

Robert Landick

List of Publications by Year in descending order

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113
papers

8,793
citations

38742

50
h-index

49909

87
g-index

125
all docs

125
docs citations

125
times ranked

4956
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 7090-7095.	7.1	375
2	Structural basis for substrate loading in bacterial RNA polymerase. Nature, 2007, 448, 163-168.	27.8	333
3	Single-Molecule Study of Transcriptional Pausing and Arrest by E. coli RNA Polymerase. Science, 2000, 287, 2497-2500.	12.6	330
4	Mechanisms of Bacterial Transcription Termination: All Good Things Must End. Annual Review of Biochemistry, 2016, 85, 319-347.	11.1	282
5	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. Science, 2014, 344, 1042-1047.	12.6	280
6	Sequence-Resolved Detection of Pausing by Single RNA Polymerase Molecules. Cell, 2006, 125, 1083-1094.	28.9	252
7	The Transcriptional Regulator RfaH Stimulates RNA Chain Synthesis after Recruitment to Elongation Complexes by the Exposed Nontemplate DNA Strand. Cell, 2002, 109, 193-203.	28.9	229
8	The regulatory roles and mechanism of transcriptional pausing. Biochemical Society Transactions, 2006, 34, 1062-1066.	3.4	228
9	RNA polymerase mutants found through adaptive evolution reprogram <i>Escherichia coli</i> for optimal growth in minimal media. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20500-20505.	7.1	219
10	Regulator Trafficking on Bacterial Transcription Units In Vivo. Molecular Cell, 2009, 33, 97-108.	9.7	217
11	Allosteric Control of RNA Polymerase by a Site That Contacts Nascent RNA Hairpins. Science, 2001, 292, 730-733.	12.6	205
12	An α Helix to β Barrel Domain Switch Transforms the Transcription Factor RfaH into a Translation Factor. Cell, 2012, 150, 291-303.	28.9	201
13	Structure of a bacterial RNA polymerase holoenzyme open promoter complex. ELife, 2015, 4, .	6.0	196
14	A Central Role of the RNA Polymerase Trigger Loop in Active-Site Rearrangement during Transcriptional Pausing. Molecular Cell, 2007, 27, 406-419.	9.7	189
15	Architecture of a transcribing-translating expressome. Science, 2017, 356, 194-197.	12.6	163
16	Discontinuous movements of DNA and RNA in RNA polymerase accompany formation of a paused transcription complex. Cell, 1995, 81, 341-350.	28.9	161
17	RNA Polymerase Accommodates a Pause RNA Hairpin by Global Conformational Rearrangements that Prolong Pausing. Molecular Cell, 2018, 69, 802-815.e5.	9.7	152
18	Structural Basis for Transcript Elongation Control by NusG Family Universal Regulators. Cell, 2018, 173, 1650-1662.e14.	28.9	143

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19	Structural Basis of Transcriptional Pausing in Bacteria. <i>Cell</i> , 2013, 152, 431-441.	28.9	139
20	Role of the RNA polymerase trigger loop in catalysis and pausing. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 99-104.	8.2	138
21	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, 9545-9550.	7.1	133
22	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, 12344-12355.	3.4	132
23	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.	7.1	126
24	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, 6555-6560.	7.1	118
25	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, 4663-4667.	7.1	115
26	A Two-Way Street: Regulatory Interplay between RNA Polymerase and Nascent RNA Structure. <i>Trends in Biochemical Sciences</i> , 2016, 41, 293-310.	7.5	113
27	Bridged filaments of histone-like nucleoid structuring protein pause RNA polymerase and aid termination in bacteria. <i>ELife</i> , 2015, 4, .	6.0	112
28	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.	4.2	110
29	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.	3.4	96
30	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.	8.2	92
31	Termination-altering amino acid substitutions in the beta' subunit of Escherichia coli RNA polymerase identify regions involved in RNA chain elongation.. <i>Genes and Development</i> , 1994, 8, 2913-2927.	5.9	91
32	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.	2.5	91
33	Multiple interactions stabilize a single paused transcription intermediate in which hairpin to 3' end spacing distinguishes pause and termination pathways. <i>Journal of Molecular Biology</i> , 1997, 268, 54-68.	4.2	90
34	The Downstream DNA Jaw of Bacterial RNA Polymerase Facilitates Both Transcriptional Initiation and Pausing. <i>Journal of Biological Chemistry</i> , 2002, 277, 37456-37463.	3.4	86
35	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, 7833-7838.	7.1	85
36	Mycobacterial RNA Polymerase Requires a U-Tract at Intrinsic Terminators and Is Aided by NusG at Suboptimal Terminators. <i>MBio</i> , 2014, 5, e00931.	4.1	85

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37	RNA polymerase motions during promoter melting. <i>Science</i> , 2017, 356, 863-866.	12.6	85
38	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, 265-282.	4.2	84
39	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, 12619-12624.	7.1	84
40	Fidaxomicin jams <i>Mycobacterium tuberculosis</i> RNA polymerase motions needed for initiation via RbpA contacts. <i>ELife</i> , 2018, 7, .	6.0	83
41	Bacterial RNA polymerase can retain $\sim 70\%$ throughout transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 602-607.	7.1	79
42	Complete genome sequence and the expression pattern of plasmids of the model ethanologen <i>Zymomonas mobilis</i> ZM4 and its xylose-utilizing derivatives 8b and 2032. <i>Biotechnology for Biofuels</i> , 2018, 11, 125.	6.2	79
43	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, 708-725.	4.2	77
44	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, .	7.1	76
45	Directed Evolution Reveals Unexpected Epistatic Interactions That Alter Metabolic Regulation and Enable Anaerobic Xylose Use by <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2016, 12, e1006372.	3.5	75
46	Mechanisms of Transcriptional Pausing in Bacteria. <i>Journal of Molecular Biology</i> , 2019, 431, 4007-4029.	4.2	70
47	Mechanism for the Regulated Control of Bacterial Transcription Termination by a Universal Adaptor Protein. <i>Molecular Cell</i> , 2018, 71, 911-922.e4.	9.7	65
48	RNA Polymerase Clamps Down. <i>Cell</i> , 2001, 105, 567-570.	28.9	63
49	RNA Transcript 3'-Proximal Sequence Affects Translocation Bias of RNA Polymerase. <i>Biochemistry</i> , 2011, 50, 7002-7014.	2.5	63
50	DksA Guards Elongating RNA Polymerase against Ribosome-Stalling-Induced Arrest. <i>Molecular Cell</i> , 2014, 53, 766-778.	9.7	63
51	H-NS and RNA polymerase: a love-hate relationship?. <i>Current Opinion in Microbiology</i> , 2015, 24, 53-59.	5.1	62
52	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of <i>Saccharomyces cerevisiae</i> Used in Biofuels Research. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1757-1766.	1.8	61
53	The <i>Salmonella typhimurium</i> his operon leader region contains an RNA hairpin-dependent transcription pause site. <i>Journal of Biological Chemistry</i> , 1989, 264, 20796-20804.	3.4	61
54	The elemental mechanism of transcriptional pausing. <i>ELife</i> , 2019, 8, .	6.0	58

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55	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.	14.5	55
56	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.	3.4	55
57	The Role of the Lid Element in Transcription by E. coli RNA Polymerase. <i>Journal of Molecular Biology</i> , 2006, 361, 644-658.	4.2	52
58	Cys-Pair Reporters Detect a Constrained Trigger Loop in a Paused RNA Polymerase. <i>Molecular Cell</i> , 2013, 50, 882-893.	9.7	52
59	Transcription of Bacterial Chromatin. <i>Journal of Molecular Biology</i> , 2019, 431, 4040-4066.	4.2	51
60	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.	7.1	49
61	Direct Versus Limited-step Reconstitution Reveals Key Features of an RNA Hairpin-stabilized Paused Transcription Complex. <i>Journal of Biological Chemistry</i> , 2007, 282, 19020-19028.	3.4	48
62	Pausing guides RNA folding to populate transiently stable RNA structures for riboswitch-based transcription regulation. <i>ELife</i> , 2017, 6, .	6.0	48
63	Aromatic inhibitors derived from ammonia-pretreated lignocellulose hinder bacterial ethanologensis by activating regulatory circuits controlling inhibitor efflux and detoxification. <i>Frontiers in Microbiology</i> , 2014, 5, 402.	3.5	46
64	Life times of metastable states guide regulatory signaling in transcriptional riboswitches. <i>Nature Communications</i> , 2018, 9, 944.	12.8	46
65	Trigger-helix folding pathway and SI3 mediate catalysis and hairpin-stabilized pausing by Escherichia coli RNA polymerase. <i>Nucleic Acids Research</i> , 2014, 42, 12707-12721.	14.5	43
66	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.	7.1	38
67	Downstream DNA Selectively Affects a Paused Conformation of Human RNA Polymerase II. <i>Journal of Molecular Biology</i> , 2004, 341, 429-442.	4.2	37
68	Active-Site Dynamics in RNA Polymerases. <i>Cell</i> , 2004, 116, 351-353.	28.9	37
69	Transcriptional pausing without backtracking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8797-8798.	7.1	36
70	OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. <i>Metabolic Engineering</i> , 2019, 52, 324-340.	7.0	36
71	Transcriptional Pausing as a Mediator of Bacterial Gene Regulation. <i>Annual Review of Microbiology</i> , 2021, 75, 291-314.	7.3	34
72	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.	7.1	33

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73	TRANSCRIPTION:Shifting RNA Polymerase into Overdrive. <i>Science</i> , 1999, 284, 598-599.	12.6	32
74	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, 1163-1179.	4.2	32
75	Alternative transcription cycle for bacterial RNA polymerase. <i>Nature Communications</i> , 2020, 11, 448.	12.8	31
76	Natural Variation in the Multidrug Efflux Pump <i><i>SGE1</i></i> Underlies Ionic Liquid Tolerance in Yeast. <i>Genetics</i> , 2018, 210, 219-234.	2.9	30
77	The Battle of RNA Synthesis: Virus versus Host. <i>Viruses</i> , 2017, 9, 309.	3.3	26
78	Regulated redirection of central carbon flux enhances anaerobic production of bioproducts in <i>Zymomonas mobilis</i> . <i>Metabolic Engineering</i> , 2020, 61, 261-274.	7.0	26
79	The antibiotic sorangicin A inhibits promoter DNA unwinding in a <i><i>Mycobacterium tuberculosis</i></i> rifampicin-resistant RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30423-30432.	7.1	25
80	P1 Ref Endonuclease: A Molecular Mechanism for Phage-Enhanced Antibiotic Lethality. <i>PLoS Genetics</i> , 2016, 12, e1005797.	3.5	24
81	Basis of narrow-spectrum activity of fidaxomicin on <i>Clostridioides difficile</i> . <i>Nature</i> , 2022, 604, 541-545.	27.8	24
82	NTP-entry routes in multi-subunit RNA polymerases. <i>Trends in Biochemical Sciences</i> , 2005, 30, 651-654.	7.5	23
83	Functional Divergence in the Growing Family of RNA Polymerases. <i>Structure</i> , 2009, 17, 323-325.	3.3	23
84	Mapping <i>E. coli</i> RNA Polymerase and Associated Transcription Factors and Identifying Promoters Genome-Wide. <i>Methods in Enzymology</i> , 2011, 498, 449-471.	1.0	22
85	Crabtree/Warburg-like aerobic xylose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2021, 68, 119-130.	7.0	22
86	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.	4.2	21
87	Efficient reconstitution of transcription elongation complexes for single-molecule studies of eukaryotic RNA polymerase II. <i>Transcription</i> , 2012, 3, 146-153.	3.1	20
88	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.	7.1	19
89	A Markerless Method for Genome Engineering in <i>Zymomonas mobilis</i> ZM4. <i>Frontiers in Microbiology</i> , 2019, 10, 2216.	3.5	19
90	Genome-Scale Transcription-Translation Mapping Reveals Features of <i>Zymomonas mobilis</i> Transcription Units and Promoters. <i>MSystems</i> , 2020, 5, .	3.8	19

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91	The Shrewd Grasp of RNA Polymerase. <i>Science</i> , 1996, 273, 202-203.	12.6	15
92	Multiomeric Fermentation Using Chemically Defined Synthetic Hydrolyzates Revealed Multiple Effects of Lignocellulose-Derived Inhibitors on Cell Physiology and Xylose Utilization in <i>Zymomonas mobilis</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2596.	3.5	15
93	Genome-wide mapping of the distribution of CarD, RNAP σ^H , and RNAP σ^D on the <i>Mycobacterium smegmatis</i> chromosome using chromatin immunoprecipitation sequencing. <i>Genomics Data</i> , 2014, 2, 110-113.	1.3	14
94	A majority of <i>Rhodobacter sphaeroides</i> 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.	7.1	14
95	The Structure of Bacterial RNA Polymerase. , 0, , 283-296.		14
96	Delayed inhibition mechanism for secondary channel factor regulation of ribosomal RNA transcription. <i>ELife</i> , 2019, 8, .	6.0	12
97	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.	1.8	11
98	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, .	7.1	11
99	Chemical-genetic interrogation of RNA polymerase mutants reveals structure-function relationships and physiological tradeoffs. <i>Molecular Cell</i> , 2021, 81, 2201-2215.e9.	9.7	10
100	Systems Metabolic Engineering of <i>Escherichia coli</i> Improves Coconversion of Lignocellulose-Derived Sugars. <i>Biotechnology Journal</i> , 2019, 14, e1800441.	3.5	9
101	Genome-Wide Identification of Transcription Start Sites in Two <i>Alphaproteobacteria</i> , <i>Rhodobacter sphaeroides</i> 2.4.1 and <i>Novosphingobium aromaticivorans</i> DSM 12444. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	8
102	A Long Time in the Making—The Nobel Prize for RNA Polymerase. <i>Cell</i> , 2006, 127, 1087-1090.	28.9	5
103	Building a better stop sign: understanding the signals that terminate transcription. <i>Nature Methods</i> , 2013, 10, 618-619.	19.0	5
104	Heterologous expression of a glycosyl hydrolase and cellular reprogramming enable <i>Zymomonas mobilis</i> growth on cellobiose. <i>PLoS ONE</i> , 2020, 15, e0226235.	2.5	4
105	Conserved Trigger Loop Histidine of RNA Polymerase II Functions as a Positional Catalyst Primarily through Steric Effects. <i>Biochemistry</i> , 2021, 60, 3323-3336.	2.5	4
106	Bacterial Transcription Continues to Surprise: Activation by Alarmone-Mediated σ^H -Factor Tethering. <i>Molecular Cell</i> , 2021, 81, 8-9.	9.7	1
107	Mechanism for the Regulated Control of Transcription Termination by a Universal Adapter Protein. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
108	Seeing gene expression in cells: the future of structural biology. <i>Faculty Reviews</i> , 2021, 10, 79.	3.9	1

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109	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.	0.9	0
110	RNA Polymerases from <i>Bacillus subtilis</i> and <i>Escherichia coli</i> Differ in Recognition of Regulatory Signals In Vitro. <i>Journal of Bacteriology</i> , 2001, 183, 1504-1504.	2.2	0
111	Single Molecule Studies Reveal the Mechanism and Energetics of Transcriptional Termination. <i>FASEB Journal</i> , 2008, 22, 399.1.	0.5	0
112	Role of the RNA polymerase trigger loop in transcript elongation, cleavage, and pausing. <i>FASEB Journal</i> , 2009, 23, 430.2.	0.5	0
113	Conserved mechanisms of transcriptional pausing regulate diverse RNA polymerases. <i>FASEB Journal</i> , 2019, 33, 624.2.	0.5	0