

A pause sequence enriched at translation start sites driv

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Closed for business: exit-channel coupling to active site conformation in bacterial RNA polymerase. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 741-742.	3.6	0
2	Control of transcription elongation by GreA determines rate of gene expression in <i>Streptococcus pneumoniae</i> . <i>Nucleic Acids Research</i> , 2014, 42, 10987-10999.	6.5	48
3	Genomic Looping: A Key Principle of Chromatin Organization. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2014, 24, 344-359.	1.0	22
4	Trigger-helix folding pathway and S13 mediate catalysis and hairpin-stabilized pausing by <i>Escherichia coli</i> RNA polymerase. <i>Nucleic Acids Research</i> , 2014, 42, 12707-12721.	6.5	43
6	RNA polymerase pausing and nascent-RNA structure formation are linked through clamp-domain movement. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 794-802.	3.6	92
7	Molecular basis of transcription pausing. <i>Science</i> , 2014, 344, 1226-1227.	6.0	2
8	Kinetic competition during the transcription cycle results in stochastic RNA processing. <i>ELife</i> , 2014, 3, .	2.8	177
9	Backtracking behavior in viral RNA-dependent RNA polymerase provides the basis for a second initiation site. <i>Nucleic Acids Research</i> , 2015, 43, gkv1098.	6.5	37
10	Visualizing translocation dynamics and nascent transcript errors in paused RNA polymerases in vivo. <i>Genome Biology</i> , 2015, 16, 98.	3.8	82
11	Regulation of Transcription Elongation and Termination. <i>Biomolecules</i> , 2015, 5, 1063-1078.	1.8	51
12	New Insights into the Functions of Transcription Factors that Bind the RNA Polymerase Secondary Channel. <i>Biomolecules</i> , 2015, 5, 1195-1209.	1.8	34
13	The primary σ factor in <i>Escherichia coli</i> can access the transcription elongation complex from solution in vivo. <i>ELife</i> , 2015, 4, .	2.8	20
14	Untangling reaction pathways through modern approaches to high-throughput single-molecule force-spectroscopy experiments. <i>Current Opinion in Structural Biology</i> , 2015, 34, 116-122.	2.6	36
15	RNA polymerase-induced remodelling of NusA produces a pause enhancement complex. <i>Nucleic Acids Research</i> , 2015, 43, 2829-2840.	6.5	31
16	Unraveling the mechanistic features of RNA polymerase II termination by the 5'â€²-3'â€² exoribonuclease Rat1. <i>Nucleic Acids Research</i> , 2015, 43, 2625-2637.	6.5	26
17	Mutations in the CRE pocket of bacterial RNA polymerase affect multiple steps of transcription. <i>Nucleic Acids Research</i> , 2015, 43, 5798-5809.	6.5	24
18	Distinct pathways of RNA polymerase regulation by a phage-encoded factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2017-2022.	3.3	18
19	Bacterial global regulators DksA/ppGpp increase fidelity of transcription. <i>Nucleic Acids Research</i> , 2015, 43, 1529-1536.	6.5	51

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20	Two transcription pause elements underlie a γ -dependent pause cycle. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4374-80.	3.3	33
21	Sequence-Dependent Promoter Escape Efficiency Is Strongly Influenced by Bias for the Pretranslocated State during Initial Transcription. Biochemistry, 2015, 54, 4267-4275.	1.2	17
22	Regulation of Transcript Elongation. Annual Review of Microbiology, 2015, 69, 49-69.	2.9	64
23	RNA Exosome Regulates AID DNA Mutator Activity in the B Cell Genome. Advances in Immunology, 2015, 127, 257-308.	1.1	29
24	Quantitative characterization of gene regulation by Rho dependent transcription termination. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2015, 1849, 940-954.	0.9	7
25	Native Elongating Transcript Sequencing Reveals Human Transcriptional Activity at Nucleotide Resolution. Cell, 2015, 161, 541-554.	13.5	342
26	A Kissing Loop Is Important for btuB Riboswitch Ligand Sensing and Regulatory Control. Journal of Biological Chemistry, 2015, 290, 26739-26751.	1.6	17
27	Methodology for the analysis of transcription and translation in transcription-coupled-to-translation systems in vitro. Methods, 2015, 86, 51-59.	1.9	9
28	Confidence, tolerance, and allowance in biological engineering: The nuts and bolts of living things. BioEssays, 2015, 37, 95-102.	1.2	22
29	H-NS Facilitates Sequence Diversification of Horizontally Transferred DNAs during Their Integration in Host Chromosomes. PLoS Genetics, 2016, 12, e1005796.	1.5	25
30	Misincorporation by RNA polymerase is a major source of transcription pausing in vivo. Nucleic Acids Research, 2016, 45, gkw969.	6.5	31
31	RNA polymerase gate loop guides the nontemplate DNA strand in transcription complexes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14994-14999.	3.3	20
32	Single-Molecule Real-Time 3D Imaging of the Transcription Cycle by Modulation Interferometry. Cell, 2016, 167, 1839-1852.e21.	13.5	32
33	Mechanisms of Bacterial Transcription Termination: All Good Things Must End. Annual Review of Biochemistry, 2016, 85, 319-347.	5.0	282
34	A Comprehensive, CRISPR-based Functional Analysis of Essential Genes in Bacteria. Cell, 2016, 165, 1493-1506.	13.5	593
35	Coupling of RNA Polymerase II Transcription Elongation with Pre-mRNA Splicing. Journal of Molecular Biology, 2016, 428, 2623-2635.	2.0	245
36	Regulatory effects of cotranscriptional σ RNA structure formation and transitions. Wiley Interdisciplinary Reviews RNA, 2016, 7, 562-574.	3.2	19
37	What have single-molecule studies taught us about gene expression?. Genes and Development, 2016, 30, 1796-1810.	2.7	48

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38	RNA polymerase supply and flux through the <i>lac</i> operon in <i>Escherichia coli</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20160080.	1.8	5
39	The physiology of growth arrest: uniting molecular and environmental microbiology. <i>Nature Reviews Microbiology</i> , 2016, 14, 549-562.	13.6	176
40	Co-transcriptional splicing and the CTD code. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2016, 51, 395-411.	2.3	42
41	RNA Polymerase Pausing during Initial Transcription. <i>Molecular Cell</i> , 2016, 63, 939-950.	4.5	96
42	Base-pair-resolution genome-wide mapping of active RNA polymerases using precision nuclear run-on (PRO-seq). <i>Nature Protocols</i> , 2016, 11, 1455-1476.	5.5	392
43	Regulation of transcriptional pausing through the secondary channel of RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8699-8704.	3.3	18
44	Control of transcriptional pausing by biased thermal fluctuations on repetitive genomic sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7409-E7417.	3.3	8
45	The ribosome in action: Tuning of translational efficiency and protein folding. <i>Protein Science</i> , 2016, 25, 1390-1406.	3.1	154
46	A universal transcription pause sequence is an element of initiation factor λ 70-dependent pausing. <i>Nucleic Acids Research</i> , 2016, 44, 6732-6740.	6.5	11
47	Bayesian Markov models consistently outperform PWMs at predicting motifs in nucleotide sequences. <i>Nucleic Acids Research</i> , 2016, 44, 6055-6069.	6.5	72
48	Ribonucleoprotein particles of bacterial small non-coding RNA <i>IsrA</i> (IS61 or <i>McaS</i>) and its interaction with RNA polymerase core may link transcription to mRNA fate. <i>Nucleic Acids Research</i> , 2016, 44, 2577-2592.	6.5	18
49	A Two-Way Street: Regulatory Interplay between RNA Polymerase and Nascent RNA Structure. <i>Trends in Biochemical Sciences</i> , 2016, 41, 293-310.	3.7	113
50	Large-Effect Beneficial Synonymous Mutations Mediate Rapid and Parallel Adaptation in a Bacterium. <i>Molecular Biology and Evolution</i> , 2016, 33, 1542-1553.	3.5	58
51	Genome-wide profiling of RNA polymerase transcription at nucleotide resolution in human cells with native elongating transcript sequencing. <i>Nature Protocols</i> , 2016, 11, 813-833.	5.5	65
52	Mammalian NET-seq analysis defines nascent RNA profiles and associated RNA processing genome-wide. <i>Nature Protocols</i> , 2016, 11, 413-428.	5.5	86
53	Real-Time Observation of Backtracking by Bacterial RNA Polymerase. <i>Biochemistry</i> , 2016, 55, 647-658.	1.2	13
54	Effects of cooperation between translating ribosome and RNA polymerase on termination efficiency of the Rho-independent terminator. <i>Nucleic Acids Research</i> , 2016, 44, 2554-2563.	6.5	33
55	Transcriptional pausing at the translation start site operates as a critical checkpoint for riboswitch regulation. <i>Nature Communications</i> , 2017, 8, 13892.	5.8	67

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56	A link between transcription fidelity and pausing <i>in vivo</i> . <i>Transcription</i> , 2017, 8, 99-105.	1.7	13
57	Structure and Function of RNA Polymerases and the Transcription Machineries. <i>Sub-Cellular Biochemistry</i> , 2017, 83, 225-270.	1.0	27
58	Elucidation of bacterial translation regulatory networks. <i>Current Opinion in Systems Biology</i> , 2017, 2, 84-90.	1.3	5
59	Gfh factors and NusA cooperate to stimulate transcriptional pausing and termination. <i>FEBS Letters</i> , 2017, 591, 946-953.	1.3	8
60	Conserved functions of the trigger loop and Gre factors in RNA cleavage by bacterial RNA polymerases. <i>Journal of Biological Chemistry</i> , 2017, 292, 6744-6752.	1.6	12
61	Transcription elongation. <i>Transcription</i> , 2017, 8, 150-161.	1.7	14
62	Macromolecular Protein Complexes. <i>Sub-Cellular Biochemistry</i> , 2017, , .	1.0	5
63	σ ³⁸ -dependent promoter-proximal pausing by bacterial RNA polymerase. <i>Nucleic Acids Research</i> , 2017, 45, 3006-3016.	6.5	10
64	Deep sequencing approaches for the analysis of prokaryotic transcriptional boundaries and dynamics. <i>Methods</i> , 2017, 120, 76-84.	1.9	10
65	Conformational Dynamics of mRNA in Gene Expression as New Pharmaceutical Target. <i>Chemical Record</i> , 2017, 17, 817-832.	2.9	13
66	Modular Organization of the NusA- and NusG-Stimulated RNA Polymerase Pause Signal That Participates in the <i>Bacillus subtilis</i> trp Operon Attenuation Mechanism. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	14
67	Trigger loop of RNA polymerase is a positional, not acid-base, catalyst for both transcription and proofreading. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5103-E5112.	3.3	49
68	Production and characterization of a highly pure RNA polymerase holoenzyme from <i>Mycobacterium tuberculosis</i> . <i>Protein Expression and Purification</i> , 2017, 134, 1-10.	0.6	7
69	Pause & go: from the discovery of RNA polymerase pausing to its functional implications. <i>Current Opinion in Cell Biology</i> , 2017, 46, 72-80.	2.6	113
70	Initiation of mtDNA transcription is followed by pausing, and diverges across human cell types and during evolution. <i>Genome Research</i> , 2017, 27, 362-373.	2.4	41
71	Trigger loop dynamics can explain stimulation of intrinsic termination by bacterial RNA polymerase without terminator hairpin contact. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9233-E9242.	3.3	19
72	Genome-Wide Spectra of Transcription Insertions and Deletions Reveal That Slippage Depends on RNA:DNA Hybrid Complementarity. <i>MBio</i> , 2017, 8, .	1.8	8
73	Evolutionary Origins of Two-Barrel RNA Polymerases and Site-Specific Transcription Initiation. <i>Annual Review of Microbiology</i> , 2017, 71, 331-348.	2.9	26

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74	A structure-based kinetic model of transcription. <i>Transcription</i> , 2017, 8, 1-8.	1.7	11
75	The Battle of RNA Synthesis: Virus versus Host. <i>Viruses</i> , 2017, 9, 309.	1.5	26
76	Sequence-specific thermodynamic properties of nucleic acids influence both transcriptional pausing and backtracking in yeast. <i>PLoS ONE</i> , 2017, 12, e0174066.	1.1	3
77	Transcription-translation coupling: direct interactions of RNA polymerase with ribosomes and ribosomal subunits. <i>Nucleic Acids Research</i> , 2017, 45, 11043-11055.	6.5	64
78	RNA secondary structures regulate three steps of Rho-dependent transcription termination within a bacterial mRNA leader. <i>Nucleic Acids Research</i> , 2017, 45, 631-642.	6.5	15
79	Genome-wide relationship between R-loop formation and antisense transcription in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2018, 46, 3400-3411.	6.5	30
80	RNA Polymerase Accommodates a Pause RNA Hairpin by Global Conformational Rearrangements that Prolong Pausing. <i>Molecular Cell</i> , 2018, 69, 802-815.e5.	4.5	152
81	Uneven Braking Spins RNA Polymerase into a Pause. <i>Molecular Cell</i> , 2018, 69, 723-725.	4.5	4
82	Missing the Mark: PRDM9-Dependent Methylation Is Required for Meiotic DSB Targeting. <i>Molecular Cell</i> , 2018, 69, 725-727.	4.5	2
83	Structural Basis for NusA Stabilized Transcriptional Pausing. <i>Molecular Cell</i> , 2018, 69, 816-827.e4.	4.5	140
84	Effects of mRNA Degradation and Site-Specific Transcriptional Pausing on Protein Expression Noise. <i>Biophysical Journal</i> , 2018, 114, 1718-1729.	0.2	27
85	The transcription-repair coupling factor Mfd associates with RNA polymerase in the absence of exogenous damage. <i>Nature Communications</i> , 2018, 9, 1570.	5.8	55
86	Pausing controls branching between productive and non-productive pathways during initial transcription in bacteria. <i>Nature Communications</i> , 2018, 9, 1478.	5.8	61
87	<i>Escherichia coli</i> transcription factor NusG binds to 70S ribosomes. <i>Molecular Microbiology</i> , 2018, 108, 495-504.	1.2	65
88	Rebuilding the bridge between transcription and translation. <i>Molecular Microbiology</i> , 2018, 108, 467-472.	1.2	29
89	Single-molecule FRET studies on the cotranscriptional folding of a thiamine pyrophosphate riboswitch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 331-336.	3.3	49
90	The evolutionary impact of intragenic FliA promoters in proteobacteria. <i>Molecular Microbiology</i> , 2018, 108, 361-378.	1.2	14
91	DNA template sequence control of bacterial RNA polymerase escape from the promoter. <i>Nucleic Acids Research</i> , 2018, 46, 4469-4486.	6.5	29

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92	Transcription fidelity and its roles in the cell. <i>Current Opinion in Microbiology</i> , 2018, 42, 13-18.	2.3	25
93	Transcription pausing: biological significance of thermal fluctuations biased by repetitive genomic sequences. <i>Transcription</i> , 2018, 9, 196-203.	1.7	3
94	StpA and Hha stimulate pausing by RNA polymerase by promoting DNA-DNA bridging of H-NS filaments. <i>Nucleic Acids Research</i> , 2018, 46, 5525-5546.	6.5	55
95	A Genome-Wide Assay Specifies Only GreA as a Transcription Fidelity Factor in <i>Escherichia coli</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2257-2264.	0.8	19
96	NETSeq reveals heterogeneous nucleotide incorporation by RNA polymerase I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11633-E11641.	3.3	22
97	Gene regulation by a glycine riboswitch singlet uses a finely tuned energetic landscape for helical switching. <i>Rna</i> , 2018, 24, 1813-1827.	1.6	18
98	Locking the nontemplate DNA to control transcription. <i>Molecular Microbiology</i> , 2018, 109, 445-457.	1.2	16
99	Ligand Modulates Cross-Coupling between Riboswitch Folding and Transcriptional Pausing. <i>Molecular Cell</i> , 2018, 72, 541-552.e6.	4.5	48
100	Hierarchical mechanism of amino acid sensing by the T-box riboswitch. <i>Nature Communications</i> , 2018, 9, 1896.	5.8	30
101	RNA-DNA and DNA-DNA base-pairing at the upstream edge of the transcription bubble regulate translocation of RNA polymerase and transcription rate. <i>Nucleic Acids Research</i> , 2018, 46, 5764-5775.	6.5	12
102	Polymerase pausing induced by sequence-specific RNA-binding protein drives heterochromatin assembly. <i>Genes and Development</i> , 2018, 32, 953-964.	2.7	33
103	A multivariate prediction model for Rho-dependent termination of transcription. <i>Nucleic Acids Research</i> , 2018, 46, 8245-8260.	6.5	30
104	Pause sequences facilitate entry into long-lived paused states by reducing RNA polymerase transcription rates. <i>Nature Communications</i> , 2018, 9, 2930.	5.8	42
105	Structure of activated transcription complex Pol II-DSIF-PAF-SPT6. <i>Nature</i> , 2018, 560, 607-612.	13.7	300
106	Structure of paused transcription complex Pol II-DSIF-NELF. <i>Nature</i> , 2018, 560, 601-606.	13.7	262
107	Structural Basis for Transcript Elongation Control by NusG Family Universal Regulators. <i>Cell</i> , 2018, 173, 1650-1662.e14.	13.5	143
108	Mechanisms of Transcriptional Pausing in Bacteria. <i>Journal of Molecular Biology</i> , 2019, 431, 4007-4029.	2.0	70
109	Transcription of Bacterial Chromatin. <i>Journal of Molecular Biology</i> , 2019, 431, 4040-4066.	2.0	51

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110	mTERF5 Acts as a Transcriptional Pausing Factor to Positively Regulate Transcription of Chloroplast psbEFLJ. <i>Molecular Plant</i> , 2019, 12, 1259-1277.	3.9	53
111	RNA Polymerase Clamp Movement Aids Dissociation from DNA but Is Not Required for RNA Release at Intrinsic Terminators. <i>Journal of Molecular Biology</i> , 2019, 431, 696-713.	2.0	21
112	cis Elements that Mediate RNA Polymerase II Pausing Regulate Human Gene Expression. <i>American Journal of Human Genetics</i> , 2019, 105, 677-688.	2.6	26
114	Long-Distance Cooperative and Antagonistic RNA Polymerase Dynamics via DNA Supercoiling. <i>Cell</i> , 2019, 179, 106-119.e16.	13.5	77
115	Oxazinomycin arrests RNA polymerase at the polythymidine sequences. <i>Nucleic Acids Research</i> , 2019, 47, 10296-10312.	6.5	11
116	An evolving tale of two interacting RNAs—themes and variations of the Tâ€box riboswitch mechanism. <i>IUBMB Life</i> , 2019, 71, 1167-1180.	1.5	15
117	The Mechanisms of Substrate Selection, Catalysis, and Translocation by the Elongating RNA Polymerase. <i>Journal of Molecular Biology</i> , 2019, 431, 3975-4006.	2.0	56
118	Promoter-proximal pausing of RNA polymerase II: a nexus of gene regulation. <i>Genes and Development</i> , 2019, 33, 960-982.	2.7	373
119	Role of a hairpin-stabilized pause in the <i>Escherichia coli</i> thiC riboswitch function. <i>RNA Biology</i> , 2019, 16, 1066-1073.	1.5	14
120	RNA polymerase pausing at a protein roadblock can enhance transcriptional interference by promoter occlusion. <i>FEBS Letters</i> , 2019, 593, 903-917.	1.3	5
121	Ancient Transcription Factors in the News. <i>MBio</i> , 2019, 10, .	1.8	23
122	RhoTermPredict: an algorithm for predicting Rho-dependent transcription terminators based on <i>Escherichia coli</i> , <i>Bacillus subtilis</i> and <i>Salmonella enterica</i> databases. <i>BMC Bioinformatics</i> , 2019, 20, 117.	1.2	32
123	An Overview of Methodologies in Studying lncRNAs in the High-Throughput Era: When Acronyms ATTACK!. <i>Methods in Molecular Biology</i> , 2019, 1933, 1-30.	0.4	13
124	Mechanisms of Bacterial Transcription Termination. <i>Journal of Molecular Biology</i> , 2019, 431, 4030-4039.	2.0	111
125	<i>Escherichia coli</i> as a platform for the study of phosphoinositide biology. <i>Science Advances</i> , 2019, 5, eaat4872.	4.7	12
126	Processing generates 3' ends of RNA masking transcription termination events in prokaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4440-4445.	3.3	37
127	A ligand-gated strand displacement mechanism for ZTP riboswitch transcription control. <i>Nature Chemical Biology</i> , 2019, 15, 1067-1076.	3.9	47
128	Determining the effects of DNA sequence on Hel308 helicase translocation along single-stranded DNA using nanopore tweezers. <i>Nucleic Acids Research</i> , 2019, 47, 2506-2513.	6.5	32

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129	Analysis of Mammalian Native Elongating Transcript sequencing (mNET-seq) high-throughput data. <i>Methods</i> , 2020, 178, 89-95.	1.9	11
130	The Biogenesis of SRP RNA Is Modulated by an RNA Folding Intermediate Attained during Transcription. <i>Molecular Cell</i> , 2020, 77, 241-250.e8.	4.5	19
131	Antitermination protein P7 of bacteriophage Xp10 distinguishes different types of transcriptional pausing by bacterial RNA polymerase. <i>Biochimie</i> , 2020, 170, 57-64.	1.3	0
132	NusG-dependent RNA polymerase pausing is a frequent function of this universally conserved transcription elongation factor. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2020, 55, 716-728.	2.3	18
133	Escherichia coli NusG Links the Lead Ribosome with the Transcription Elongation Complex. <i>IScience</i> , 2020, 23, 101352.	1.9	43
134	XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for Initial-Transcription Pausing. <i>Molecular Cell</i> , 2020, 79, 797-811.e8.	4.5	20
135	Origins and Molecular Evolution of the NusG Paralog RfaH. <i>MBio</i> , 2020, 11, .	1.8	15
136	Motif 1 Binding Protein suppresses wingless to promote eye fate in <i>Drosophila</i> . <i>Scientific Reports</i> , 2020, 10, 17221.	1.6	8
137	NusG controls transcription pausing and RNA polymerase translocation throughout the <i>Bacillus subtilis</i> genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21628-21636.	3.3	38
138	A Tale of Good Fortune in the Era of DNA. <i>Annual Review of Microbiology</i> , 2020, 74, 1-19.	2.9	4
139	Seqâ€™ing identity and function in a repeat-derived noncoding RNA world. <i>Chromosome Research</i> , 2020, 28, 111-127.	1.0	3
140	A unified view of the sequence and functional organization of the human RNA polymerase II promoter. <i>Nucleic Acids Research</i> , 2020, 48, 7767-7785.	6.5	29
142	Downstream sequence-dependent RNA cleavage and pausing by RNA polymerase I. <i>Journal of Biological Chemistry</i> , 2020, 295, 1288-1299.	1.6	13
143	Identifying Transcription Error-Enriched Genomic Loci Using Nuclear Run-on Circular-Sequencing Coupled with Background Error Modeling. <i>Journal of Molecular Biology</i> , 2020, 432, 3933-3949.	2.0	2
144	Extending the Repertoire of mTERF Proteins with Functions in Organellar Gene Expression. <i>Molecular Plant</i> , 2020, 13, 817-819.	3.9	8
145	The Molecular Function of Plant mTERFs as Key Regulators of Organellar Gene Expression. <i>Plant and Cell Physiology</i> , 2021, 61, 2004-2017.	1.5	15
146	Basic mechanisms and kinetics of pause-interspersed transcript elongation. <i>Nucleic Acids Research</i> , 2021, 49, 15-24.	6.5	9
147	Understanding the molecular mechanisms of transcriptional bursting. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 21399-21406.	1.3	3

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149	Coupled Transcription-Translation in Prokaryotes: An Old Couple With New Surprises. <i>Frontiers in Microbiology</i> , 2020, 11, 624830.	1.5	40
150	Structural basis for transcription complex disruption by the Mfd translocase. <i>ELife</i> , 2021, 10, .	2.8	36
151	Nascent RNA sequencing identifies a widespread sigma70-dependent pausing regulated by Gre factors in bacteria. <i>Nature Communications</i> , 2021, 12, 906.	5.8	11
152	Conserved DNA sequence features underlie pervasive RNA polymerase pausing. <i>Nucleic Acids Research</i> , 2021, 49, 4402-4420.	6.5	29
153	Modelling single-molecule kinetics of helicase translocation using high-resolution nanopore tweezers (SPRNT). <i>Essays in Biochemistry</i> , 2021, 65, 109-127.	2.1	8
154	Understanding transcription across scales: From base pairs to chromosomes. <i>Molecular Cell</i> , 2021, 81, 1601-1616.	4.5	10
155	A translational riboswitch coordinates nascent transcriptionâ€“translation coupling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
156	The Dynamic SecYEG Translocon. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 664241.	1.6	39
157	Long-Range Supercoiling-Mediated RNA Polymerase Cooperation in Transcription. <i>Journal of Physical Chemistry B</i> , 2021, 125, 4692-4700.	1.2	10
158	The intricate relationship between transcription and translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	4
159	Reading and surviving the harsh conditions in desert biological soil crust: the cyanobacterial viewpoint. <i>FEMS Microbiology Reviews</i> , 2021, 45, .	3.9	22
160	Quantitative mapping of mRNA 3â€™ ends in <i>Pseudomonas aeruginosa</i> reveals a pervasive role for premature 3â€™ end formation in response to azithromycin. <i>PLoS Genetics</i> , 2021, 17, e1009634.	1.5	7
162	Two distinct mechanisms of RNA polymerase II elongation stimulation in vivo. <i>Molecular Cell</i> , 2021, 81, 3096-3109.e8.	4.5	53
163	Trade-offs among transcription elongation rate, number, and duration of ubiquitous pauses on highly transcribed bacterial genes. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2150020.	0.3	0
164	Transcriptional Pausing as a Mediator of Bacterial Gene Regulation. <i>Annual Review of Microbiology</i> , 2021, 75, 291-314.	2.9	34
165	Bacterial transcription during growth arrest. <i>Transcription</i> , 2021, 12, 232-249.	1.7	7
166	Obligate movements of an active siteâ€“linked surface domain control RNA polymerase elongation and pausing via a Phe pocket anchor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
167	Î²-CASP proteins removing RNA polymerase from DNA: when a torpedo is needed to shoot a sitting duck. <i>Nucleic Acids Research</i> , 2021, 49, 10221-10234.	6.5	3

#	ARTICLE	IF	CITATIONS
168	Macromolecular assemblies supporting transcription-translation coupling. <i>Transcription</i> , 2021, 12, 103-125.	1.7	12
169	Illuminating Enhancer Transcription at Nucleotide Resolution with. <i>Methods in Molecular Biology</i> , 2021, 2351, 41-65.	0.4	0
170	NusG, an Ancient Yet Rapidly Evolving Transcription Factor. <i>Frontiers in Microbiology</i> , 2020, 11, 619618.	1.5	30
171	A Single-Molecule View on Cellular and Viral RNA Synthesis. <i>Biological and Medical Physics Series</i> , 2019, , 109-141.	0.3	5
172	Design Principles for Single-Stranded RNA Origami Structures. <i>Lecture Notes in Computer Science</i> , 2014, , 1-19.	1.0	21
173	Downstream sequence-dependent RNA cleavage and pausing by RNA polymerase I. <i>Journal of Biological Chemistry</i> , 2020, 295, 1288-1299.	1.6	16
174	Mfd regulates RNA polymerase association with hard-to-transcribe regions in vivo, especially those with structured RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
182	Temperature-Dependent Model of Multi-step Transcription Initiation in <i>Escherichia coli</i> Based on Live Single-Cell Measurements. <i>PLoS Computational Biology</i> , 2016, 12, e1005174.	1.5	33
183	Transcription facilitated genome-wide recruitment of topoisomerase I and DNA gyrase. <i>PLoS Genetics</i> , 2017, 13, e1006754.	1.5	56
184	Bridged filaments of histone-like nucleoid structuring protein pause RNA polymerase and aid termination in bacteria. <i>ELife</i> , 2015, 4, .	2.8	112
185	Architecture and RNA binding of the human negative elongation factor. <i>ELife</i> , 2016, 5, .	2.8	54
186	Pausing guides RNA folding to populate transiently stable RNA structures for riboswitch-based transcription regulation. <i>ELife</i> , 2017, 6, .	2.8	48
187	Operon mRNAs are organized into ORF-centric structures that predict translation efficiency. <i>ELife</i> , 2017, 6, .	2.8	128
188	The universally-conserved transcription factor RfaH is recruited to a hairpin structure of the non-template DNA strand. <i>ELife</i> , 2018, 7, .	2.8	45
189	The elemental mechanism of transcriptional pausing. <i>ELife</i> , 2019, 8, .	2.8	58
190	Analysing the fitness cost of antibiotic resistance to identify targets for combination antimicrobials. <i>Nature Microbiology</i> , 2021, 6, 1410-1423.	5.9	16
191	Quantitative analysis of asynchronous transcription-translation and transcription processivity in <i>Bacillus subtilis</i> under various growth conditions. <i>IScience</i> , 2021, 24, 103333.	1.9	9
192	Transcription and splicing dynamics during early <i>Drosophila</i> development. <i>Rna</i> , 2022, 28, 139-161.	1.6	11

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208	sRNA-mediated regulation of gal mRNA in E. coli: Involvement of transcript cleavage by RNase E together with Rho-dependent transcription termination. <i>PLoS Genetics</i> , 2021, 17, e1009878.	1.5	13
210	Conserved Trigger Loop Histidine of RNA Polymerase II Functions as a Positional Catalyst Primarily through Steric Effects. <i>Biochemistry</i> , 2021, 60, 3323-3336.	1.2	4
211	Transcription complexes as RNA chaperones. <i>Transcription</i> , 2021, 12, 126-155.	1.7	4
212	Accuracy, readability, and acceptability in translation. , 2020, , .		0
213	Requirements for efficient ligand-gated co-transcriptional switching in designed variants of the B. subtilis pbuE adenine-responsive riboswitch in E. coli. <i>PLoS ONE</i> , 2020, 15, e0243155.	1.1	12
216	Dynamic competition between a ligand and transcription factor NusA governs riboswitch-mediated transcription regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
217	DNA Supercoiling Drives a Transition between Collective Modes of Gene Synthesis. <i>Physical Review Letters</i> , 2021, 127, 218101.	2.9	12
221	Unique properties of spacer acquisition by the type III-A CRISPR-Cas system. <i>Nucleic Acids Research</i> , 2022, 50, 1562-1582.	6.5	8
222	Transcription factors modulate RNA polymerase conformational equilibrium. <i>Nature Communications</i> , 2022, 13, 1546.	5.8	20
223	Transcriptome-Wide Effects of NusA on RNA Polymerase Pausing in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2022, 204, e0053421.	1.0	9
224	Purification of synchronized <i>Escherichia coli</i> transcription elongation complexes by reversible immobilization on magnetic beads. <i>Journal of Biological Chemistry</i> , 2022, 298, 101789.	1.6	3
225	Ubiquitous mRNA decay fragments in <i>E. coli</i> redefine the functional transcriptome. <i>Nucleic Acids Research</i> , 2022, 50, 5029-5046.	6.5	15
226	High-throughput single-molecule experiments reveal heterogeneity, state switching, and three interconnected pause states in transcription. <i>Cell Reports</i> , 2022, 39, 110749.	2.9	18
227	In vivo regulation of bacterial Rho-dependent transcription termination by the nascent RNA. <i>Journal of Biological Chemistry</i> , 2022, 298, 102001.	1.6	8
228	Single-Molecule Detection in the Study of Gene Expression. , 2022, , 127-141.		0
231	Site-specific photolabile roadblocks for the study of transcription elongation in biologically complex systems. <i>Communications Biology</i> , 2022, 5, 457.	2.0	4
232	Transcription elongation is finely tuned by dozens of regulatory factors. <i>ELife</i> , 2022, 11, .	2.8	8
234	Suppressor mutations in <i>Escherichia coli</i> RNA polymerase alter transcription initiation but do not affect translesion RNA synthesis in vitro. <i>Journal of Biological Chemistry</i> , 2022, , 102099.	1.6	0

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235	Structural and mechanistic basis of λ -dependent transcriptional pausing. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	6
236	Failure of Translation Initiation of the Next Gene Decouples Transcription at Intercistronic Sites and the Resultant mRNA Generation. MBio, 2022, 13, .	1.8	5
237	Investigating the role of RNA structures in transcriptional pausing using in vitro assays and in silico analyses. RNA Biology, 2022, 19, 916-927.	1.5	0
238	Alkaline pH has an unexpected effect on transcriptional pausing during synthesis of the Escherichia coli pH-responsive riboswitch. Journal of Biological Chemistry, 2022, 298, 102302.	1.6	1
240	Isolation of synchronized E. coli elongation complexes for solid-phase and solution-based in vitro transcription assays. Methods in Enzymology, 2022, , 159-192.	0.4	2
242	Transcription-Translation Coupling in Bacteria. Annual Review of Genetics, 2022, 56, 187-205.	3.2	15
243	Stochastic dynamics and ribosome-RNAP interactions in transcription-translation coupling. Biophysical Journal, 2023, 122, 254-266.	0.2	3
246	Thermodynamic model of bacterial transcription. Physical Review E, 2022, 106, .	0.8	1
248	Rate of transcription elongation and sequence-specific pausing by RNA polymerase I directly influence rRNA processing. Journal of Biological Chemistry, 2022, 298, 102730.	1.6	4
249	Structural basis for intrinsic transcription termination. Nature, 2023, 613, 783-789.	13.7	12
250	Rho-dependent transcription termination is the dominant mechanism in Mycobacterium tuberculosis. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2023, 1866, 194923.	0.9	4
251	Allosteric mechanism of transcription inhibition by NusG-dependent pausing of RNA polymerase. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	8
252	Transcriptional pause extension benefits the stand-by rather than catch-up Rho-dependent termination. Nucleic Acids Research, 2023, 51, 2778-2789.	6.5	4
253	An ensemble of interconverting conformations of the elemental paused transcription complex creates regulatory options. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	3.3	5
254	A trailing ribosome speeds up RNA polymerase at the expense of transcript fidelity via force and allostery. Cell, 2023, 186, 1244-1262.e34.	13.5	15
255	Correlative <i>Escherichia coli</i> Transcription Rate and Bubble Conformation Remodeled by NusA and NusG. Journal of Physical Chemistry B, 2023, 127, 2909-2917.	1.2	1