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The prototypic class Ia ribonucleotide reductase from *Escherichia coli*: still surprising after all these years

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allostery, oligomerization, protein-protein interactions, conformational equilibrium, feedback regulation, nucleotide biosynthesis

Abbreviations used:
RNR, ribonucleotide reductase
NDP, ribonucleoside 5’-diphosphate
PCET, proton-coupled electron transfer
PELDOR, pulsed electron-electron double resonance
AUC, analytical ultracentrifugation
SAXS, small-angle X-ray scattering
EM, electron microscopy

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Abstract
Ribonucleotide reductases (RNRs) are key players in nucleic acid metabolism, converting ribonucleotides to deoxyribonucleotides. As such, they maintain the intracellular balance of deoxyribonucleotides to ensure the fidelity of DNA replication and repair. The best-studied RNR is the class Ia enzyme from *Escherichia coli*, which employs two subunits to catalyze its radical-based reaction: $\beta_2$ houses the diferric-tyrosyl radical cofactor and $\alpha_2$ contains the active site. Recent applications of biophysical methods to the study of this RNR have revealed the importance of oligomeric state to overall enzyme activity and suggest unprecedented subunit configurations are in play. Although it has been five decades since the isolation of nucleotide reductase activity in extracts of *E. coli*, this prototypic RNR continues to surprise us after all these years.
Introduction

In all organisms, propagation of genetic material from one generation to the next requires DNA replication. The accuracy of the genetic copy and the repair of mistakes depend on balanced levels of ribonucleotides and deoxyribonucleotides [1-3]. One remarkable enzyme, ribonucleotide reductase (RNR), converts all four ribonucleotides into deoxyribonucleotide precursors for DNA synthesis and repair. Because of its crucial metabolic role in dividing cells, RNR has an important place in medicine as the target of several clinically used cancer drugs, such as gemcitabine and clofarabine [4, 5].

All RNRs employ a radical-based mechanism for catalysis and are classified by the metalloc cofactor used to generate an essential thyl radical within a structurally conserved α/β-barrel substrate-binding domain [6-8]. Once the thyl radical is generated, nucleotide reduction proceeds through a conserved mechanism (Fig. 1) [9, 10]. Eukaryotes and some aerobic prokaryotes employ class Ia RNRs, which utilize a diferric-thyrosyl radical cofactor for the reduction of ribonucleoside diphosphates (NDPs) [11]. In addition to having a complex catalytic mechanism, RNRs employ sophisticated allosteric regulation to maintain the appropriate nucleotide balance in the cell (recently summarized in [12]). Here, we focus on the E. coli enzyme, which has long served as the prototype for class Ia RNRs, and review how structural biology techniques have illuminated its catalytic mechanism and allosteric regulation.

Surprising structures of domains

In class Ia RNRs, thyl radical generation in the active site is achieved by intermolecular interactions between two separate proteins: the nucleotide-binding protein encoded by the gene nrdA and the radical-generating protein encoded by the gene nrdB [13]. For the canonical class Ia enzymes, including the prototypic E. coli enzyme, the NrdA and NrdB proteins form homodimers called α2 and β2, respectively (Fig. 2). A diferric-thyrosyl radical cofactor is assembled in β2 at Tyr122 in the presence of molecular oxygen, Fe(II), and an electron source [14-16]. For each turnover, the formation of the active holocomplex triggers long-range proton-coupled electron transfer (PCET), reducing the Tyr122 radical in β2 and oxidizing Cys439 in the active site of α2 to form the essential thyl radical [17].

A number of crystal structures of the individual α2 and β2 subunits have been determined for the E. coli enzyme. The β2 structure is often described as a heart-shaped dimer (Fig. 2B) [18]. One surprise from the β2 structure was that the tyrosine residue (Tyr122) that harbors the tyrosyl radical is buried in the center of each β protomer, adjacent to its diiron center, 10 Å from the surface. This observation suggested the need for the radical to transfer through other residues to reach the surface of β2 en route to the substrate-binding site of α2. Such a long-range electron transfer was unprecedented at the time it was proposed [8] but is now well supported by experimental evidence [19-21]. Another finding from the β2 structure was that the 32 C-terminal residues were not observed due to their thermal lability (Fig. 2B, dotted curves) [18]. Earlier studies demonstrated that C-terminal residues of β2 were critical for its interaction with α2 [22, 23]. Just upstream from this C-terminal sequence within the unstructured tail is the absolutely conserved Tyr356 that subsequent studies have shown to be part of the radical relay between the RNR subunits [19, 24, 25].

Shortly after the first β2 structure, an equally surprising α2 structure was reported [8] (Fig. 2A). The α2 structure was the first example of the 10-stranded α/β barrel that is now known to be characteristic of all three classes of RNR [6, 7]. Cys439, the residue that harbors the catalytic thyl radical, was located at the tip of a “finger loop” poking into the middle of the barrel. This
residue was located adjacent to the absolutely conserved Cys225 and Cys462 residues that provide the reducing equivalents for nucleotide reduction (Fig. 1, 2A) [10]. In this structure Cys225 and Cys462 were observed in their oxidized state as a disulfide bonded cystine. Furthermore, the positions of Tyr730 and Tyr731 relative to Cys439 implicated their involvement in PCET from \( \beta_2 \) to \( \alpha_2 \) (Fig. 2A). Like \( \beta_2 \), \( \alpha_2 \) has an unstructured C-terminal tail that also contains residues involved in catalysis. Two cysteine residues, Cys754 and Cys759, in the flexible \( \alpha_2 \) tail are responsible for accessing the active site to reduce the Cys225-Cys462 disulfide at the end of each catalytic cycle (Fig. 1) [10, 26]. Additionally, the structure of \( \alpha_2 \) was obtained by co-crystallization with a 20-residue C-terminal peptide of \( \beta_2 \), revealing an important determinant of the \( \alpha_2-\beta_2 \) interaction [23], but again density for Tyr356 was not observed (Fig. 2A, orange ribbons).

Early experiments with the \( E. \ coli \) class Ia enzyme revealed that deoxynucleotide effectors and ATP are responsible for regulating substrate specificity as well as overall enzyme activity [12, 27]. Nucleotide-binding sites in \( E. \ coli \) \( \alpha_2 \) were located by further crystallographic work [28]. Crystals of \( \alpha_2 \) co-crystallized or soaked with the effector, dTTP, yielded information about the allosteric site known as the “specificity site”. The resultant structures showed dTTP bound at either end of a four-helix bundle formed at the \( \alpha_2 \) dimer interface, approximately 15 Å from the active site (Fig. 2A) [28]. The specificity effector bound at this site appears to communicate with the active site by ordering the conformation of flexible loops, including one termed “loop 2”, which is adjacent to the active site [28]. Consistent with the ancient origin of RNR, this specificity-regulating feature is conserved in the other RNR classes [7, 12, 29, 30]. However, although GDP reduction is promoted by dTTP, structures determined from crystals soaked with this substrate/effector pair showed low substrate occupancy, even for a Cys292-Ala mutant with enhanced GDP affinity and using dithiothreitol to reduce the active site disulfide [28]. Thus, we do not yet have a molecular level picture of how effectors at this site determine substrate specificity for the \( E. \ coli \) enzyme. The \( \alpha_2 \) subunit also has a third nucleotide-binding site that accepts ATP to activate or dATP to inhibit overall catalytic activity (Fig. 2A) [12]. This “activity site” was located in the same study using crystals soaked with the substrate, CDP, and the ATP analog, AMP-PNP [28]. In the resulting structure, AMP-PNP was observed at the N-terminus of the protein in the so-called “cone domain”, a four-helix bundle that is found across class Ia enzymes [31]. However, it was not evident from this structure how binding of ATP or dATP to the cone domain would communicate a signal to the distant active site over approximately 40 Å. In addition, although ATP is also the specificity effector for CDP, AMP-PNP was only weakly present at the specificity site, and the substrate molecule was not observed in the active site [28].

**Insight into the structural components of an active RNR complex**

To afford enzymatic turnover, \( \alpha_2 \) and \( \beta_2 \) must interact allowing for radical transfer to the active site. However, structural data describing the active complex of \( E. \ coli \) class Ia RNR has been challenging to obtain. Seminal studies on this RNR led to the proposal that active enzyme exists as an \( \alpha_2\beta_2 \) complex [32, 33]. Using sucrose gradient centrifugation, mixtures of \( \alpha_2 \) and \( \beta_2 \) in the absence of nucleotides or in the presence of ATP or dTTP were shown to sediment at around 8.8-9.7 S with an apparent 1:1 subunit stoichiometry [33]. In a later study, analytical ultracentrifugation (AUC) was repeated in the absence of sucrose, which can perturb protein-protein interactions, to show again that an equimolar mixture of \( \alpha_2 \) and \( \beta_2 \) sedimented at around...
10 S with an apparent molecular weight that is consistent with an αβ oligomerization state [32]. Together, these studies suggested that the active quaternary structure is an αβ complex.

The determination of the individual α2 and β2 structures that followed two decades later showed that the two dimeric proteins were complementary in shape and therefore could plausibly form an active αβ complex [8, 18]. When the two structures are docked along their 2-fold symmetry axes, the lobes of the heart-shaped β2 neatly fit in the concave pockets containing the active sites of α2 (Fig. 3A) [8]. Importantly, the subunit arrangement in this model places residues that are important for radical transfer in close proximity across the α2-β2 interface. In the proposed PCET pathway, radical propagation occurs along conserved aromatic residues: from Tyr122→Trp48→Tyr356 in β2 to Tyr731→Tyr730→Cys439 in α2 [17]. These residues form a conduit in the αβ docking model, with the surface-exposed Trp48 of β2 within ~23 Å from Tyr731 of α2, a reasonable distance for PCET if bridged by Tyr356 on the flexible C-terminal tail of β2 (Fig. 3A). Site-directed mutation of each of these conserved residues eliminated activity to background levels, consistent with their proposed involvement in the PCET pathway [25, 34-36]. More recently, incorporation of unnatural amino acids that act as radical traps at Tyr356, Tyr731, and Tyr730 has permitted the direct demonstration of redox-coupling between these residues [20, 21, 24]. Furthermore, these mutants enabled measurements of Tyr122-Tyr731 and Tyr122-Tyr730 distances by pulsed electron-electron double resonance (PELDOR) spectroscopy [19, 37]. These measured distances were consistent with those predicted by the αβ docking model and thus provided the first experimental support for the subunit arrangement in this model.

Recently, AUC studies of class Ia RNR were reinitiated, and showed that the sedimentation value of equimolar mixtures of α2 and β2 in the presence of activating allosteric effectors is highly dependent on protein concentration and able to exceed 11.5 S, the theoretical value for the globular αβ complex predicted by the docking model [38]. This concentration-dependent behavior indicated that the active complex is embedded in an equilibrium mixture and able to interconvert not only with dissociated species but also with a higher order complex, offering an explanation for the elusiveness of the active complex to crystallographic techniques that benefit from homogeneous samples.

Small-angle X-ray scattering (SAXS) was used to extract structural information for the active complex from the equilibrium mixture and provide the first structural evidence that the active complex is well described by the αβ docking model [38]. Under assay conditions where α2 and β2 should be 97% in an active conformation, the resultant shape reconstruction shows a globular molecule, consistent with the close subunit arrangement in the docking model (Fig. 3B, left). The excess density seen in this shape reconstruction was shown to be due to the presence of a small population of the higher order complex interconverting with the predominant αβ complex [38]. When data are subjected to a global analysis, the contribution of the higher order complex can be quantified and therefore subtracted from the SAXS data, yielding a shape reconstruction that represents the active complex on its own (Fig. 3A, right).

First structures of the dATP-inhibited state of E. coli RNR complex
In addition to the quest for a structure of active E. coli class Ia RNR, a structure depicting both α2 and β2 in a dATP-inhibited state has been long sought. Early ultracentrifugation studies provided the first evidence that allosteric inhibition of class Ia RNR by dATP is coupled with higher order oligomerization [32, 33]. Recently, the role of oligomerization in the activity regulation of the E. coli enzyme was revisited with multiple biophysical techniques [38, 39]. These studies have
converged on a consistent picture involving the formation of an \( \alpha_4\beta_4 \) complex under dATP inhibition [38, 39] and have led to the elucidation of the first structures of this complex [38].

A number of low-resolution techniques were used to determine the oligomerization state of the dATP-inhibited \( E. coli \) enzyme. In a gas-phase electrophoretic mobility macromolecule analysis (GEMMA) study, a heavy complex was observed in the presence of inhibiting dATP concentrations with an electrophoretic mobility diameter that is consistent with a molecular weight of 510 kDa [39]. This heavy complex was shown to have an \( \alpha_4\beta_4 \) subunit stoichiometry with the use of a \( \beta \) construct tagged with the 57-kDa NusA protein in order to distinguish the \( \alpha \)-monomer from the similarly sized \( \beta_2 \) [39]. More recently, AUC and SAXS were used to confirm the molecular weight and subunit composition of the dATP-inhibited \( \alpha_4\beta_4 \) complex and further show the stability of this species in solution over a wide range of RNR concentrations [38]. Furthermore, both the sedimentation rate and the power-law dependence observed in the X-ray scattering indicated that this \( \alpha_4\beta_4 \) complex is highly non-globular in shape [38].

The first structures of the dATP-inhibited \( \alpha_4\beta_4 \) were determined by single particle electron microscopy (EM) and X-ray crystallography, revealing a ring-shaped complex with an alternating arrangement of \( \alpha_2 \) and \( \beta_2 \) subunits (Fig. 4) [38]. In this study, the \( \alpha_4\beta_4 \) rings were the dominant species observed in EM images of \( \alpha_2 \) and \( \beta_2 \) mixtures under dATP inhibition. A three-dimensional EM reconstruction of this species generated at 23-Å resolution was fit with crystal structures of the individual subunits, yielding a pseudo-atomic model. This pseudo-atomic model was nearly superimposable with a 5.7-Å resolution crystal structure of the \( \alpha_4\beta_4 \) ring obtained by co-crystallizing \( \alpha_2 \) and \( \beta_2 \) with dATP, demonstrating the structural stability of this complex even at the dilute protein concentrations used for EM. Furthermore, the theoretical sedimentation rate and X-ray scattering profile predicted from these structures closely matched experimental AUC and SAXS data, indicating that this \( \alpha_4\beta_4 \) ring exists in solution at physiologically relevant RNR and dATP concentrations [38]. Moreover, a low-resolution molecular envelope obtained from SAXS resembled the both EM model and crystal structure, showing consistency among the three structural techniques [38].

The structures obtained from this study provide insight into how dATP inhibits the prototypic class Ia enzyme from \( E. coli \) [38]. The ring is formed by contacts made by \( \beta_2 \) to the \( \alpha_2 \) N-terminal cone domains housing the activity sites, such that Trp48 in \( \beta_2 \) and Tyr731 in \( \alpha_2 \) face a large solvent-exposed hole (Fig. 4). In the crystal structure, dATP is observed in both the activity and specificity sites in the crystal structure. Consistent with this result, the \( \alpha_4\beta_4 \) complex was shown by SAXS to maximally form at above 4 molar equivalents of dATP per \( \alpha_2 \). Additionally, in the crystal structure, C-terminal residues of \( \beta_2 \) were observed at the peptide-binding site of each \( \alpha \)-protomer (Fig. 4). However, there is broken electron density between Leu339 and Ser363 that again prevented visualization of the elusive Tyr356. While nucleotide reduction by the class Ia RNR depends on the juxtaposition of \( \alpha_2 \) and \( \beta_2 \) to permit the round-trip radical relay from Tyr122 to Cys439, the distance between the closest visible residues in the PCET pathway (Trp48 in \( \beta_2 \) and Tyr731 in \( \alpha_2 \)) in the \( \alpha_4\beta_4 \) complex is \( \approx 55 \) Å (Fig. 4). The \( \approx 55 \) Å distance is too long to accommodate the radical transfer even with a bridging Tyr356 and would require the implausible scenario of radical transfer through bulk solvent [40]. Together, these structures suggest that the dATP-binding at the activity sites inhibits RNR by stabilizing an open subunit arrangement of \( \alpha_2 \) and \( \beta_2 \) that physically separates the PCET residues, preventing radical transfer.

**Model for allosteric regulation**
These recent developments in the structural characterization of *E. coli* class Ia RNR have provided a new understanding of allosteric activity regulation for this protein. We now know that the prototypic class Ia RNR from *E. coli* exists in at least three states that are supported by direct structural observation: the dissociated α2 and β2 subunits [8, 18], the active α2β2 complex [38], and the inhibited α4β4 complex [38]. Furthermore, it was shown by AUC and SAXS that in the presence of activating effectors or in the absence of any effectors, the *E. coli* enzyme exists as an equilibrium mixture of α2, β2, α2β2, and α4β4, whose distributions are sensitive to protein concentration. In contrast, dATP is uniquely able to push the equilibrium towards a single α4β4 state [38]. From these data a three-state model emerges for the allosteric regulation of overall activity in *E. coli* class Ia RNR. Here active α2β2 complex is an intermediate between the dissociated state and the inhibited α4β4 complex (Fig. 5). While increases in protein or dATP levels shift the equilibrium to the right, according to this model, ATP may upregulate the *E. coli* enzyme by competing with dATP for binding at the activity site and shifting the equilibrium away from the inhibited α4β4 complex. Thus, in the cell, RNR may act like a molecular thermostat that senses the balance between ribonucleotide and deoxyribonucleotide pools by the competitive binding of ATP and dATP for the activity site, which in turn modulates the equilibrium between the active α2β2 and inhibited α4β4 complexes.

In *E. coli*, the *nrdA* and *nrdB* genes are on the same operon and are thus co-expressed [13]. The ability to form αβ4 provides the *E. coli* enzyme with a clever mechanism for regulating activity by keeping its subunits together but in a nonproductive arrangement. The structure of the dATP-inhibited α4β4 suggests that interconversion between these states can readily occur. Each contact at the cone domains containing the activity site buries a ~500 Å2 interface involving only a handful of residues from each subunit. In addition to the contacts involving the activity site, interconversion between α2β2 and α4β4 may be facilitated by the flexible C-terminal tails of β2. While both C-terminal tails from a single β2 may be interacting with a single α2 in the compact active complex, the crystal structure of the α4β4 complex suggests that the C-terminal tails of a single β2 may be used to recruit two α2 subunits. The C-terminal tails may allow α2 and β2 to remain flexibly linked in order to rapidly switch from a closed to open conformation and vice versa (Fig. 5).

**Future directions**

Recent advances bring clarity to the early observations that suggested a link between activity regulation and oligomerization in the class Ia RNR of *E. coli*, yet many important problems remain to be solved [38]. High-resolution structures of α2 both alone and in complex with β2 in the presence and absence of the activity site effectors, ATP and dATP, are needed to understand at an atomic level the conformational changes in the activity site. In existing *E. coli* α2 crystal structures, the cone domains containing the activity sites make lattice packing interactions [8, 28], and therefore new crystallization conditions might be required to unambiguously resolve details of effector-induced rearrangements at the cone domain. While structures of α2 with specificity effector/substrate pairs have been determined for the yeast class Ia RNR [41], the effect of β2 in an active α2β2 complex on specificity regulation is not yet known for any class Ia enzyme. Furthermore, species-specific differences between the sequences at the specificity site [41, 42] suggest that a more complete model of specificity regulation in the *E. coli* enzyme will require structures with full occupancy substrate/effectors pairs.

Eukaryotic class Ia RNRs subscribe to a qualitatively similar regime of activity and specificity regulation as their prokaryotic homologs [43-45]. However, the relationship between
oligomerization and allostery in the eukaryotic class Ia RNRs is not as well defined as in prokaryotes. In contrast to the *E. coli* homolog that requires both subunits to form the inhibited oligomer [33, 38, 39], the eukaryotic α₂ alone can oligomerize under both ATP-activation and dATP-inhibition [42, 43, 46-48]. Recently, the dATP-stabilized complex from yeast was shown to be a hexameric ring of α subunits with the cone domains again forming intersubunit contacts [42]. Without structural information on the active form of eukaryotic class Ia RNRs, however, it is not yet clear why this dATP-induced α₆ arrangement would be inactive. A comparison between the structures of the dATP- and ATP-induced complexes is needed to understand its unique twist to this developing saga of allosteric regulation. Excitingly, differences in the allosteric regulation of eukaryotic and prokaryotic class Ia RNRs may permit the future design of allosteric inhibitors that target specific RNRs, such as the RNRs of pathogens.

Finally, little is known about the interaction between the α₂ and β₂ subunits in the active complex. The long-sought atomic resolution structure of the active α₂β₂ would reveal the positions of residues involved in PCET and might provide critical insight into the conformational changes that trigger radical transmission. In particular, the position of Tyr356 on the C-terminal tail of β₂ has not yet been visualized in any of the available structures. Moreover, mounting evidence establishes that only one of the two active sites in RNR is engaged in radical transfer and substrate reduction at a time [37, 49-52]. Such half-sites reactivity suggests asymmetry in the interaction between α₂ and β₂ that might finally be explained by a high-resolution structure of the active complex. Presumably, the difficulty in obtaining a high-resolution structure of an active complex derives from the dynamic properties of the subunit interactions, the full nature of which was recently emphasized in AUC and SAXS studies [38].

Although five decades have passed since the discovery of the prototypic class Ia enzyme from *E. coli*, RNRs continue to amaze us with their elaborate modes of allosteric regulation, dramatic conformational changes, and complex radical transfer pathways. In the latest chapter, two decades since the first structures of *E. coli* α₂ and β₂ were determined [8, 18], we now have the first low-resolution reconstruction of an active α₂β₂ complex and the first X-ray and EM structures of the dATP-inhibited α₄β₄ complex for the *E. coli* enzyme [38]. These studies reveal the transient nature of the active complex and an unanticipated ring-shaped structure for the dATP-inhibited complex, adding a new twist to the RNR story and promising more surprises to come in the future.

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References


Figure legends

**Figure 1.** Catalytic mechanism of *E. coli* class Ia RNR. Class Ia RNRs act on all four ribonucleoside diphosphates (B = A, T, G, C). Hydrogen abstraction at the 3′ position of the substrate is initiated by the essential thyl radical (C439). Two additional cysteines at the α2 active site (C225, C462) act as a redox sulfhydryl pair and are directly involved in the reduction of NDPs to deoxyribonucleoside diphosphates (dNDPs). Re-reduction of the active site disulfide occurs via disulfide exchange with two cysteine residues on the C-terminal tails of the nucleotide-binding subunit, α2. The C-terminal tail disulfide is re-reduced in a thioredoxin/thioredoxin reductase/NADPH-dependent or equivalent reaction. Kinases and additional enzymes convert the dNDP products of RNR into the direct precursors for DNA, deoxyribonucleoside triphosphates (dNTPs).

**Figure 2.** Structures of the class Ia *E. coli* RNR subunits. (a) Crystal structures of α2 (generated by superposition of PDB: 4R1R, 3R1R) [28]. Monomers are colored light blue and gray with N-terminal cone domains in green. C-terminal peptides of β are colored in orange. Bound nucleotides are colored by atoms (gray carbon, blue nitrogen red oxygen, orange phosphorus). dTTP is bound in the specificity site, GDP is bound in the specificity site, and AMP-PNP is bound in the activity site. Key residues are shown in dark blue. (b) Crystal structure of β2 (PDB: 1RIB) [18]. Monomers are colored red and orange. Flexible C-terminal tails (illustrated as dashed lines) are responsible for interacting with the α2 subunit and contain the Y356 residue that is critical for radical propagation. Key residues are shown in dark blue with Fe atoms adjacent to Y122 colored in green.

**Figure 3.** Structural insight into the active complex. (a) In the proposed α2β2 model for the active complex (shown with same coloring as in Fig. 2), the structures of the individual subunits were rigid-body docked along their symmetry axes, bringing the residues involved in radical transfer as close as possible across the subunit interface [8]. The shortest W48-Y731 distance (indicated with double arrows) in this model is 23 Å. (b) Left: The compact subunit arrangement in the proposed docking model is consistent with a low-resolution shape reconstruction of the active complex obtained by SAXS and also fits SAXS data in a global analysis [38]. The disconnected density in this reconstruction is due the presence of a small population of inhibited complexes in equilibrium with the active complex. Right: The molecular envelope shown here is the average of ten *ab initio* DAMMIF models generated from data on 6 µM RNR in the presence of the substrate CDP [38], with the contributions from a small population of inhibited complexes subtracted.

**Figure 4.** Crystal structure of the dATP-inhibited α4β4 complex. The inhibited complex (PDB: 3UUS) is a ring of alternating subunits making contact at the activity site [38] (shown with same coloring as in Fig. 2). dATP is bound in both the activity and specificity sites. The C-terminal tails of β2 (shown in orange/red) are bound in the previously determined peptide-binding sites on α2. The shortest W48-Y731 distance is 55 Å (indicated by double arrows), much too long for radical transfer even with a bridging Y356.

**Figure 5.** Model for allosteric regulation of activity in *E. coli* class Ia RNR (shown with same coloring as in Fig. 2).
thioredoxin/thioredoxin reductase
NADPH
dATP in activity site

55 Å

dATP in specificity site

β₂ C-terminus
dissociated subunits

active complex

dATP-inactive complex