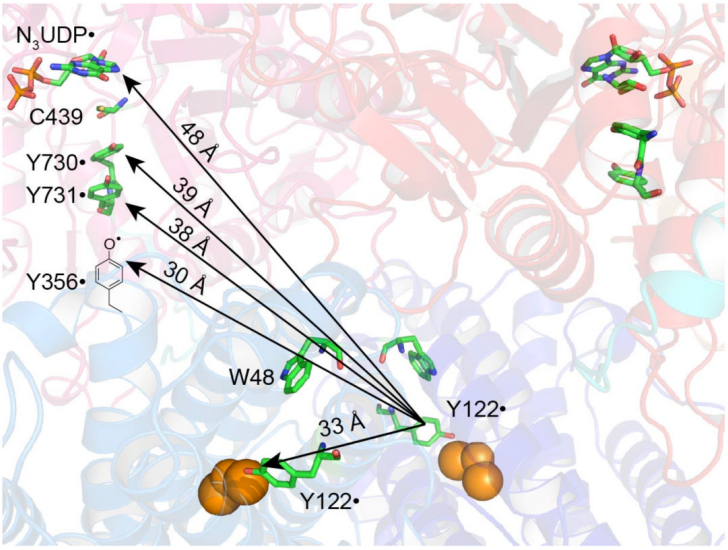

Figure 8.

Validating the docking model by PELDOR spectroscopy. By exploiting the half-sites reactivity of RNR, diagonal distances between Y_{122}• on one α/β pair and $DOPA_{356}$•, NH_2Y_{731}•, NH_2Y_{730}•, and an active-site N• on the second α/β pair have been measured.[20,23] The pathway residues and S were built in from the docking model,[2] in which Y_{356} is invisible.

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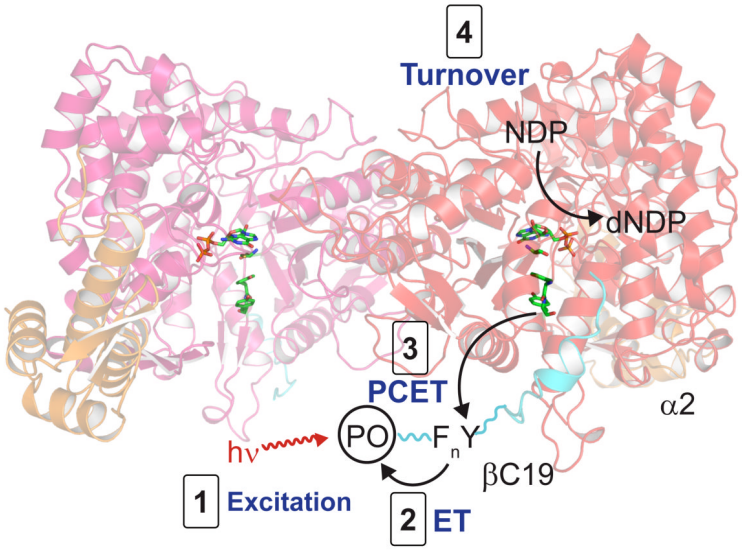

Figure 9.

Photo-initiated radical propagation in PO-Y-βC19 photopeptides. A photooxidant (PO, black circle) is appended to the N-terminus of a peptide corresponding to residues 356-375 of β2 (βC19, cyan), with either Y or F_nY at position 356. Light excitation (step **1**) induces oxidation of the residue at position 356 (**2**), a fraction of which is reduced by Y_{731} of α2 (**3**). The photopeptide/wt-α2 complex is capable of generating dNDP (**4**), providing direct evidence for radical injection from the peptide. Figure constructed from PDB ID 1RLR.[2]

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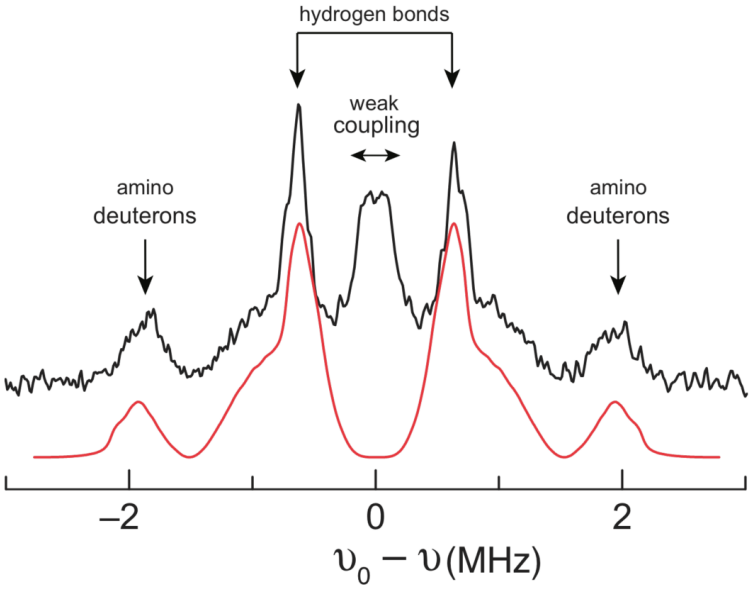

Figure 10.

The 94 GHz [2H]-MIMS ENDOR spectrum of NH_2Y_{730}• in the active α2β2 complex reveals the details of its intra- and intermolecular H-bonds. Experimental data are shown in black and a simulation in red. The two prominent peaks centered around 0.6 MHz fall in a region expected for coupled H bonds. The detailed analysis of the experimental spectrum and its simulation is described in reference 21.

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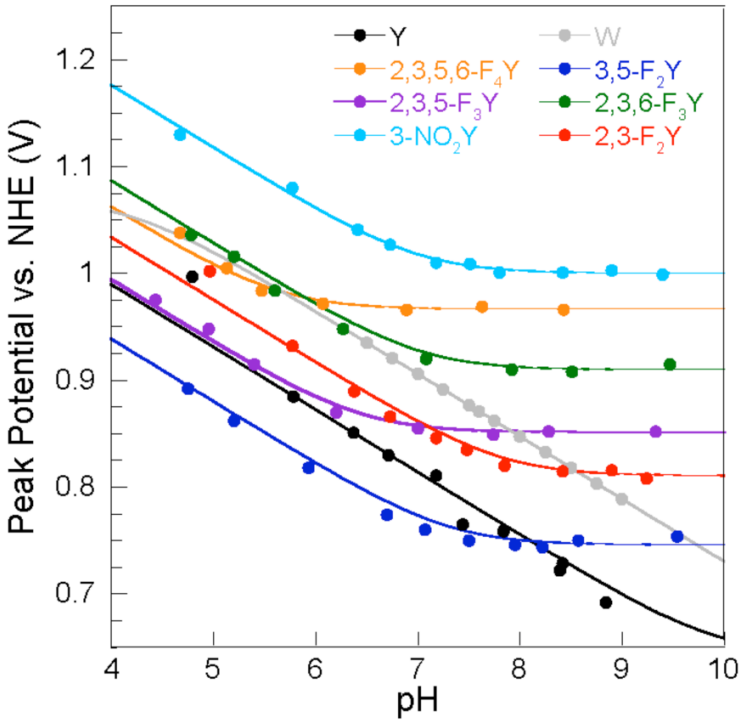

Figure 11.
Solution peak potentials (E_ps) of Y, W, and UAAs blocked with N-acetyl and C-amide functionalities.[15,18]

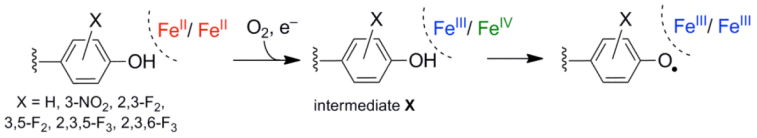

Figure 12.

Assembly of the diferric-Y_{122}• (or NO_2Y_{122}• or F_nY_{122}•) cofactor from diferrous-β2, O_2 and reductant.

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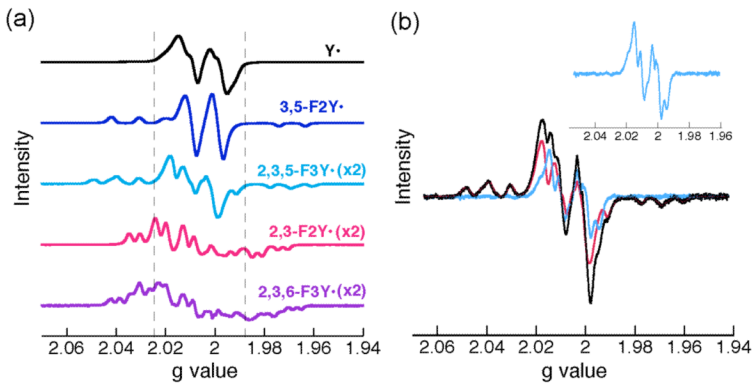
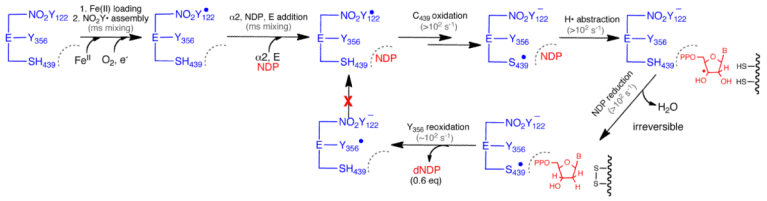


Figure 13.

(a) X-band EPR spectra (77 K) for *E. coli* Y_{122}• and F_nY_{122}•s normalized for radical concentration. Dashed lines highlight the increased spectral width of the F_nY_{122}•s.[13,14] (b) EPR spectrum of the reaction of Y_{122}(2,3,5)F_3Y-β2, wt-α2, CDP, and ATP quenched at 25 s. The reaction spectrum (black) is a composite of two species: 2,3,5-F_3Y_{122}• (pink) and a new radical (blue, magnified in inset), assigned as Y_{356}•.[13]



Scheme 1.

Kinetic model for radical initiation in the reaction of $Y_{122}NO_2Y$-β2 with wt-α2, S, and E.[29]

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Table 1

pK_as and E_ps of UAAs

UAA[a]	pK_a[b]	E_p *vs* NHE (V)[c]	ΔE_p *vs* Y/Y• (mV)[c]
Y	9.9	0.83	-
DOPA	9.7	0.57	−260
NH_2Y	~10	0.64	−190
3,5-F_2Y	7.2	0.77	−60
2,3-F_2Y	7.8	0.86	+30
2,3,5-F_3Y	6.4	0.86	+30
2,3,6-F_3Y	7.0	0.93	+100
2,3,5,6-F_4Y	5.6	0.97	+140
NO_2Y	7.2	1.02	+190

[a] For Y, NO_2Y, and F_nYs, measurements made on N-acetyltyrosinamide forms.

[b] The solution pK_as reported here are perturbed by <+1 unit at positions 356, 730, and 731 and by >+2.5 units at position 122.

[c] At pH 7, as reported in references 15,17-19 and references therein.