Robert Landick

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6,683 80 46 113 h-index g-index citations papers 6.08 8,058 14.8 125 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
113	Pausing by bacterial RNA polymerase is mediated by mechanistically distinct classes of signals. Proceedings of the National Academy of Sciences of the United States of America, 2000 , 97, 7090-5	11.5	335
112	Single-molecule study of transcriptional pausing and arrest by E. coli RNA polymerase. <i>Science</i> , 2000 , 287, 2497-500	33.3	293
111	Structural basis for substrate loading in bacterial RNA polymerase. <i>Nature</i> , 2007 , 448, 163-8	50.4	287
110	Sequence-resolved detection of pausing by single RNA polymerase molecules. <i>Cell</i> , 2006 , 125, 1083-94	56.2	229
109	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. <i>Science</i> , 2014 , 344, 1042-7	33.3	209
108	The transcriptional regulator RfaH stimulates RNA chain synthesis after recruitment to elongation complexes by the exposed nontemplate DNA strand. <i>Cell</i> , 2002 , 109, 193-203	56.2	200
107	The regulatory roles and mechanism of transcriptional pausing. <i>Biochemical Society Transactions</i> , 2006 , 34, 1062-6	5.1	190
106	Allosteric control of RNA polymerase by a site that contacts nascent RNA hairpins. <i>Science</i> , 2001 , 292, 730-3	33.3	185
105	Regulator trafficking on bacterial transcription units in vivo. <i>Molecular Cell</i> , 2009 , 33, 97-108	17.6	173
104	Mechanisms of Bacterial Transcription Termination: All Good Things Must End. <i>Annual Review of Biochemistry</i> , 2016 , 85, 319-47	29.1	170
103	A central role of the RNA polymerase trigger loop in active-site rearrangement during transcriptional pausing. <i>Molecular Cell</i> , 2007 , 27, 406-19	17.6	166
102	RNA polymerase mutants found through adaptive evolution reprogram Escherichia coli for optimal growth in minimal media. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 20500-5	11.5	153
101	An Ihelix to Ibarrel domain switch transforms the transcription factor RfaH into a translation factor. <i>Cell</i> , 2012 , 150, 291-303	56.2	147
100	Discontinuous movements of DNA and RNA in RNA polymerase accompany formation of a paused transcription complex. <i>Cell</i> , 1995 , 81, 341-50	56.2	147
99	Structure of a bacterial RNA polymerase holoenzyme open promoter complex. <i>ELife</i> , 2015 , 4,	8.9	130
98	Structural basis of transcriptional pausing in bacteria. <i>Cell</i> , 2013 , 152, 431-41	56.2	117
97	Role of the RNA polymerase trigger loop in catalysis and pausing. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 99-104	17.6	117

(2007-1999)

96	Folding of a large ribozyme during transcription and the effect of the elongation factor NusA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 9545-50	11.5	116
95	Co-overexpression of Escherichia coli RNA polymerase subunits allows isolation and analysis of mutant enzymes lacking lineage-specific sequence insertions. <i>Journal of Biological Chemistry</i> , 2003 , 278, 12344-55	5.4	115
94	Architecture of a transcribing-translating expressome. <i>Science</i> , 2017 , 356, 194-197	33.3	110
93	Translation activates the paused transcription complex and restores transcription of the trp operon leader region. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1985 , 82, 4663-7	11.5	101
92	Dissection of the his leader pause site by base substitution reveals a multipartite signal that includes a pause RNA hairpin. <i>Journal of Molecular Biology</i> , 1993 , 233, 25-42	6.5	100
91	Trigger loop dynamics mediate the balance between the transcriptional fidelity and speed of RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6555-60	11.5	98
90	Correcting direct effects of ethanol on translation and transcription machinery confers ethanol tolerance in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E2576-85	11.5	96
89	RNA Polymerase Accommodates a Pause RNA Hairpin by Global Conformational Rearrangements that Prolong Pausing. <i>Molecular Cell</i> , 2018 , 69, 802-815.e5	17.6	85
88	GreA-induced transcript cleavage in transcription complexes containing Escherichia coli RNA polymerase is controlled by multiple factors, including nascent transcript location and structure. <i>Journal of Biological Chemistry</i> , 1994 , 269, 22282-94	5.4	85
87	A Two-Way Street: Regulatory Interplay between RNA Polymerase and Nascent RNA Structure. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 293-310	10.3	83
86	Bridged filaments of histone-like nucleoid structuring protein pause RNA polymerase and aid termination in bacteria. <i>ELife</i> , 2015 , 4,	8.9	82
85	Structural Basis for Transcript Elongation Control by NusG Family Universal Regulators. <i>Cell</i> , 2018 , 173, 1650-1662.e14	56.2	81
84	Roles of RNA:DNA hybrid stability, RNA structure, and active site conformation in pausing by human RNA polymerase II. <i>Journal of Molecular Biology</i> , 2001 , 311, 265-82	6.5	81
83	Termination-altering amino acid substitutions in the betavoubunit of Escherichia coli RNA polymerase identify regions involved in RNA chain elongation. <i>Genes and Development</i> , 1994 , 8, 2913-2	7 ^{12.6}	81
82	The downstream DNA jaw of bacterial RNA polymerase facilitates both transcriptional initiation and pausing. <i>Journal of Biological Chemistry</i> , 2002 , 277, 37456-63	5.4	79
81	Multiple interactions stabilize a single paused transcription intermediate in which hairpin to 3\hstartendrighted no spacing distinguishes pause and termination pathways. <i>Journal of Molecular Biology</i> , 1997 , 268, 54-68	6.5	76
80	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	17.6	70
79	Real-time footprinting of DNA in the first kinetically significant intermediate in open complex formation by Escherichia coli RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7833-8	11.5	70

78	The NusA N-terminal domain is necessary and sufficient for enhancement of transcriptional pausing via interaction with the RNA exit channel of RNA polymerase. <i>Journal of Molecular Biology</i> , 2010 , 401, 708-25	6.5	68
77	Structure and function of CarD, an essential mycobacterial transcription factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12619-24	11.5	64
76	Engineering and two-stage evolution of a lignocellulosic hydrolysate-tolerant Saccharomyces cerevisiae strain for anaerobic fermentation of xylose from AFEX pretreated corn stover. <i>PLoS ONE</i> , 2014 , 9, e107499	3.7	64
75	Mycobacterial RNA polymerase requires a U-tract at intrinsic terminators and is aided by NusG at suboptimal terminators. <i>MBio</i> , 2014 , 5, e00931	7.8	61
74	RNA polymerase clamps down. <i>Cell</i> , 2001 , 105, 567-70	56.2	58
73	DksA guards elongating RNA polymerase against ribosome-stalling-induced arrest. <i>Molecular Cell</i> , 2014 , 53, 766-78	17.6	52
72	RNA transcript 3Wproximal sequence affects translocation bias of RNA polymerase. <i>Biochemistry</i> , 2011 , 50, 7002-14	3.2	51
71	The Salmonella typhimurium his operon leader region contains an RNA hairpin-dependent transcription pause site. <i>Journal of Biological Chemistry</i> , 1989 , 264, 20796-20804	5.4	51
70	RNA polymerase motions during promoter melting. <i>Science</i> , 2017 , 356, 863-866	33.3	50
69	The Salmonella typhimurium his operon leader region contains an RNA hairpin-dependent transcription pause site. Mechanistic implications of the effect on pausing of altered RNA hairpins. <i>Journal of Biological Chemistry</i> , 1989 , 264, 20796-804	5.4	49
68	Directed Evolution Reveals Unexpected Epistatic Interactions That Alter Metabolic Regulation and Enable Anaerobic Xylose Use by Saccharomyces cerevisiae. <i>PLoS Genetics</i> , 2016 , 12, e1006372	6	49
67	Fidaxomicin jams RNA polymerase motions needed for initiation via RbpA contacts. <i>ELife</i> , 2018 , 7,	8.9	46
66	H-NS and RNA polymerase: a love-hate relationship?. Current Opinion in Microbiology, 2015, 24, 53-9	7.9	45
65	The role of the lid element in transcription by E. coli RNA polymerase. <i>Journal of Molecular Biology</i> , 2006 , 361, 644-58	6.5	45
64	Direct versus limited-step reconstitution reveals key features of an RNA hairpin-stabilized paused transcription complex. <i>Journal of Biological Chemistry</i> , 2007 , 282, 19020-8	5.4	42
63	Mechanism for the Regulated Control of Bacterial Transcription Termination by a Universal Adaptor Protein. <i>Molecular Cell</i> , 2018 , 71, 911-922.e4	17.6	41
62	Bacterial RNA polymerase can retain IIO throughout transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 602-7	11.5	40
61	Cys-pair reporters detect a constrained trigger loop in a paused RNA polymerase. <i>Molecular Cell</i> , 2013 , 50, 882-93	17.6	40

(2021-2018)

60	Complete genome sequence and the expression pattern of plasmids of the model ethanologen ZM4 and its xylose-utilizing derivatives 8b and 2032. <i>Biotechnology for Biofuels</i> , 2018 , 11, 125	7.8	39
59	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	20.1	36
58	Transcriptional pausing without backtracking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 8797-8	11.5	35
57	Downstream DNA selectively affects a paused conformation of human RNA polymerase II. <i>Journal of Molecular Biology</i> , 2004 , 341, 429-42	6.5	35
56	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of Saccharomyces cerevisiae Used in Biofuels Research. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 1757-66	3.2	35
55	Active-site dynamics in RNA polymerases. <i>Cell</i> , 2004 , 116, 351-3	56.2	34
54	Pausing guides RNA folding to populate transiently stable RNA structures for riboswitch-based transcription regulation. <i>ELife</i> , 2017 , 6,	8.9	32
53	The elemental mechanism of transcriptional pausing. <i>ELife</i> , 2019 , 8,	8.9	32
52	Trigger-helix folding pathway and SI3 mediate catalysis and hairpin-stabilized pausing by Escherichia coli RNA polymerase. <i>Nucleic Acids Research</i> , 2014 , 42, 12707-21	20.1	31
51	Life times of metastable states guide regulatory signaling in transcriptional riboswitches. <i>Nature Communications</i> , 2018 , 9, 944	17.4	30
50	Mechanisms of Transcriptional Pausing in Bacteria. <i>Journal of Molecular Biology</i> , 2019 , 431, 4007-4029	6.5	30
49	Transcription of Bacterial Chromatin. <i>Journal of Molecular Biology</i> , 2019 , 431, 4040-4066	6.5	30
48	Aromatic inhibitors derived from ammonia-pretreated lignocellulose hinder bacterial ethanologenesis by activating regulatory circuits controlling inhibitor efflux and detoxification. <i>Frontiers in Microbiology</i> , 2014 , 5, 402	5.7	30
47	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	11.5	29
46	CBR antimicrobials inhibit RNA polymerase via at least two bridge-helix cap-mediated effects on nucleotide addition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4178-87	11.5	29
45	Functional interplay between the jaw domain of bacterial RNA polymerase and allele-specific residues in the product RNA-binding pocket. <i>Journal of Molecular Biology</i> , 2006 , 356, 1163-79	6.5	29
44	Shifting RNA polymerase into overdrive. <i>Science</i> , 1999 , 284, 598-9	33.3	29
43	Structural basis for backtracking by the SARS-CoV-2 replication-transcription complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	29

42	Dynamics of GreB-RNA polymerase interaction allow a proofreading accessory protein to patrol for transcription complexes needing rescue. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E1081-E1090	11.5	24
41	The Battle of RNA Synthesis: Virus versus Host. <i>Viruses</i> , 2017 , 9,	6.2	21
40	NTP-entry routes in multi-subunit RNA polymerases. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 651-4	10.3	21
39	P1 Ref Endonuclease: A Molecular Mechanism for Phage-Enhanced Antibiotic Lethality. <i>PLoS Genetics</i> , 2016 , 12, e1005797	6	21
38	Natural Variation in the Multidrug Efflux Pump Underlies Ionic Liquid Tolerance in Yeast. <i>Genetics</i> , 2018 , 210, 219-234	4	19
37	OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. <i>Metabolic Engineering</i> , 2019 , 52, 324-340	9.7	19
36	Mapping E. coli RNA polymerase and associated transcription factors and identifying promoters genome-wide. <i>Methods in Enzymology</i> , 2011 , 498, 449-71	1.7	17
35	Efficient reconstitution of transcription elongation complexes for single-molecule studies of eukaryotic RNA polymerase II. <i>Transcription</i> , 2012 , 3, 146-53	4.8	17
34	Alternative transcription cycle for bacterial RNA polymerase. <i>Nature Communications</i> , 2020 , 11, 448	17.4	13
33	The Structure of Bacterial RNA Polymerase283-296		13
32	Genome-Wide Mapping of the Distribution of CarD, RNAP [Jand RNAP [bn the Chromosome using Chromatin Immunoprecipitation Sequencing. <i>Genomics Data</i> , 2014 , 2, 110-113		12
32		9.7	12
	Chromatin Immunoprecipitation Sequencing. <i>Genomics Data</i> , 2014 , 2, 110-113 Regulated redirection of central carbon flux enhances anaerobic production of bioproducts in	9.7	
31	Chromatin Immunoprecipitation Sequencing. <i>Genomics Data</i> , 2014 , 2, 110-113 Regulated redirection of central carbon flux enhances anaerobic production of bioproducts in Zymomonas mobilis. <i>Metabolic Engineering</i> , 2020 , 61, 261-274		11
31	Chromatin Immunoprecipitation Sequencing. <i>Genomics Data</i> , 2014 , 2, 110-113 Regulated redirection of central carbon flux enhances anaerobic production of bioproducts in Zymomonas mobilis. <i>Metabolic Engineering</i> , 2020 , 61, 261-274 The shrewd grasp of RNA polymerase. <i>Science</i> , 1996 , 273, 202-3 RNA Polymerase Clamp Movement Aids Dissociation from DNA but Is Not Required for RNA	33.3	11
31 30 29	Chromatin Immunoprecipitation Sequencing. <i>Genomics Data</i> , 2014 , 2, 110-113 Regulated redirection of central carbon flux enhances anaerobic production of bioproducts in Zymomonas mobilis. <i>Metabolic Engineering</i> , 2020 , 61, 261-274 The shrewd grasp of RNA polymerase. <i>Science</i> , 1996 , 273, 202-3 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 Genome-Scale Transcription-Translation Mapping Reveals Features of Zymomonas mobilis	33.3	11 11 10
31 30 29 28	Chromatin Immunoprecipitation Sequencing. <i>Genomics Data</i> , 2014 , 2, 110-113 Regulated redirection of central carbon flux enhances anaerobic production of bioproducts in Zymomonas mobilis. <i>Metabolic Engineering</i> , 2020 , 61, 261-274 The shrewd grasp of RNA polymerase. <i>Science</i> , 1996 , 273, 202-3 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 Genome-Scale Transcription-Translation Mapping Reveals Features of Zymomonas mobilis Transcription Units and Promoters. <i>MSystems</i> , 2020 , 5,	33·3 6.5 7.6	11 11 10 10

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24	Multiomic Fermentation Using Chemically Defined Synthetic Hydrolyzates Revealed Multiple Effects of Lignocellulose-Derived Inhibitors on Cell Physiology and Xylose Utilization in. <i>Frontiers in Microbiology</i> , 2019 , 10, 2596	5.7	8	
23	The antibiotic sorangicin A inhibits promoter DNA unwinding in a rifampicin-resistant RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 30423-30432	11.5	7	
22	A majority of promoters lack a crucial RNA polymerase recognition feature, enabling coordinated transcription activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 29658-29668	11.5	6	
21	Building a better stop sign: understanding the signals that terminate transcription. <i>Nature Methods</i> , 2013 , 10, 618-9	21.6	4	
20	A long time in the makingthe Nobel Prize for RNA polymerase. Cell, 2006, 127, 1087-90	56.2	4	
19	Genome-Wide Identification of Transcription Start Sites in Two, Rhodobacter sphaeroides 2.4.1 and Novosphingobium aromaticivorans DSM 12444. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	4	
18	Systems Metabolic Engineering of Escherichia coli Improves Coconversion of Lignocellulose-Derived Sugars. <i>Biotechnology Journal</i> , 2019 , 14, e1800441	5.6	3	
17	Crabtree/Warburg-like aerobic xylose fermentation by engineered Saccharomyces cerevisiae. <i>Metabolic Engineering</i> , 2021 , 68, 119-130	9.7	3	
16	CRISpy-Pop: A Web Tool for Designing CRISPR/Cas9-Driven Genetic Modifications in Diverse Populations. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 4287-4294	3.2	2	
15	Transcriptional Pausing as a Mediator of Bacterial Gene Regulation. <i>Annual Review of Microbiology</i> , 2021 , 75, 291-314	17.5	2	
14	Basis of narrow-spectrum activity of fidaxomicin on Clostridioides difficile <i>Nature</i> , 2022 ,	50.4	2	
13	Seeing gene expression in cells: the future of structural biology Faculty Reviews, 2021, 10, 79	1.2	1	
12	The elemental mechanism of transcriptional pausing		1	
11	Heterologous glycosyl hydrolase expression and cellular reprogramming resembling sucrose-induction enableZymomonas mobilisgrowth on cellobiose		1	
10	Heterologous expression of a glycosyl hydrolase and cellular reprogramming enable Zymomonas mobilis growth on cellobiose. <i>PLoS ONE</i> , 2020 , 15, e0226235	3.7	1	
9	Chemical-genetic interrogation of RNA polymerase mutants reveals structure-function relationships and physiological tradeoffs. <i>Molecular Cell</i> , 2021 , 81, 2201-2215.e9	17.6	1	
8	Obligate movements of an active site-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,	11.5	1	
7	Conserved Trigger Loop Histidine of RNA Polymerase II Functions as a Positional Catalyst Primarily through Steric Effects. <i>Biochemistry</i> , 2021 , 60, 3323-3336	3.2	Ο	

6	In Vitro Transcription Assay to Quantify Effects of H-NS Filaments on RNA Chain Elongation by RNA Polymerase. <i>Methods in Molecular Biology</i> , 2018 , 1837, 351-386	1.4
5	RNA Polymerases from Bacillus subtilis and Escherichia coli Differ in Recognition of Regulatory Signals In Vitro. <i>Journal of Bacteriology</i> , 2001 , 183, 1504-1504	3.5
4	Single Molecule Studies Reveal the Mechanism and Energetics of Transcriptional Termination. <i>FASEB Journal</i> , 2008 , 22, 399.1	0.9
3	Conserved mechanisms of transcriptional pausing regulate diverse RNA polymerases. <i>FASEB Journal</i> , 2019 , 33, 624.2	0.9
2	Role of the RNA polymerase trigger loop in transcript elongation, cleavage, and pausing. <i>FASEB Journal</i> , 2009 , 23, 430.2	0.9
1	Bacterial Transcription Continues to Surprise: Activation by Alarmone-Mediated Factor Tethering. <i>Molecular Cell</i> , 2021 , 81, 8-9	17.6