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Structures of transcription-translation coupling complexes at each stage of the translation cycle

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Abstract:

Bacterial transcription and translation are frequently linked through a transcribing RNA polymerase following the leading ribosome, a process termed transcription-translation coupling (TTC). Two distinct TTC structures, the collied-TTC (TTC-A) and the coupled-TTC (TTC-B), have been reported, but the biological significance of both complexes is still subject to uncertainty. Furthermore, the ribosomes in all of them are in a static state. The underlying translation dynamics within these TTCs remain elusive. Here we report cryo-EM structures of transcription-translation complexes from E.coli at various stages of the translation elongation cycle. The results show five states of TTC-B representing the whole stages of translation elongation cycle. TTC-B is compatible with ribosome conformational changes during the translation elongation and coordinates transcription elongation with translation elongation. The results show two distinct TTC-A in translational pre-translocation and translocation intermediate states in which the RNAP becomes unstable as the translation progresses. The results further show that TTC-A is the key state where the ribsomes could exert mechanical force on RNAP leading to the potential transition between TTC-A and TTC-B within mRNA spacer ranging from 7 to 9 codons and the TTC-A-dependent transcription termination within mRNA spacer shorter than 7 codons. Taken together, our results provide a comprehensive blueprint detailing the dynamic interplay of translation coupled with transcription.

Introduction

In bacteria, the absence of a nuclear envelop, allows the first ribosome (leading ribosome) translating mRNA closely coordinate with RNA polymerase (RNAP)[1,2]. This coordination allows for the synchronization of transcription and translation rates by the lead ribosome[3-13]. The physical interactions between these two macromolecular machines are indispensable for both transcription and translation processes, and it has been reported that the coupling transcription with translation can regulate gene expression[4,7-9,12,14-21]. It does so by mediating the transcription attenuation[22,23], preventing premature transcription termination[24-27], reactivating halted or paused RNAP[14,19,20], protecting RNA from degradation, and inhibiting the formation of deleterious R-loops[4,28,29].

NusG plays a crucial role in mediating the coordination between transcription and translation in *E. coli.*[3,6,13,30,31]. It is the only transcription factor that is conserved across all domains of life, including bacteria, archaea, and eukaryotes[30,32,33]. NusG facilitates connection between RNAP and the leading ribosome. This is achieved through the interaction of its the N-terminal domain (NTD) with RNAP and the simultaneous engagement of its C-terminal domain (CTD) with ribosomal protein S10 [6,10,31]. Additionally, NusA, another transcription elongation factor in *E. coli*, can also modulate of transcription-translation coupling. While NusA can augment and support the bridging function of NusG, it cannot replace it entirely [34,35].

Recently, using cryo-EM, researchers have begun to reveal atomic structures of *E. coli* transcription-translation complexes (TTCs)[35-37]. The insightful results delineate two distinct classes of TTCs. Firstly, "Collided Complexes" (referred to as TTC-A or “expressome”) are captured with short mRNA spacers between RNAP and the ribosome[35-37]. These complexes are notable for being incompatible with NusG bridging and NusA binding. Molecular modeling suggests that TTC-A would conflict with transcriptional processes in *E.coli*, including elongation, pausing, and termination[35]. Secondly, "Coupled Complexes” (referred to as TTC-B), characterized with longer mRNA spacers, are dependent on NusG and is capable of accommodating NusA[35,37]. Significantly, TTC-B is compatible with the full transcriptional cycle in *E.coli*[35,37].

Despite the wealth of available TTC structures, several fundamental questions remain unanswered, particularly concerning the dynamic interplay between ribosome movement and RNAP activity during translation elongation. As the ribosome deciphers the nascent mRNA, it undergoes a coordinated choreography of conformational changes -- binding and releasing of translation factors and tRNAs, translocating of the ribosome along the mRNA that further involves ratcheting of the 30S ribosomal subunit by ~9° relative to 50S subunit and the 30S head swivel by ~20° relative to the body[38-41]. Strikingly, all

reported TTCs show ribosomes in a static, non-rotated state with the initiator tRNA bound to the P site of the ribosome[35-37]. How these dynamic structural changes within the ribosome are accommodated within the coupled complex remains a puzzle.

Another critical question relates to the mechanistic basis of RNAP enhancement by the leading ribosome. The physical link between RNAP and the leading ribosome is postulated to promote transcription elongation by pushing a slow or paused RNAP[14,19,20]. Recently, the coupled ribosome was further revealed to be able to terminate the stalled RNAP which was arrested due to template-strand DNA damage[21]. However, the precise mechanism by which the ribosome exerts this mechanical force on RNAP remains obscure.

Finally, the comprehensive understanding of the transcription-translation coupling process and the biological significance of both "collided" and "coupled" TTCs are still subjects of uncertainty. The complete scope and implications of these complex interactions in cellular context are yet to be fully understood.

Here, to address these critical questions, we systematically assembled TTCs by incorporating the 70S ribosome, initiator tRNA fMet-tRNA^{fMet}, ternary complex EF-Tu•Phe-tRNA^{Phe}•GTP, and elongation factor EF-G into RNAP transcription elongation complex (Supplementary Fig. 1, 2, and 3)[38,42]. Using GTP analogs (GDPCP), antibiotics (viomycin and fusidic acid)[43-45], we captured a series of *E.coli* TTC cryo-EM structures at various stages of the translation elongation cycle, including the pre-translocation state (PRE state), the translation intermediate state (CHI state) and the post-translocation state (POST state). Our results unveil that (i) the ribosome within TTC-B is capable of pass-through translocation trajectory, accommodating mRNA with a codon spacer ranging from 7 to 10; NusA and NusG finely tune the RNAP orientations relative to ribosome, further supporting the functional significance of TTC-B in coupled transcription-translation. (ii) The TTC-A represents a state wherein the ribosome applies mechanical force on RNAP through mRNA, holding the ribosome in the PRE or early CHI state with mRNA having a codon spacer of 7 to 9. (iii) both TTC-A and TTC-B co-exist for spacer length of 7 to 9 codons, suggesting a dynamic conformational equilibrium between them; (iv) With nucleic acid scaffolds that have mRNA spacers shorter than 7 codons, the coupling complex de-couples. The new identified class of ribosomes with extracted RNA, indicates the TTC-A-dependent termination as an alternative mechanism for transcription termination.

Assembly of functional transcription-translation coupling complexes

We reconstituted TTCs using a mRNA fragment that annealed to a DNA scaffold, mimicking the elongation complex of an actively transcribing RNA polymerase. The mRNA was deliberately designed to

have a codon for phenylalanine following the initiation codon (Fig. 1A). We next employed translation elongation factor EF-G along with antibiotics to strategically capture various stages of the translation elongation cycle leading to dipeptide formation. The ternary complex EF-Tu•Phe-tRNA^{Phe}•GTP facilitated the delivery of the elongator tRNA to the A-site of the ribosome. By introducing EF-G with GTP analog, fusidic acid, or viomycin, we successfully trapped the TTC with the ribosome positioned at specific translation elongation intermediates and at the post-translocation state (Supplementary Fig. 1, 2, and 3). A summary of TTC states with specific codon spacer, antibiotics, and resolution shell can be found in Supplementary Table 1.

Structures of TTC-B in each state of translation elongation cycle

TTC-B, in the presence of NusA and NusG bridging the RNAP and ribosome (NusA-NusG-TTC-B), are obtained with nucleic acid scaffolds having mRNA spacers of 7, 8, 9, or 10 codons (Fig. 2A and Supplementary Table 1). A total number of 24 TTC-B structures were determined (Supplementary Fig. 4, and 5) and could be divided into five distinct TTC-B states (states 1-5), each representing different stages of the ribosome translation elongation cycle (Fig.2A and 2B, Supplementary Fig. 4, and 5, and Supplementary Table 1). Within each identified state, TTC-B could be further categorized into sub-class based on the relative orientation of RNAP to the ribosome (Supplementary Fig. 4, and 5). The spatial relationship of RNAP to the ribosome and the ribosomes in each state are identical in structures obtained with different spacer lengths of mRNA (Supplementary Fig. 4, and 5). In subsequent sections, we will elaborate on the ribosome elongation states 1 to 5, elucidating the conformational changes of RNAP relative to the ribosome, as mediated by the interactions of NusA and NusG.

In TTC-B state 1, the ribosome adopts a canonical non-rotated conformation (Fig.2A, first panel). High-resolution data clearly reveals the trajectory of mRNA as it emanates from RNAP transcription active center and transverses along a positively charged patch on ribosomal proteins uS3 into the mRNA entrance channel on the ribosome. Eventually, the mRNA forms base paired with the anticodon of the tRNA molecules. Within this conformation, two tRNAs adopt the classical A/A and P/P states, while a tRNA with low occupancy is found in the E-site (Fig.2B, first pane l). These observations align with previous studies on translation elongation[38,41,46,47].

The TTC-B states 2 and 3 were captured using viomycin with mRNA spacer of 9 or 10 codons. In both states, the 30S ribosomal subunit undergoes a rotation relative to the 50S subunit, anchored by EF-G to the

sarcin-ricin loop (Fig.2A, Supplementary Fig. 6A). In state 2, the domain IV of EF-G (EF-G pre state, "EF-G pre") is positioned adjacent to the A site of 30S, engaging with the anticodon stem of the A-site tRNA. The acceptor arm of $tRNA^{Phe}$ in the A site is displaced by ~25 Å towards the peptidyl transfer center (PTC), while the deacetylated P-site tRNA transitions to the E site of the 50S subunit, resulting in an A/P* and P/E configuration, respectively (Fig.2B, second panel). In state 3, the domain IV of EF-G (EF-G pre/post state, "EF-G pre/post") moves ~14 Å closer to the anticodon stem of the A site tRNA (Supplementary Fig. 6B). The conserved loop (residues 507-514 in *E.coli* EF-G) interacts extensively with the anticodon stem-loop of the A site tRNA, leading to a shift of $tRNA^{Phe}$ from A/P* state to ap/P state, and $tRNA^{fMet}$ from P/E to pe/E state (Fig. 2B, third panel).

In state 4, the domain IV of EF-G (EF-G post state, "EF-G post") moves ~18 Å further and takes the A site on 30S subunit, resulting in the $tRNA^{fMet}$ being in the P/E site (Fig. 2B, fourth panel, and Supplementary Fig. 6B). This state was captured using GDPCP, viomycin, or fusidic acid. The TTC-B states 2-4 represent transcription-translation coupling complexes with ribosomes progressing along the translocation trajectory.

In TTC-B state 5, following the translocation of tRNA by one codon, the 30S subunit reverts to the non-rotated state. Domain IV of EF-G occupies the A site, positioning $tRNA^{Phe}$ and $tRNA^{fMet}$ in P/P and E/E site, respectively (Fig.2B, fifth panel). This state was captured using GDPCP, viomycin, and fusidic acid. It represents TTCs with ribosome in post-translocation state, which is usually followed by subsequent release of EF-G, and setting the stage for the A site to accommodate an incoming aminoacyl-tRNA, thereby initiating another cycle of translation elongation[38,41,42]. Take together, The TTC-B state 1-5 represent the whole states of translation elongation cycle with transcription-translation coupling.

Throughout the translation elongation cycle, the RNAP within the TTC-B engages with 30S subunit in a flexible and yet stable manner. The RNAP densities in all five states of TTC-B are clear, enabling unambiguous rigid-body docking of atomic structures of the transcription elongation complex (TEC). The architectures of these five complexes are similar, yet not identical to previously reported TTC-B structures[35]. In these, NusG bridges RNAP and the ribosome with NusG-N binding to RNAP and NusG-C binding to ribosomal protein uS10 on 30S head; NusA further stabilizes the complexes through its AR2 and NusA-N domain binding to RNAP, and its KH1/2 domain interacting with ribosomal protein uS2 and uS5 on the 30S body. Additionally, the RNAP β' ZBD domain interacts with ribosomal protein uS3 (Fig.2A and D). Comparative analysis of the five TTC-B states provides detailed insights into the comformational dynamics between RNAP and the ribosome during the transcription elongation cycle. From TTC-B state 1 to state 2, the

30S subunit rotates ~8.6° (counter-clockwise direction from the top view on 30S), while the RNAP rotates ~7.5° in the same direction in a coordinated manner (as per superposition on 50S, Fig.2C. left). Concurrently, the 30S head domain swivels ~4.4° with RNAP rotating ~9.1° in the same direction (Fig.2C. right). These coupled movements between RNAP and the 30S subunit are fine-tuned by NusG and NusA, which rotates ~11.3° and ~2.2°, respectively (Fig.2C. right). Besides these coupled movements, The RNAP also exhibits a ~12.5° swinging movement relative to 30S throughout the translation elongation cycle (comparing the five states of TTC-B by structure superposition on 30S, Fig. 2D). In some state of TTC-B, several subclasses are also discerned (e.g. subclass1, 2, and 3 in state 1 and state 5; subclass1 and subclass2 in state 3 and 4). These subclasses differs by ~15° rotation of RNAP relative to 30S, resulting the distance between the transcription active center and the ribosome mRNA-entrance portal changes from 79 Å, to 85 Å or 90 Å, respectively (Supplementary Fig. 7). In general, the movements between RNAP and ribosome in TTC-B is relatively free but within a certain range.

The stable yet flexible interactions between RNAP and the ribosome are contingent on the subdomain architecture of NusG and NusA. The NusA protein forms an open-rectangular-frame, termed "pantograph" structure, comprising six domains: NusA-NTD, -S1, -KH1, -KH2, -AR1 and -AR2. NusA-NTD interacts with RNAP aCTD^{II} and can shift by ~22 Å across the five different states. However, the flexible linker connecting NusA-S1 and NusA-NTD (residues 133-139 in *E. coli* NusA) allows NusA-S1 to remain relatively stable to its NTD domain; The flexible linkers between the NusA KH2 and AR1 domains (residues 394-403 in *E.coli* NusA), and between the AR1 and AR2 domains (residues 428-435 in *E.coli* NusA), enable the AR2 domain to move with RNAP aCTD^{I} (within a range of ~10 Å) while maintaining the binding of the NusA-KH2 domain with ribosomal proteins uS5 and uS2 (Fig.2D and 2E). NusG, similar with NusA, has a flexible linker (residues 116-128 in *E.coli* NusG) between its NTD and CTD, allowing the NusG NTD to shift ~26 Å in response to the swinging of RNAP without disturbing the interactions between the NusG CTD and uS10 (Fig.2D and 2F).

Based on the these observations that TTC-B is compatible with ribosome conformational changes during the translation elongation cycle and coordinates transcription elongation with translation elongation, we propose that TTC-B modulates NusG-dependent, NusA-dependent dynamic transcription-translation coupling in *E.coli*.

Structures of TTC-A in early stage of translation elongation cycle

In addition to TTC-B, we also captured two distinct collided coupling states (TTC-A) in a ratchet state[39] with EF-G, the pre-translocation and translocation intermediate, specifically designated as state 2 and state 3. A notable feature of both states is the absence of NusA and the lack of interaction between the NusG-CTD and ribosomal protein uS10, rendering them unable to sustain the canonical TTC-B state (Supplementary Fig. 8). The overall architectures of these states are distinctly different from the previously identified collided coupling state (referred to as TTC-A state 1 for clarity). In TTC-A state 1, the ribosome is in a non-ratcheted conformation, while the action of EF-G propels it into the ratcheted one in TTC-A states 2 and 3. Specifically, in TTC-A state 2, EF-G is in the 'EF-G pre' state, with two tRNAs occupying the A/P* and P/E sites, respectively (Fig. 3A left). In TTC-A state 3, the 30S subunit is also in a rotated state, with EF-G assuming the 'EF-G pre/post' state, and the two tRNAs situated in the A/P and P/E sites, respectively (Fig. 3A right).

The spatial relationships between RNAP to the ribosome in these newly identified states of TTC-A also contrasts with that in the previously characterized "initiation-like" TTC-A state 1[35-37], where RNAP is more flexible and has reduced protein-protein interactions with the 30S subunit. Specifically, RNAP in TTC-A state 2 exhibits a ~2.5° counterclockwise rotation compared to TTC-A state 1 (from the top view, as compared in the two states of TTC-A by structure superposition on 30S, Supplementary Fig. 8A). From state 2 to state 3, RNAP undergoes further rotation of ~4.1° and shifts ~2.1Å relative to the ribosome. These RNAP movements relative to the 30S lead to the disruption of interfaces between RNAP β' ZBD domain and ribosomal protein S4 (Fig. 3D), and between RNAP αI and ribosomal protein S10 (Fig. 3E), resulting in a significantly poorer density in these regions of RNAP. Although we reconstituted TTC with varying mRNA spacer length (7-10 codons) and different GTP analogs or antibiotics, only TTC-A states 2 and 3 (CHI-states) were captured. This suggests that TTC-A cannot be formed during later stages of the translation elongation process.

Functional relationship between TTC-A and TTC-B

The simultaneous capture of both TTC-A and TTC-B in the presence of a codon spacer ranging from 7 to 9 codons raises intriguing possibilities about potential state transformations during the translation elongation process (Fig. 3F). In our earlier work[35], TTC-A was exclusively observed in state 1 using a spacer-7 codons mRNA (Fig. 3F, upper panel). However, in this study, both TTC-A and TTC-B were obtained using a spacer-7 codons mRNA, with a near-equal particle distribution of 50.5% for TTC-A and 49.5% for TTC-B (as depicted in Fig. 3F, lower panel and Supplementary Table 1). These findings imply that the introduction of translation factors EF-Tu and EF-G might induce a significant remodeling of the overall architecture of TTC, potentially

facilitating the transition from TTC-A into TTC-B during translation elongation. Notably, when using a codon spacer of 9 codons, previous experiments[35] yielded only the TTC-B state (Fig. 3F, upper panel), while the current study achieved a simultaneous capture of both TTC-A and TTC-B states. Despite TTC-B is dominant (92.5%) in this scenario, the presence of TTC-A (7.5%) is a crucial observation (as depicted in Fig. 3F, lower panel and Supplementary Fig. 1). This co-occurrence suggests that even during active translation transcription coupling, as typified by the TTC-B state, translation elongation factors may potentially disrupt the stabilizing interactions mediated by NusA and NusG, thereby leading to a state transition from TTC-B to TTC-A. This transition indicates a dynamic and potentially reversible interaction between the components of the transcription-translation machinery.

In light of our observations regarding TTC-A states 2 and 3, we propose a model where RNAP undergoes a counterclockwise rotation during the transition from TTC-A to TTC-B and conversely, a clockwise rotation during the transition from TTC-B to TTC-A (Supplementary Fig. 8B).

TTC-A may also play a pivotal role in the termination of transcription. Our previous research, employing a nucleic acid scaffold with a mRNA spacer of 5 and 6 codons, yielded exclusively non-rotated TTC-A structures (Fig. 3F, upper panel). However, in the current study with the same configuration, where we energized the ribosome with translation elongation factors, we observed a complete absence of TTCs (Fig. 3F, Supplementary Fig. 9). Further analysis identified two distinct classes of ribosomes within the same cryo-EM dataset. The first class, displaying no mRNA density around the ribosome's mRNA entry channel, represents what we termed the "un-coupled" ribosome (Supplementary Fig. 10B). These could be free, non-translating ribosomes and are also observed in other TTC-A datasets with 7 to 9 codon spacers. The second class is more biologically significant and presents robust mRNA density interacting with the positively charged patch of the ribosomal proteins uS3, extending from the mRNA entry channel to the decoding center. We refer to this second class as 'de-coupled' ribosomes (Supplementary Fig. 10A), hypothesizing that they emerge from transcription termination, triggered by the ribosome exerting mechanical foce on the TEC, consequently disrupting it and extracting the RNA. The findings of our study suggest that within the transcription-translation coupling complex, the ribosome can promote the termination of TEC as an alternative mechanism for transcription termination. In this scenario, the ribosome, through continuous translation in the TTC-A state, shortens the mRNA length between RNAP and the ribosome to a critical point (7-condon spacer) where the transition from TTC-A to TTC-B is not viable.

In summary, our comprehensive investigation has unveiled two distinct types of TTCs, each

characterized by ribosomes in various states of translating elongation cycle. The first type, TTC-B, is formed using nucleic acid scaffolds with mRNA spacers ranging from 7 to 10. In this state, RNAP is stabilized by connecting to the ribosome's 30S body via NusA and to the 30S head via NusG. This architecture is adeptly adapted to accommodate changes in ribosome conformation throughout the translation elongation cycle, ensuring compatibility with ongoing transcription elongation. Consequently, TTC-B represents the functional, active state during the transcription-translation coupling (Fig.4). In contrast, TTC-A is obtained with nucleic acid scaffolds with 7 or 9 spacer codons. In TTC-A, dynamic changes in ribosome conformation during translation, particularly during mRNA translocation, would exert mechanical force on RNAP, potentially transforming the TTC-A state into TTC-B. Furthermore, with a spacer shorter than 7 codons, TTC-A may no longer be able to transform into TTC-B. In such cases, the elongation ribosome could terminate the RNAP by dissociating the mRNA from the RNAP transcription active center. Therefore, the TTC-A represents a crucial functional state within the pathway, where the ribosome engages with the halted or backtracked RNAP. This interaction can result in either the reactivation of RNAP or its termination (Fig.4).

Discussion

During transcription elongation, RNA polymerase (RNAP) adds ribonucleoside triphosphates (rNTPs) to the growing RNA chain, incorporating one rNTP per cycle[48]. While during translation elongation, ribosomes use the synthesized mRNA as a template to add amino acids to the growing nascent peptide chain, incorporating one codon (three ribonucleotides) per cycle[38]. In addition, both RNAP and ribosome undergo inter-domain movements during the synthesizing cycle[31,38,39,41]. Thus, in order to coordinate the synchronization of active transcription and translation, the transcription-translation coupling process needs a very special connections between RNAP and ribosome.

Our results reveal that the interactions between RNAP and ribosome in TTC-B are relatively flexible yet within a certain range. These interactions, mediated by NusA and NusG, allow the coupling complex to adjust to the changes in ribosome tertiary structure that occur during the translation elongation cycle. Furthermore, the TTC-B contains several subclasses which differs by ~15° rotation of RNAP relative to 30S, resulting the distance between the transcription active center and the ribosome mRNA-entrance portal changes from 79 Å, to 85 Å or 90 Å, respectively (Supplementary Fig. 6A and 6B). Since the average distance between two nucleotide is ~3.4Å, the difference in length between subclass1 and subclass3 is ~3-4 nt. These specific architectures enable TTC-B accommodating 3-4 nucleotide difference in mRNA within subclasses. Taken

together, TTC-B is accommodated to the different synthesizing patterns between transcription (1nt per cycle) and translation (3nt or 1 codon per cycle) without disrupting their own activities. On the other hand, in TTC-A, the interactions between RNAP and ribosome are extensive tight[35-37]. In addition, in TTC-A, the mRNA moves directly from the RNAP transcription active center to the translation active site. As a result, there is less room for the mRNA to adapt to any changes during the translation elongation cycle. It is consistent with our observations that the coupling complex can hardly remain in TTC-A without experiencing any conformational changes for later stages of translation elongation process.

With respect to functional consequences, TTCs were noted for their role in reactivating backtracked RNAP, enhancing transcription processivity at the expense of RNA synthesis fidelity through mechanical and allosteric mechanisms[14,19,20]. Our results suggests the potential equilibrium between TTC-A and TTC-B, determined by specific codon spacer lengths, may be critical in facilitating the reactivation of backtracked RNAP during TTC. This dynamic suggests that the translating ribosome acts as a propelling force for RNAP, and upon the restart of RNAP, both the RNAP and ribosome revert to the functional TTC-B state, thereby maintaining the efficiency and integrity of the transcription-translation coupling process.

Transcription termination in bacterial is crucial for regulating gene expression, recycling RNAP, preventing transcription-replication collisions, thereby maintaining genome stability[16,17]. Transcription in bacteria can be terminated via two primary mechanisms: intrinsic (or Rho-independent) termination, relying on the interaction of nucleic acid with RNAP, and Rho-dependent termination, mediated by the ring-shaped hexameric ATP-dependent helicase Rho[24-27]. Our molecular modeling suggests that neither of these TTCs (TTC-A or TTC-B) is compatible with Rho factors, involved in Rho-dependent transcription termination (Supplementary Fig. 11). TTC-A is also incompatible with intrinsic termination elements[35]. The findings of our study suggest that within the transcription-translation coupling complex, the ribosome can promote the termination of TEC as an alternative mechanism for transcription termination. In this scenario, the ribosome, through continuous translation in the TTC-A state, shortens the mRNA length between RNAP and the ribosome to a critical point (7 codon spacer) where the transition from TTC-A to TTC-B is not viable. We suggest the structural and mechanistic studies that involve the reactivating or terminating backtracked RNAP by the transcription-translation coupling, will be facilitated by assembling the same complex as our study but using the backtracked RNAP with mRNA spacer length of 5 or 6 codons (Fig 4).

Taken together, our results answer the previously open questions regarding whether transcription-translation complexes accommodate changes in ribosome throughout the translation elongation

cycle, provide a foundation for understanding the role of TTC-A and TTC-B in the process of transcription-translation coupling, suggest the potential transcription termination function by TTC-A, and set the stage for, and point to the most effective approaches for, future work to define the mechanisms of reactivating or terminating backtracked RNAP by the transcription-translation coupling.

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Figures legends:

Fig. 1. Structure determination: transcription-translation complexes (TTCs)

(A) Nucleic-acid scaffolds. Each scaffold comprises nontemplate- (gray) and template-strand (blue) oligodeoxyribonucleotides and one of six oligoribonucleotides (red), corresponding to mRNA. Dashed black box labeled "TEC" represents a portion of nucleic-acid scaffold that forms TEC upon the addition of RNAP. It includes a 10 nt nontemplate- and template-strand ssDNA segments forming "transcription bubble", a 9 nt of mRNA engaged with the template-strand DNA as RNA- DNA "hybrid", and 5 nt of mRNA, on diagonal, in the RNAP RNA-exit channel. The orange line labeled "Met" represents the mRNA AUG codon intended to occupy ribosome P site upon the addition of ribosome and fMet-tRNA^{fMet}. The dark green lines labeled “Phe” represents mRNA UUU codon intended to occupy ribosome A site upon addition of Phe-tRNA^{Phe}, The purple line labeled “Leu” represents mRNA CUU codon.The "spacer" denotes mRNA length between the TEC and the initiation codon AUG counted by codons.

(B) Schematic of TTCs reconstitution. In the first step (left panel), RNAP core in complex with nucleic acid scaffold forms TEC. In the second step (second panel), TEC binds with ribosome 70S through NusA and NusG bridging, and mRNA AUG codon pairs with anticodon of fMet-tRNA^{fMet} in the P site of 30S ribosomal subunit. In the third step (third panel), the EF-Tu ternary complex delivers Phe-tRNA^{Phe} into the decoding center on 30S ribosomal subunit. In the fourth step (right panel), EF-G motivates translocation of mRNA and paired tRNAs. RNAP in TEC is represented in gray, non-template strand DNA, template strand DNA, and RNA are in black, blue, and red, respectively. The codons AUG, UUU, and CUU are in orange, green, and purple, respectively. The non-rotated 30S subunit is shown in yellow, rotated 30S subunit in wheat, and 50S subunit in dark gray. NusA is shown in light blue, NusG in magenta, fMet-tRNA^{fMet} in orange, Phe-tRNA^{Phe} in forest, and EF-G in cyan.

Fig. 2. Cryo-EM structures of TTC-B

(A) Side view of the TTC-B model layered on the top of cryoEM maps. The five representative panel, from left to right, are TTC-B in state1 at 4.5 Å resolution (n = 9), state2 at 4.9 Å (n = 9), state3 at 5.2 Å (n = 10), state4 at 4.9 Å (n = 9), and state5 at 4.6 Å (n = 9), respectively. Color-coding is the same as in Figure 1, except when stated differently. Ribosome stalk is omitted for clarity in this and all subsequent images.

(B) Close-up view of mRNA connecting the RNAP active center and the tRNA channel in the five TTC-B states. The cryoEM map is represented by blue mesh. The disordered mRNA nucleotides indicated by dashed lines. RNAP

active-center catalytic Mg^{2+} in purple sphere. Three rectangles with dashed lines indicate A/P/E site in the ribosome.

(C) Structure comparison of TTC-B state1 and state2 by superposition of 50S subunit. Top view from mRNA entry channel of 30S subunit (left panel) and orthogonal view orientation showing the movement of RNAP and 30S subunit (right panel). The 16S rRNA in TTC-B is shown in yellow ribbon for state1 and wheat for state 2. The RNAP is shown in gray surface for state1 and cyan for state2. The NusA is shown in blue and NusG magenta with state 1 distingished with transparency. The superposition reveals a 11.3° counterclockwise rotation of NusG (magenta arrow) and a 2.2° counterclockwise rotation of NusA (blue arrow).

(D) Comparison of TTC-B state1 to 5 based on 30S subunit superimposition. Color code as in Figure 2A with states 2-4 in more transparent colors.

(E) Close-up view of points flexibility in NusA and NusG. Flexible linkages in NusA (NTD-S1 linker, AR1-KH2 linker, AR1-AR2 linker; dashed line circle) and flexible NusG bridging of RNAP and ribosome (NusG linker; dashed line circle). Colors as in Figure.2A with state2-4 in more transparent colors.

Fig. 3. Cryo-EM structures of TTC-A

(A) Cryo-EM structures of TTC-A obtained using mRNA with codon spacer of 7 to 9. Structures shown are TTC-A state2 at 7.0 Å resolution (n = 9) and state3 at 4.6 Å (n = 7). Views and colors are the same as in Figure 2A. Absence density in TTC-A state 3 is indicated by a dashed oval.

(B) Closeup view of mRNA connecting the RNAP active center and the tRNA channel in two states of TTC-A. Views and colors are same as in Figure 2B.

(C) Comparison of TTC-A state 2 and 3 by superimpose on 30S subunit. The 16S rRNA of 30S subunit in TTC-A is shown in yellow. The ribosomal protein uS3, uS4 and uS10 interacting with RNAP are highlighted in orange, dark green, and red, respectively. Superposition reveals a 4.1° rotation and 2.1 Å translation between RNAP in state2 (white surface) and RNAP in state3 (light cyan surface), as illustrated by black arrows.

(D) Absence of EM density for RNAP β' ZBD domain in TTC-A state3. EM density is represented by blue mesh. Atomic models for RNAP β' and uS4 are shown in pink and dark green ribbon, respectively. The location of missing EM density for β' ZBD is indicated by a dashed oval. The β' ZBD in TEC in the absence of ribosome (TTC-A state2) is shown in white ribbon.

(E) Absence of EM density for parts of RNAP αI domain in TTC-A state3. The cryoEM map is rerpresented by

blue mesh. The atomic models for RNAP αI and uS10 is shown in light green and red ribbon, respectively. The missing cryoEM map for parts of RNAP αI is indicated by dashed oval. The αI in TEC (TTC-A state2) is shown as white ribbon.

(F) Distribution of TTC-A and TTC-B in different spacer length. Upper panel: distribution of TTC-A and TTC-B in "translational static state" with spacer lengths of 5, 6, 7, 8, 9, or 10 codons; lower panel: distribution of TTC-A and TTC-B in "translational translocation states" TTCs with spacer lengths of 5, 6, 7, 8, 9, or 10 codons.

(G) Cryo-EM structures of "de-coupled" ribosome obtained using mRNA with codon spacer of 5 to 6. Views and colors are as in Figure 2A. Cryo-EM maps (gray surface) and fit (brick-red ribbons) for prematurely terminated mRNA are illustrated by red arrow.

Fig. 4. Schematic depiction of proposed transcription-translation coupling throughout translation elongation cycle. With a mRNA codon spacer length of 7 to 10, the TTCs are in TTC-B state. Ribosome throughout various of translation stages, including "pre-translocation" ribosome in state 1, "translocation intermediate" in state 2 to 4 and "post-translocation" in state 5. The RNAP in TTC-B remains stable with the ribosome due to NusA and NusG bridging both of them. With mRNA spacer lengths of 7, 8, and 9, the TTCs could also being in TTC-A state. A state is incompatible for ribosome pass through the translation elongation cycle but could transformed into TTC-B. With mRNA spacer length shorter than 6 (including 6 codons), TTCs cannot be formed, and the TEC is terminated by ribosome. Components used in models are further explained in the lower panel. The models with dashed line are not determined in our work.

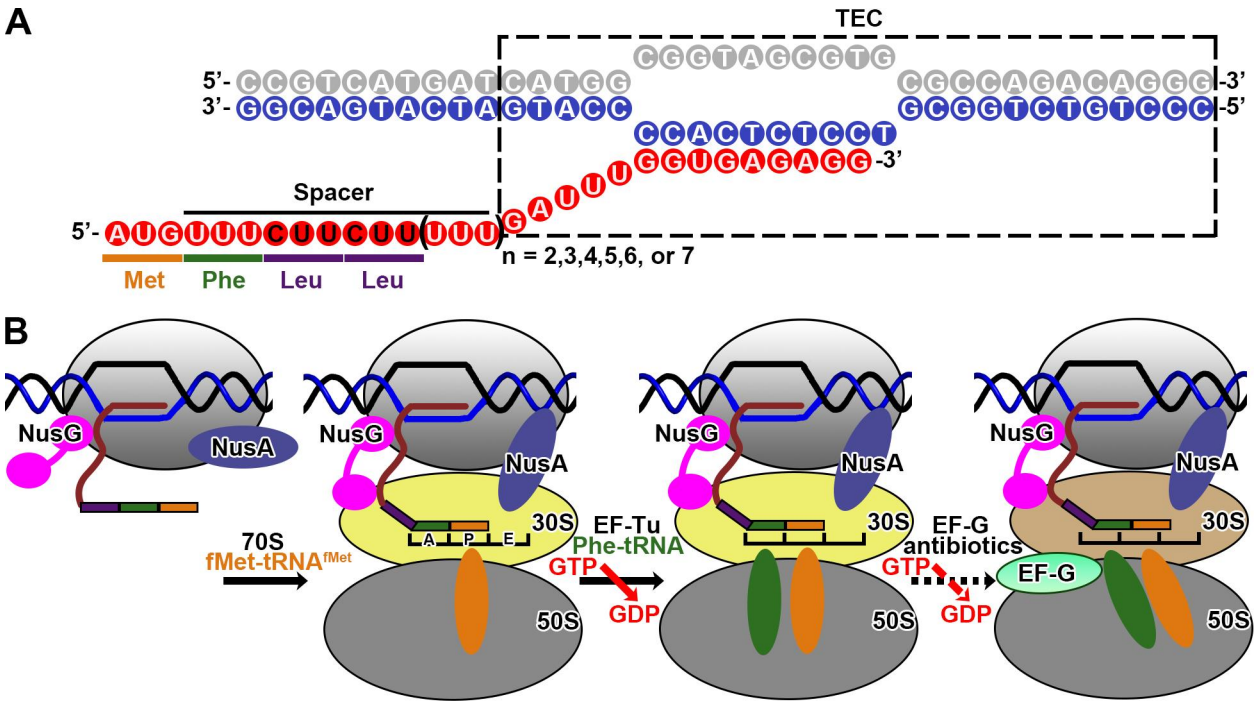
A
TEC
5'- CCGTCATGATCATGG
3'- GGCAGTACTAGTACC
CGGTAGCGTG
CCACTCTCCT
GGUGAGAGG -3'
CGCCAGACAGGG -3'
GCGGTCTGTCCC -5'
Spacer
5'- AUGUUUCUUCUU(UUU)G AUUU
n = 2,3,4,5,6, or 7
Met
Phe
Leu
Leu
B
NusG
NusA
70S
fMet-tRNAfMet
30S
50S
A
P
E
EF-Tu
Phe-tRNA
GTP
GDP
EF-G
antibiotics
EF-G

Figure 1

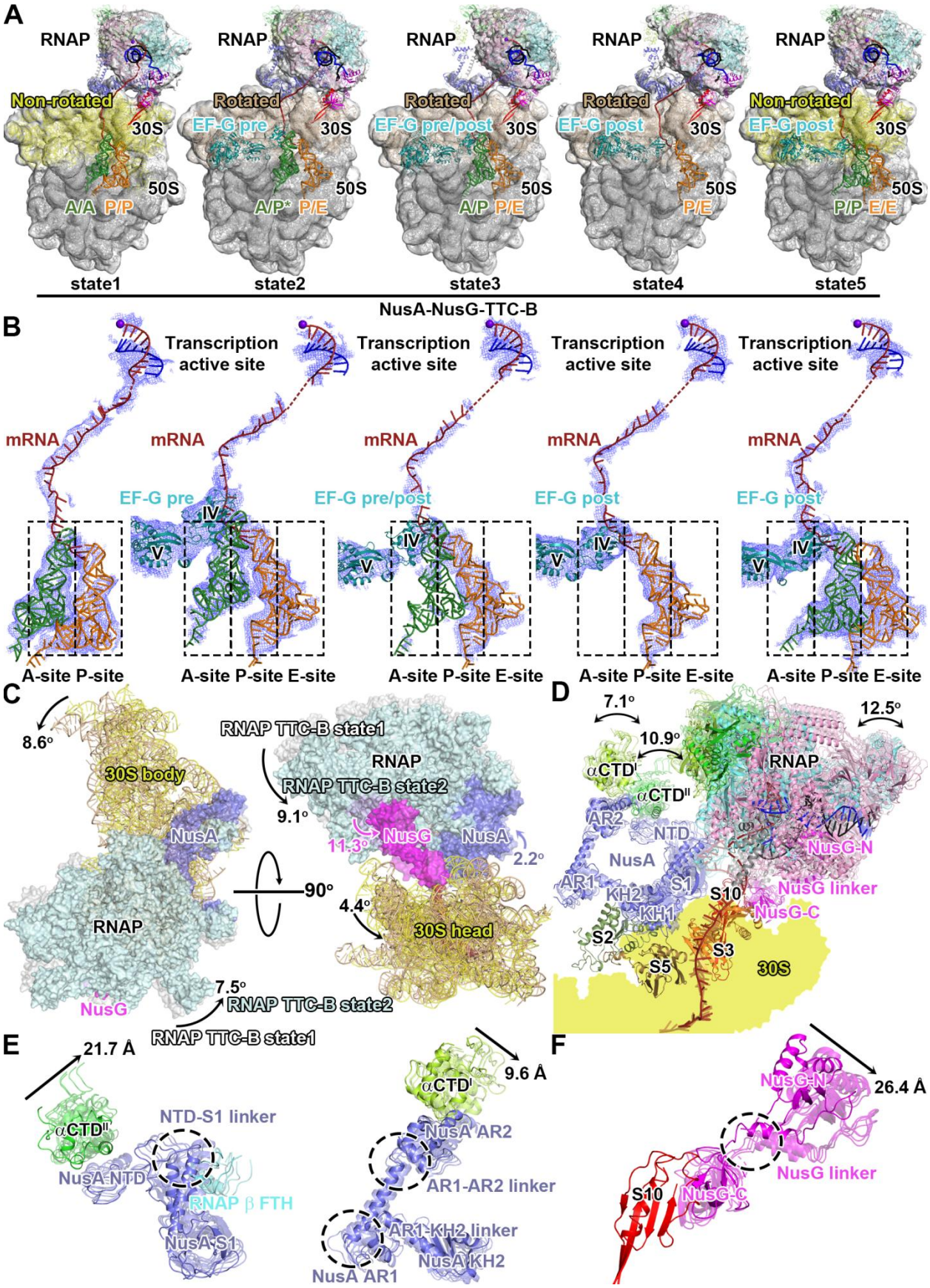
A
RNAP
Non-rotated
30S
50S
A/A P/P
state1
Rotated
EF-G pre
A/P* P/E
state2
EF-G pre/post
A/P P/E
state3
EF-G post
P/E
state4
Non-rotated
EF-G post
P/P E/E
state5
NusA-NusG-TTC-B
B
Transcription active site
mRNA
EF-G pre
EF-G pre/post
EF-G post
IV
V
A-site P-site
A-site P-site E-site
C
8.6°
30S body
NusA
RNAP
NusG
RNAP TTC-B state1
RNAP
RNAP TTC-B state2
9.1°
11.3°
NusG
NusA
2.2°
90°
4.4°
30S head
7.5°
RNAP TTC-B state2
RNAP TTC-B state1
D
7.1°
10.9°
12.5°
αCTD^I
αCTD^II
RNAP
AR2
NTD
NusA
NusG-N
AR1
KH2
S1
S10
NusG linker
KH1
NusG-C
S2
S3
S5
30S
E
21.7 Å
αCTD^II
NTD-S1 linker
NusA-NTD
RNAP β FTH
NusA-S1
9.6 Å
αCTD^I
NusA AR2
AR1-AR2 linker
AR1-KH2 linker
NusA KH2
NusA AR1
F
26.4 Å
NusG-N
NusG linker
S10
NusG-C

Figure 2

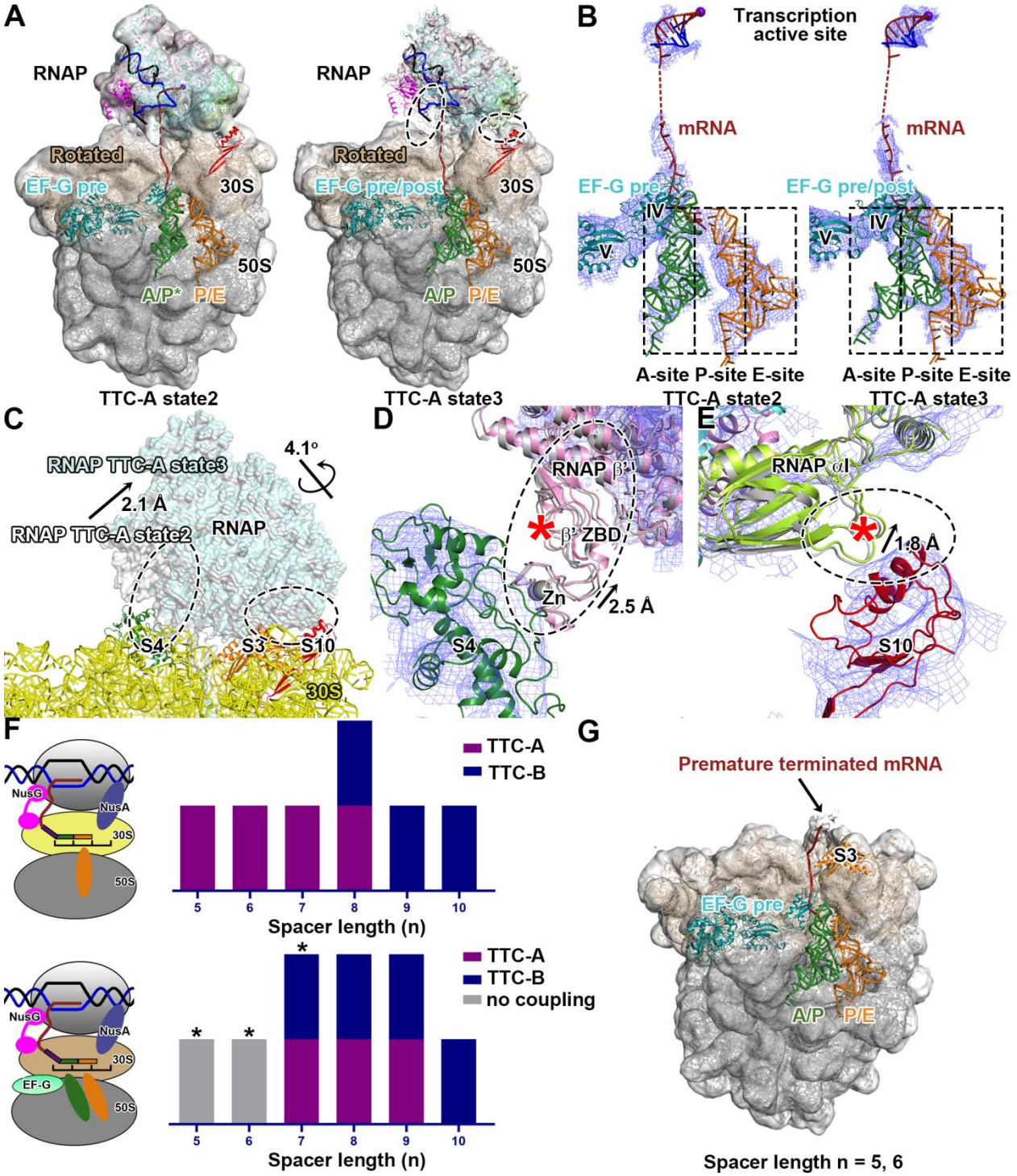
A
RNAP
Rotated
EF-G pre
30S
50S
A/P*
P/E
TTC-A state2
RNAP
Rotated
EF-G pre/post
30S
50S
A/P
P/E
TTC-A state3
B
Transcription active site
mRNA
EF-G pre
IV
V
A-site P-site E-site
TTC-A state2
mRNA
EF-G pre/post
IV
V
A-site P-site E-site
TTC-A state3
C
RNAP TTC-A state3
4.1°
2.1 Å
RNAP TTC-A state2
RNAP
S4
S3
S10
30S
D
RNAP β'
β' ZBD
Zn
2.5 Å
S4
E
RNAP αI
1.8 Å
S10
F
NusG
NusA
30S
50S
TTC-A
TTC-B
5
6
7
8
9
10
Spacer length (n)
NusG
NusA
30S
EF-G
50S
TTC-A
TTC-B
no coupling
5
6
7
8
9
10
Spacer length (n)
G
Premature terminated mRNA
S3
EF-G pre
A/P
P/E
Spacer length n = 5, 6

Figure 3

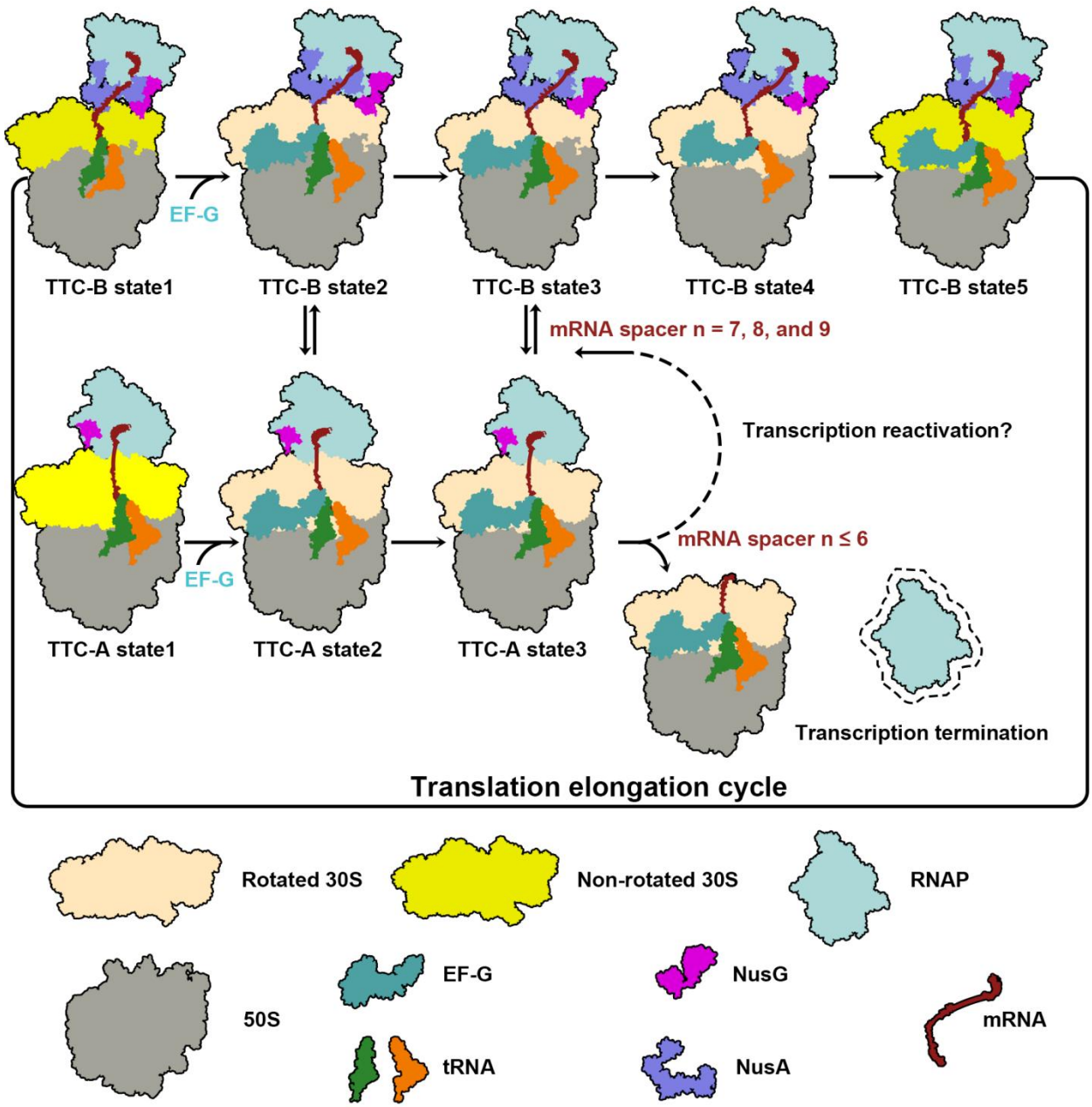
EF-G
TTC-B state1
TTC-B state2
TTC-B state3
TTC-B state4
TTC-B state5
mRNA spacer n = 7, 8, and 9
Transcription reactivation?
mRNA spacer n ≤ 6
EF-G
TTC-A state1
TTC-A state2
TTC-A state3
Transcription termination
Translation elongation cycle
Rotated 30S
Non-rotated 30S
RNAP
50S
EF-G
NusG
mRNA
tRNA
NusA

Figure 4