Supplemental Information for:

Trigger-helix folding pathway and SI3 mediate catalysis and hairpin-stabilized pausing by *Escherichia coli* RNA polymerase

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Supplemental information:

- Figure S1. Elongation by wild-type, F937-736, and 6Ala RNAPs
- Figure S2. Exonuclease digestion of ECs formed with wild-type and F937-736 RNAPs
- Figure S3. Δ SI3a and Δ SI3b show increased elongation rate on longer templates.
- Figure S4. Test of wild-type and PGPP RNAPs for possible misincorporation.
- Table S1. Strains, plasmids, and oligonucleotides
- Table S2. Nucleotide addition rate measurements
- Table S3. Kinetics of pausing at the his pause signal



A Scaffold^{long} = complementary Scaf^{GTP}+50 bp

Fig. S1. Elongation by wild-type, F937-736, and 6Ala RNAPs

(A) Schematic of ScaffoldLong, a derivative of ScaffoldGTP with additional downstream DNA (42 basepairs) and a fully complementary NT strand.

(B) Schematic of reaction. RNAPs were reconstituted at G13, elongated to G15 with addition of 10µM 32P-GTP, and given 1 mM all four NTPs at time zero.

(C) Reaction products were halted at the times indicated and separated by denaturing polyacrylamide electrophoresis. The red boxes indicate the apparent products from the crosslinked F937-736 RNAP.



FL C C А G Т С A Т G С -15 -14 А G G A

Fig. S2. Exonuclease digestion of ECs formed with wild-type and F937-736 RNAPs.

(A) Schematic of exonuclease assay. After reconstitution of complexes and crosslinking, exonuclease is added at time zero, with samples removed during digestion.

(B) Samples separated on 20% PAGE, time points as indicated.

(C) Mapping of cleavage products by separation alongside an A/G marker.



Fig. S3. Δ SI3a and Δ SI3b show increased elongation rate on longer templates. Top. Schematic of promoter-driven template containing a large fragment of rpoB to allow transcription of a 668-nt transcript (pIA146; Table S1).



Fig. S4. Test of wild-type and PGPP RNAPs for possible misincorporation. Transcription reactions with wild-type or PGPP RNAPs were performed on ScaffoldGTP, as in Figure 4. Reactions were incubated with 10 mM of both ATP and UTP up to 1 second but no extension beyond U17 (to misin-corporate a G) was detected. Thus, we see no evidence for purine-for-purine misincorporation.

Table S1. Strains, Plasmids, and Oligonucleotides

Stock			Source or	
#	Name	Description	Note	
Strains	Strains			
1607	DH10b	F- mcrAΔ(mrr-hsdRMS-mcrBC) φ80 lacZΔM15 ΔlacX74		
		deoR recA1 araD139D(araA-leu)7697 galU galK rpsL		
		endA1 nupG		
	C2566	C2566,T7 Express. fhuA2 lacZ::T7 gene1 [lon] ompT gal	New	
		sulA11 R(mcr-73::miniTn10TetS)2 [dcm] R(zgb-	England	
		210::Tn10TetS) endA1 Δ(mcrC-mrr)114::IS10. recA-	Biolabs	
2657	RL2657	recA derivative of C2566	This work	
<u>Plasmi</u>	ds_			
2956	pRM756	Expresses wild-type <i>E. coli</i> RNAP ($\alpha_2\beta\beta'\omega$) with His ₁₀ tag	This work	
		on the β' C-terminus		
2995	pRM795	Expresses wild-type <i>E. coli</i> RNAP ($\alpha_2\beta\beta'\omega$) with His ₁₀ and	(Ref. 2)	
		HMK tags on the β C-terminus		
4963	pDJ124	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	(Ref. 2)	
		(α2ββ ['] ω) containing β' 1937C Q736C		
4291	pMTF028	pRM756 derivative that expresses mutant <i>E. coli</i> RNAP	This work	
		(α2ββ'ω) containing β' G1136P, G1137P (GGPP)		
4954	pDJ115	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	(Ref. 2)	
		(α2ββ ['] ω) containing β' I937C P1139C		
2961	pRM761	pRM756 derivative that expresses mutant <i>E. coli</i> RNAP	This work	
		(α2ββ'ω) containing β' L930P, T931P (LTPP)		
5126	pRM826	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work	
		(α2ββ'ω) containing β' (KDPP)		
5127	pRM827	pRM795 derivative that expresses mutant E. coli RNAP	This work	
		(α2ββ'ω) containing β' (DIPP)		
5132	pRM832	pRM795 derivative that expresses mutant E. coli RNAP	This work	
		$(\alpha 2\beta \beta' \omega)$ containing β' (PGPP)		

2959	pRM759	pRM756 derivative that expresses mutant <i>E. coli</i> RNAP	(This work
		$(α_2 β β' ω)$ containing β' Δ943-1130 (ΔSI3a)	and Ref. 3)
2993	pRM793	pRM756 derivative that expresses mutant <i>E. coli</i> RNAP	(This work
		$(α_2ββ'ω)$ containing β' Δ945-1132 (ΔSI3b)	and Ref. 4)
5140	pRM840	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ'ω) containing β' (DIPP) Δ945-1132 (ΔSI3b)	
5154	pRM854	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ´ω) containing β' L930P, T931P (LTPP) 937C 736C	
5144	pRM844	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ'ω) containing β' (DIPP) 937C 736C	
4967	pDJ128	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ'ω) containing β' 937C 736C Δ 945-1132 (Δ SI3b)	
5162	pRM862	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ'ω) containing β' (DIPP) Δ945-1132 (ΔSI3b) 937C	
		736C	
5155	pRM855	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ'ω) containing β' (LTPP) Δ945-1132 (ΔSI3b) 937C	
		736C	
4288	pMTF025	pRM756 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		$(\alpha_2 \beta \beta' \omega)$ containing β' 6Ala (924A, 926A, 927A, 11336A,	
		1137A, 1139A)	
5226	pRM926	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ´ω) containing β' 6Ala 937C 736C Δ 945-1132	
		(ΔSI3b)	
5227	pRM927	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ'ω) containing β' 6Ala 937C 736C	
2996	pRM796	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		(α2ββ΄ω) containing β' 6Ala Δ945-1132 (ΔSI3b)	
5225	pRM925	pRM795 derivative that expresses mutant <i>E. coli</i> RNAP	This work
		$(\alpha 2\beta \beta' \omega)$ containing β' 6Ala 937C 1139C (924A, 926A,	
		927A, 11336A, 1137A, but 1139C)	
3737	pIA423	Expresses wild-type <i>E. coli</i> RNAP ($\alpha_2\beta\beta'$) with CBP/intein	(Ref. 3)

		on th			
3798	pIA373	pIA4	23 derivative that expresses mutant <i>E. coli</i> RNAP	(Ref. 5)	
		(α ₂ β			
		term	terminus		
47512	pJZ1	pIA4	23 derivative that expresses mutant <i>E. coli</i> RNAP	(This work	
		(α ₂ β	β´ Δ1149-1190, Δjaw and Δ943-1130, ΔSI3a) with	and Ref.	
		CBP	CBP/intein on the β C-terminus		
761	pIA146	pT7.	pT7A1-668nt template plasmid		
775	pIA171	pT7.	pT7A1- <i>his</i> P template plasmid		
3774	pIA349	pT7.	A1-ops P-his P –his T template plasmid	(Ref. 6)	
Oligon	ucleotides (5	´→3´)	<u> </u>		
5069	NT, Scaffold ^F	PEC	GGTCAGTACGTCCATTCGATCTTCGGAAGAGATTCAGAG		
	and Scaffold ^{UTP}				
5420	T, Scaffold ^{PEC}		CTCTGAATCTCTTCCAGCACACATCAGGACGTACTGACC		
4903	T, Scaffold ^{UTP}		CTCTGAATCTCTTCCCCTCTAGCTTAGGACGTACTGACC		
7636	RNA13,		CGAUAGCUAGAGG		
	Scaffold ^{GTP} and				
	Scaffold ^{Long}				
8079	RNA13 (EC-dG)		CGAUAGCUAGAG3'dG		
4865	RNA29,		CCUGACUAGUCUUUCAGGCGAUGUGUGCU		
	Scaffold ^{PEC}				
4867	RNA27,		CCUGACUAGUCUUUCAGGCGAUGUGUGCU		
	Scaffold ^{PEC}				
7712	NT, Scaffold ^{UTP}		GGTCAGTACGTGGCTtcgatcttcTGTACAGCAATCAGAGTACC		
7713	T, Scaffold ^{UTP}		GGTACTCTGATTGCTGTACATGCCCGGCTAGCCACGTACTGACC		
7718	RNA14,		UUUUUUAGCCGGG		
	Scaffold ^{UTP}				
8576	NT, Scaffold ^{Long}		GGTCAGTACGTCCTAAGCTAGAGGGGAAGAGATTCAGAGGACTAG		
			AGTGCTTGGCGAACCGGTGTTTGACGTCCAGGAATGTCAAATCCGT		
			GGCGTGACC		
8493	T, Scaffold ^{Long}		ggtcacgccacggatttgacattcctggacgtcaaacaccggttcg		

	CCAAGCACTCTAGTCCTCTGAATCTCTTCCCCTCTAGCTTAGGACG
	TACTGACC

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G14 and G15 nucleotide addition rates			
RNAP	V ^{app} max G14 s ⁻¹	V ^{app} _{max} G15 s ⁻¹	
WT	560 ± 10	170 ± 30	
F937-736ox	12 ± 1	15 ± 1	
F937-736red	300 ± 70	240 ± 30	
WTox	530 ± 120	140 ± 30	
6Ala	1.7 ± 0.3	7.3 ± 1.1	
LTPP	0.031 ± 0.006	0.081 ± 0.013	
DIPP	0.36 ± 0.06	0.99 ± 0.18	
PGPP	580 ± 50	26 ± 4	
ΔSI3	550 ± 50	88 ± 3	
U17 nucleotid	le addition rates		
RNAP	V ^{obs} max s ⁻¹	k ^{obs} UTP mM	
WT	360 ± 100	1.4 ± 0.6	
LTPP	0.008 ± 0.002	1.3 ± 1.0	
ΔTL	0.008 ± 0.000	2.3 ± 0.1	
6Ala	0.41 ± 0.06	0.35 ± 0.11	
KDPP	0.32 ± 0.02	0.27 ± 0.04	
DIPP	0.18 ± 0.01	0.17 ± 0.10	
GGPP	0.21 ± 0.01	0.28 ± 0.06	
PGPP	480 ± 50	0.45 ± 0.13	
∆SI3	750 ± 70	1.2 ± 0.2	
DIPP ASI 3	0.61 ± 0.03	0.13 ± 0.02	
6Ala ∆Sl3	0.31 ± 0.02	0.62 ± 0.14	
ΔSI3 550 ± 50		88 ± 3	
U17 nucleotide addition, 10 mM UTP			
RNAP	V ^{app} _{max} s ⁻¹ , 10 mM UTP		
∆SI3a	$680 \pm 70 (V_{max}^{obs} = 750 \pm 70 \text{ s}^{-1})$		
∆SI3b	560 ± 100		

Table S2. Nucleotide addition rate measurements

A. <i>his</i> pause escape, elongating through the pause					
RNAP	Bypass fraction	Pause fraction, E	Pause escape rate, k _e		
			s ⁻¹		
F937-736red	0.08 ± 0.03	0.75 ± 0.01	0.010 ± 0.005		
F937-736ox	0.68 ± 0.10	0.21 ± 0.02	0.002 ± 0.001		
F937-736rred	0.10 ± 0.03 0.87 ± 0.03		0.002 ± 0.001		
B. <i>his</i> pause escape, elongating through the pause					
RNAP	Pause fraction,	Pause escape rate, k _e s ⁻¹			
	E				
WT	0.75 ± 0.01	0.010 ± 0.001			
∆Sl3a	0.65 ± 0.09	0.016 ± 0.02			
∆SI3b	0.67 ± 0.01	0.020 ± 0.04			
C. <i>his</i> pause escape, starting at the pause					
RNAP	Fast escape rate,	Pause	Pause escape rate, k _e		
	s⁻¹	fraction, E	s ⁻¹		
WТ	NA	0.94 ± 0.02	0.015 ± 0.002		
PGPP	0.20 ± 0.07	0.26 ± 0.03	0.025 ± 0.002		
F773V	0.27 ± 0.01	0.24 ± 0.02	0.020 ± 0.004		

Table S3. Kinetics of pausing at the *his* pause signal