

# 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	Basis of narrow-spectrum activity of fidaxomicin on <i>Clostridioides difficile</i> . <i>Nature</i> , 2022, 604, 541-545.	27.8	24
2	Bacterial Transcription Continues to Surprise: Activation by Alarmone-Mediated $\sigma$ -Factor Tethering. <i>Molecular Cell</i> , 2021, 81, 8-9.	9.7	1
3	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
4	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
5	Transcriptional Pausing as a Mediator of Bacterial Gene Regulation. <i>Annual Review of Microbiology</i> , 2021, 75, 291-314.	7.3	34
6	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
7	Crabtree/Warburg-like aerobic xylose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2021, 68, 119-130.	7.0	22
8	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
9	Seeing gene expression in cells: the future of structural biology. <i>Faculty Reviews</i> , 2021, 10, 79.	3.9	1
10	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
11	The antibiotic sorangicin A inhibits promoter DNA unwinding in a <i>Mycobacterium tuberculosis</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
12	Genome-Scale Transcription-Translation Mapping Reveals Features of <i>Zymomonas mobilis</i> Transcription Units and Promoters. <i>MSystems</i> , 2020, 5, .	3.8	19
13	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
14	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
15	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
16	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
17	Alternative transcription cycle for bacterial RNA polymerase. <i>Nature Communications</i> , 2020, 11, 448.	12.8	31
18	Mechanisms of Transcriptional Pausing in Bacteria. <i>Journal of Molecular Biology</i> , 2019, 431, 4007-4029.	4.2	70

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19	Transcription of Bacterial Chromatin. <i>Journal of Molecular Biology</i> , 2019, 431, 4040-4066.	4.2	51
20	Systems Metabolic Engineering of <i>Escherichia coli</i> Improves Coconversion of Lignocellulose-Derived Sugars. <i>Biotechnology Journal</i> , 2019, 14, e1800441.	3.5	9
21	A Markerless Method for Genome Engineering in <i>Zymomonas mobilis</i> ZM4. <i>Frontiers in Microbiology</i> , 2019, 10, 2216.	3.5	19
22	Multimic 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
23	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
24	OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. <i>Metabolic Engineering</i> , 2019, 52, 324-340.	7.0	36
25	Delayed inhibition mechanism for secondary channel factor regulation of ribosomal RNA transcription. <i>ELife</i> , 2019, 8, .	6.0	12
26	The elemental mechanism of transcriptional pausing. <i>ELife</i> , 2019, 8, .	6.0	58
27	Conserved mechanisms of transcriptional pausing regulate diverse RNA polymerases. <i>FASEB Journal</i> , 2019, 33, 624.2.	0.5	0
28	Life times of metastable states guide regulatory signaling in transcriptional riboswitches. <i>Nature Communications</i> , 2018, 9, 944.	12.8	46
29	RNA Polymerase Accommodates a Pause RNA Hairpin by Global Conformational Rearrangements that Prolong Pausing. <i>Molecular Cell</i> , 2018, 69, 802-815.e5.	9.7	152
30	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
31	Fidaxomicin jams <i>Mycobacterium tuberculosis</i> RNA polymerase motions needed for initiation via RbpA contacts. <i>ELife</i> , 2018, 7, .	6.0	83
32	Natural Variation in the Multidrug Efflux Pump <i>SGE1</i> Underlies Ionic Liquid Tolerance in Yeast. <i>Genetics</i> , 2018, 210, 219-234.	2.9	30
33	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
34	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
35	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
36	Structural Basis for Transcript Elongation Control by NusG Family Universal Regulators. <i>Cell</i> , 2018, 173, 1650-1662.e14.	28.9	143

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37	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
38	Architecture of a transcribing-translating expressome. <i>Science</i> , 2017, 356, 194-197.	12.6	163
39	RNA polymerase motions during promoter melting. <i>Science</i> , 2017, 356, 863-866.	12.6	85
40	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
41	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
42	The Battle of RNA Synthesis: Virus versus Host. <i>Viruses</i> , 2017, 9, 309.	3.3	26
43	Pausing guides RNA folding to populate transiently stable RNA structures for riboswitch-based transcription regulation. <i>ELife</i> , 2017, 6, .	6.0	48
44	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
45	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
46	Mechanisms of Bacterial Transcription Termination: All Good Things Must End. <i>Annual Review of Biochemistry</i> , 2016, 85, 319-347.	11.1	282
47	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
48	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
49	P1 Ref Endonuclease: A Molecular Mechanism for Phage-Enhanced Antibiotic Lethality. <i>PLoS Genetics</i> , 2016, 12, e1005797.	3.5	24
50	Structure of a bacterial RNA polymerase holoenzyme open promoter complex. <i>ELife</i> , 2015, 4, .	6.0	196
51	H-NS and RNA polymerase: a love-hate relationship?. <i>Current Opinion in Microbiology</i> , 2015, 24, 53-59.	5.1	62
52	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
53	Bridged filaments of histone-like nucleoid structuring protein pause RNA polymerase and aid termination in bacteria. <i>ELife</i> , 2015, 4, .	6.0	112
54	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

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55	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
56	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
57	DksA Guards Elongating RNA Polymerase against Ribosome-Stalling-Induced Arrest. <i>Molecular Cell</i> , 2014, 53, 766-778.	9.7	63
58	A pause sequence enriched at translation start sites drives transcription dynamics in vivo. <i>Science</i> , 2014, 344, 1042-1047.	12.6	280
59	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
60	Genome-wide mapping of the distribution of CarD, RNAP $\sigma^A$ , and RNAP $\sigma^H$ on the Mycobacterium smegmatis chromosome using chromatin immunoprecipitation sequencing. <i>Genomics Data</i> , 2014, 2, 110-113.	1.3	14
61	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
62	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
63	Structural Basis of Transcriptional Pausing in Bacteria. <i>Cell</i> , 2013, 152, 431-441.	28.9	139
64	Cys-Pair Reporters Detect a Constrained Trigger Loop in a Paused RNA Polymerase. <i>Molecular Cell</i> , 2013, 50, 882-893.	9.7	52
65	Building a better stop sign: understanding the signals that terminate transcription. <i>Nature Methods</i> , 2013, 10, 618-619.	19.0	5
66	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
67	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
68	An $\alpha$ Helix to $\beta$ Barrel Domain Switch Transforms the Transcription Factor RfaH into a Translation Factor. <i>Cell</i> , 2012, 150, 291-303.	28.9	201
69	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
70	RNA Transcript 3'-Proximal Sequence Affects Translocation Bias of RNA Polymerase. <i>Biochemistry</i> , 2011, 50, 7002-7014.	2.5	63
71	Mapping E. coli RNA Polymerase and Associated Transcription Factors and Identifying Promoters Genome-Wide. <i>Methods in Enzymology</i> , 2011, 498, 449-471.	1.0	22
72	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

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73	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
74	The NusA N-Terminal Domain Is Necessary and Sufficient for Enhancement of Transcriptional Pausing via Interaction with the RNA Exit Channel of RNA Polymerase. Journal of Molecular Biology, 2010, 401, 708-725.	4.2	77
75	Transcriptional pausing without backtracking. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8797-8798.	7.1	36
76	Functional Divergence in the Growing Family of RNA Polymerases. Structure, 2009, 17, 323-325.	3.3	23
77	Regulator Trafficking on Bacterial Transcription Units In Vivo. Molecular Cell, 2009, 33, 97-108.	9.7	217
78	Role of the RNA polymerase trigger loop in transcript elongation, cleavage, and pausing. FASEB Journal, 2009, 23, 430.2.	0.5	0
79	Single Molecule Studies Reveal the Mechanism and Energetics of Transcriptional Termination. FASEB Journal, 2008, 22, 399.1.	0.5	0
80	Direct Versus Limited-step Reconstitution Reveals Key Features of an RNA Hairpin-stabilized Paused Transcription Complex. Journal of Biological Chemistry, 2007, 282, 19020-19028.	3.4	48
81	Real-time footprinting of DNA in the first kinetically significant intermediate in open complex formation by <i>Escherichia coli</i> RNA polymerase. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7833-7838.	7.1	85
82	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
83	Structural basis for substrate loading in bacterial RNA polymerase. Nature, 2007, 448, 163-168.	27.8	333
84	Sequence-Resolved Detection of Pausing by Single RNA Polymerase Molecules. Cell, 2006, 125, 1083-1094.	28.9	252
85	A Long Time in the Making—The Nobel Prize for RNA Polymerase. Cell, 2006, 127, 1087-1090.	28.9	5
86	The regulatory roles and mechanism of transcriptional pausing. Biochemical Society Transactions, 2006, 34, 1062-1066.	3.4	228
87	Functional Interplay between the Jaw Domain of Bacterial RNA Polymerase and Allele-specific Residues in the Product RNA-binding Pocket. Journal of Molecular Biology, 2006, 356, 1163-1179.	4.2	32
88	The Role of the Lid Element in Transcription by <i>E. coli</i> RNA Polymerase. Journal of Molecular Biology, 2006, 361, 644-658.	4.2	52
89	NTP-entry routes in multi-subunit RNA polymerases. Trends in Biochemical Sciences, 2005, 30, 651-654.	7.5	23
90	Downstream DNA Selectively Affects a Paused Conformation of Human RNA Polymerase II. Journal of Molecular Biology, 2004, 341, 429-442.	4.2	37

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91	Active-Site Dynamics in RNA Polymerases. <i>Cell</i> , 2004, 116, 351-353.	28.9	37
92	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
93	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
94	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.	28.9	229
95	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
96	RNA Polymerase Clamps Down. <i>Cell</i> , 2001, 105, 567-570.	28.9	63
97	Allosteric Control of RNA Polymerase by a Site That Contacts Nascent RNA Hairpins. <i>Science</i> , 2001, 292, 730-733.	12.6	205
98	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
99	Pausing by bacterial RNA polymerase is mediated by mechanistically distinct classes of signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 7090-7095.	7.1	375
100	Single-Molecule Study of Transcriptional Pausing and Arrest by <i>E. coli</i> RNA Polymerase. <i>Science</i> , 2000, 287, 2497-2500.	12.6	330
101	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
102	TRANSCRIPTION: Shifting RNA Polymerase into Overdrive. <i>Science</i> , 1999, 284, 598-599.	12.6	32
103	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
104	The Shrewd Grasp of RNA Polymerase. <i>Science</i> , 1996, 273, 202-203.	12.6	15
105	Discontinuous movements of DNA and RNA in RNA polymerase accompany formation of a paused transcription complex. <i>Cell</i> , 1995, 81, 341-350.	28.9	161
106	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
107	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
108	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

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109	The Salmonella typhimurium his operon leader region contains an RNA hairpin-dependent transcription pause site. Journal of Biological Chemistry, 1989, 264, 20796-20804.	3.4	61
110	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. Journal of Biological Chemistry, 1989, 264, 20796-804.	3.4	55
111	Translation activates the paused transcription complex and restores transcription of the trp operon leader region.. Proceedings of the National Academy of Sciences of the United States of America, 1985, 82, 4663-4667.	7.1	115
112	The Structure of Bacterial RNA Polymerase. , 0, , 283-296.		14
113	Mechanism for the Regulated Control of Transcription Termination by a Universal Adapter Protein. SSRN Electronic Journal, 0, , .	0.4	1