

# Richard H Ebright

## List of Publications by Year in descending order

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179  
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17,266  
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9264  
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209  
all docs

209  
docs citations

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times ranked

9935  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription activation by catabolite activator protein (CAP). Journal of Molecular Biology, 1999, 293, 199-213.	4.2	709
2	Dynamically driven protein allostery. Nature Structural and Molecular Biology, 2006, 13, 831-838.	8.2	574
3	Accurate FRET Measurements within Single Diffusing Biomolecules Using Alternating-Laser Excitation. Biophysical Journal, 2005, 88, 2939-2953.	0.5	440
4	Promoter structure, promoter recognition, and transcription activation in prokaryotes. Cell, 1994, 79, 743-746.	28.9	432
5	Initial Transcription by RNA Polymerase Proceeds Through a DNA-Scrunching Mechanism. Science, 2006, 314, 1144-1147.	12.6	400
6	Abortive Initiation and Productive Initiation by RNA Polymerase Involve DNA Scrunching. Science, 2006, 314, 1139-1143.	12.6	346
7	New core promoter element in RNA polymerase II-dependent transcription: sequence-specific DNA binding by transcription factor $\sigma^{48}$ . Genes and Development, 1998, 12, 34-44.	5.9	336
8	Structural Basis of Transcription Initiation. Science, 2012, 338, 1076-1080.	12.6	333
9	Catabolite activator protein: DNA binding and transcription activation. Current Opinion in Structural Biology, 2004, 14, 10-20.	5.7	291
10	Transcription Activation at Class II CAP-Dependent Promoters: Two Interactions between CAP and RNA Polymerase. Cell, 1996, 87, 1123-1134.	28.9	279
11	Structural Organization of Bacterial RNA Polymerase Holoenzyme and the RNA Polymerase-Promoter Open Complex. Cell, 2002, 108, 599-614.	28.9	279
12	Transcription activation at Class I CAP-dependent promoters. Molecular Microbiology, 1993, 8, 797-802.	2.5	262
13	Structure of the CAP-DNA Complex at 2.5 Å Resolution: A Complete Picture of the Protein-DNA Interface. Journal of Molecular Biology, 1996, 260, 395-408.	4.2	262
14	Mutations that alter the DNA sequence specificity of the catabolite gene activator protein of E. coli. Nature, 1984, 311, 232-235.	27.8	252
15	Domain organization of RNA polymerase $\sigma^{48}$ subunit: C-terminal 85 amino acids constitute a domain capable of dimerization and DNA binding. Cell, 1994, 78, 889-896.	28.9	251
16	Mechanism of ATP-Dependent Promoter Melting by Transcription Factor IIH. Science, 2000, 288, 1418-1421.	12.6	236
17	Random mutagenesis of gene-sized DNA molecules by use of PCR with Taq DNA polymerase. Nucleic Acids Research, 1991, 19, 6052-6052.	14.5	235
18	Structural Basis of Transcription Activation: The CAP- $\alpha$ CTD-DNA Complex. Science, 2002, 297, 1562-1566.	12.6	234

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19	The RNA Polymerase "Switch Region" Is a Target for Inhibitors. <i>Cell</i> , 2008, 135, 295-307.	28.9	234
20	RNA Polymerase: Structural Similarities Between Bacterial RNA Polymerase and Eukaryotic RNA Polymerase II. <i>Journal of Molecular Biology</i> , 2000, 304, 687-698.	4.2	223
21	Opening and Closing of the Bacterial RNA Polymerase Clamp. <i>Science</i> , 2012, 337, 591-595.	12.6	210
22	Antibacterial Peptide Microcin J25 Inhibits Transcription by Binding within and Obstructing the RNA Polymerase Secondary Channel. <i>Molecular Cell</i> , 2004, 14, 739-751.	9.7	206
23	Structure of Antibacterial Peptide Microcin J25: A 21-Residue Lariat Protoknot. <i>Journal of the American Chemical Society</i> , 2003, 125, 12382-12383.	13.7	203
24	Bacterial RNA polymerase subunit $\alpha$ and eukaryotic RNA polymerase subunit RPB6 are sequence, structural, and functional homologs and promote RNA polymerase assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 892-897.	7.1	197
25	Structural basis for cAMP-mediated allosteric control of the catabolite activator protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6927-6932.	7.1	197
26	Transcription activation at Class II CAP-dependent promoters. <i>Molecular Microbiology</i> , 1997, 23, 853-859.	2.5	193
27	DNA-binding determinants of the $\alpha$ subunit of RNA polymerase: novel DNA-binding domain architecture. <i>Genes and Development</i> , 1996, 10, 16-26.	5.9	188
28	Bacterial promoter architecture: subsite structure of UP elements and interactions with the carboxy-terminal domain of the RNA polymerase $\alpha$ subunit. <i>Genes and Development</i> , 1999, 13, 2134-2147.	5.9	185
29	Inhibition of Bacterial RNA Polymerase by Streptolydigin: Stabilization of a Straight-Bridge-Helix Active-Center Conformation. <i>Cell</i> , 2005, 122, 541-552.	28.9	183
30	Site-Specific Incorporation of Fluorescent Probes into Protein: A Hexahistidine-Tag-Mediated Fluorescent Labeling with (Ni <sup>2+</sup> :Nitrilotriacetic Acid)-Fluorochrome Conjugates. <i>Journal of the American Chemical Society</i> , 2001, 123, 12123-12125.	13.7	182
31	Consensus DNA site for the <i>Escherichia coli</i> catabolite gene activator protein (CAP): CAP exhibits a 450-fold higher affinity for the consensus DNA site than for the <i>E. coli</i> lacDNA site. <i>Nucleic Acids Research</i> , 1989, 17, 10295-10305.	14.5	181
32	Translocation of $\lambda$ 70 with RNA Polymerase during Transcription. <i>Cell</i> , 2001, 106, 453-463.	28.9	181
33	The mechanism of RNA 5' capping with NAD <sup>+</sup> , NADH and desphospho-CoA. <i>Nature</i> , 2016, 535, 444-447.	27.8	181
34	Identification of the target of a transcription activator protein by protein-protein photocrosslinking. <i>Science</i> , 1994, 265, 90-92.	12.6	178
35	Structural Organization of the RNA Polymerase-Promoter Open Complex. <i>Cell</i> , 2000, 101, 601-611.	28.9	177
36	New target for inhibition of bacterial RNA polymerase: the "switch region"™. <i>Current Opinion in Microbiology</i> , 2011, 14, 532-543.	5.1	176

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37	Interactions between RNA polymerase and the core recognition element counteract pausing. <i>Science</i> , 2014, 344, 1285-1289.	12.6	158
38	Promoter unwinding and promoter clearance by RNA polymerase: Detection by single-molecule DNA nanomanipulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 4776-4780.	7.1	157
39	The <i>Escherichia coli</i> RNA polymerase $\sigma$ subunit: structure and function. <i>Current Opinion in Genetics and Development</i> , 1995, 5, 197-203.	3.3	151
40	Identification of the activating region of catabolite gene activator protein (CAP): isolation and characterization of mutants of CAP specifically defective in transcription activation.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 6081-6085.	7.1	150
41	Antibiotic Production by Myxobacteria Plays a Role in Predation. <i>Journal of Bacteriology</i> , 2011, 193, 4626-4633.	2.2	150
42	Fluorescence anisotropy: Rapid, quantitative assay for protein-DNA and protein-protein interaction. <i>Methods in Enzymology</i> , 1996, 274, 492-503.	1.0	137
43	Direct Observation of Abortive Initiation and Promoter Escape within Single Immobilized Transcription Complexes. <i>Biophysical Journal</i> , 2006, 90, 1419-1431.	0.5	136
44	The Initiation Factor TFE and the Elongation Factor Spt4/5 Compete for the RNAP Clamp during Transcription Initiation and Elongation. <i>Molecular Cell</i> , 2011, 43, 263-274.	9.7	136
45	Transcription activation at Class II CRP-dependent promoters: identification of determinants in the C-terminal domain of the RNA polymerase alpha subunit. <i>EMBO Journal</i> , 1998, 17, 3439-3447.	7.8	133
46	Retention of Transcription Initiation Factor $\sigma$ 70 in Transcription Elongation: Single-Molecule Analysis. <i>Molecular Cell</i> , 2005, 20, 347-356.	9.7	132
47	Structures of RNA polymerase-antibiotic complexes. <i>Current Opinion in Structural Biology</i> , 2009, 19, 715-723.	5.7	132
48	Structural Basis of Mycobacterium tuberculosis Transcription and Transcription Inhibition. <i>Molecular Cell</i> , 2017, 66, 169-179.e8.	9.7	130
49	Rapid RNA polymerase genetics: one-day, no-column preparation of reconstituted recombinant <i>Escherichia coli</i> RNA polymerase.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 4902-4906.	7.1	121
50	Antibacterial Nucleoside-Analog Inhibitor of Bacterial RNA Polymerase. <i>Cell</i> , 2017, 169, 1240-1248.e23.	28.9	121
51	The Infectious Diseases Society of America's 10 $\sigma$ 20 Initiative (10 New Systemic Antibacterial Agents US) <i>Tj ETQq1</i> 1 0.7843 2019, 69, 1-11.	5.8	120
52	Trajectory of DNA in the RNA polymerase II transcription preinitiation complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 12268-12273.	7.1	113
53	Systematic Structure-Activity Analysis of Microcin J25. <i>Journal of Biological Chemistry</i> , 2008, 283, 25589-25595.	3.4	112
54	Location, structure, and function of the target of a transcriptional activator protein.. <i>Genes and Development</i> , 1994, 8, 3058-3067.	5.9	111

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55	Incorporation of an EDTA-metal complex at a rationally selected site within a protein: application to EDTA-iron DNA affinity cleaving with catabolite gene activator protein (CAP) and Cro. <i>Biochemistry</i> , 1992, 31, 10664-10670.	2.5	109
56	High-resolution mapping of nucleoprotein complexes by site-specific protein-DNA photocrosslinking: organization of the human TBP-TFIIA-TFIIB-DNA quaternary complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 10620-10625.	7.1	106
57	Structural basis of transcription-translation coupling. <i>Science</i> , 2020, 369, 1359-1365.	12.6	101
58	Protein-protein interactions in eukaryotic transcription initiation: structure of the preinitiation complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 1119-1124.	7.1	100
59	Characterization of the activating region of Escherichia coli catabolite gene activator protein (CAP) II. Role at class I and class II CAP-dependent promoters. <i>Journal of Molecular Biology</i> , 1994, 243, 603-610.	4.2	99
60	Thermodynamic and kinetic modeling of transcriptional pausing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4439-4444.	7.1	98
61	Direct Detection of Abortive RNA Transcripts in Vivo. <i>Science</i> , 2009, 324, 927-928.	12.6	96
62	Structural basis of transcription activation. <i>Science</i> , 2016, 352, 1330-1333.	12.6	92
63	Response of RNA polymerase to ppGpp: requirement for the $\sigma$ subunit and relief of this requirement by DksA. <i>Genes and Development</i> , 2005, 19, 2378-2387.	5.9	91
64	Role of glutamic acid-181 in DNA-sequence recognition by the catabolite gene activator protein (CAP) of Escherichia coli: altered DNA-sequence-recognition properties of [Val181]CAP and [Leu181]CAP.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1987, 84, 6083-6087.	7.1	90
65	CAP interacts with RNA polymerase in solution in the absence of promoter DNA. <i>Nature</i> , 1993, 364, 548-549.	27.8	90
66	Rifamycins do not function by allosteric modulation of binding of $Mg^{2+}$ to the RNA polymerase active center. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14820-14825.	7.1	90
67	Identification of an amino acid-base contact in the GCN4-DNA complex by bromouracil-mediated photocrosslinking. <i>Nature</i> , 1992, 359, 650-652.	27.8	83
68	Identification of the functional subunit of a dimeric transcription activator protein by use of oriented heterodimers. <i>Cell</i> , 1993, 73, 375-379.	28.9	83
69	White Paper: Developing Antimicrobial Drugs for Resistant Pathogens, Narrow-Spectrum Indications, and Unmet Needs. <i>Journal of Infectious Diseases</i> , 2017, 216, 228-236.	4.0	83
70	The interaction between $\sigma^{70}$ and the $\sigma$ -flap of Escherichia coli RNA polymerase inhibits extension of nascent RNA during early elongation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4488-4493.	7.1	82
71	The Antibacterial Threaded-Iasso Peptide Capistrin Inhibits Bacterial RNA Polymerase. <i>Journal of Molecular Biology</i> , 2011, 412, 842-848.	4.2	82
72	Determinants of RNA polymerase alpha subunit for interaction with beta, beta', and sigma subunits: hydroxyl-radical protein footprinting.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 10162-10166.	7.1	81

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73	Structural Basis of Transcription Inhibition by Fidaxomicin (Lipiarmycin A3). <i>Molecular Cell</i> , 2018, 70, 60-71.e15.	9.7	81
74	Characterization of the activating region of Escherichia coli catabolite gene activator protein (CAP) I. Saturation and alanine-scanning mutagenesis. <i>Journal of Molecular Biology</i> , 1994, 243, 595-602.	4.2	80
75	Molecular basis of DNA sequence recognition by the catabolite gene activator protein: detailed inferences from three mutations that alter DNA sequence specificity.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1984, 81, 7274-7278.	7.1	79
76	The $\beta$ 70 subunit of RNA polymerase mediates a promoter-proximal pause at the lac promoter. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 544-550.	8.2	78
77	Functional Interaction between RNA Polymerase $\beta$ Subunit C-Terminal Domain and $\beta$ 70 in UP-Element- and Activator-Dependent Transcription. <i>Molecular Cell</i> , 2003, 11, 1621-1633.	9.7	77
78	The Transcription Bubble of the RNA Polymerase $\alpha$ -Promoter Open Complex Exhibits Conformational Heterogeneity and Millisecond-Scale Dynamics: Implications for Transcription Start-Site Selection. <i>Journal of Molecular Biology</i> , 2013, 425, 875-885.	4.2	77
79	Three-dimensional EM structure of an intact activator-dependent transcription initiation complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19830-19835.	7.1	76
80	Massively Systematic Transcript End Readout, $\alpha$ -MASTER $\alpha$ Transcription Start Site Selection, Transcriptional Slippage, and Transcript Yields. <i>Molecular Cell</i> , 2015, 60, 953-965.	9.7	72
81	RNA Polymerase $\beta$ Subunit: A Target of DNA Binding-Independent Activation. <i>Science</i> , 1997, 275, 1655-1657.	12.6	71
82	Transcription inhibition by the depsipeptide antibiotic salinamide A. <i>ELife</i> , 2014, 3, e02451.	6.0	71
83	Single-molecule DNA nanomanipulation: Improved resolution through use of shorter DNA fragments. <i>Nature Methods</i> , 2005, 2, 127-138.	19.0	69
84	Analogues of cyclic AMP that elicit the biochemically defined conformational change in catabolite gene activator protein (CAP) but do not stimulate binding to DNA. <i>Journal of Molecular Biology</i> , 1985, 182, 91-107.	4.2	68
85	GE23077 binds to the RNA polymerase $\alpha$ - $\beta$ and $\alpha$ - $\beta$ sites and prevents the binding of initiating nucleotides. <i>ELife</i> , 2014, 3, e02450.	6.0	68
86	Conversion of a helix-turn-helix motif sequence-specific DNA binding protein into a site-specific DNA cleavage agent.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 2882-2886.	7.1	67
87	A single substitution in the putative helix-turn-helix motif of the pleiotropic activator PrfA attenuates <i>Listeria monocytogenes</i> virulence. <i>Molecular Microbiology</i> , 1996, 20, 785-797.	2.5	67
88	Aromatic hydrogen bond in sequence-specific protein DNA recognition. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 837-841.	8.2	66
89	Determinants of the C-Terminal Domain of the Escherichia coli RNA Polymerase $\beta$ Subunit Important for Transcription at Class I Cyclic AMP Receptor Protein-Dependent Promoters. <i>Journal of Bacteriology</i> , 2002, 184, 2273-2280.	2.2	64
90	CapZyme-Seq Comprehensively Defines Promoter-Sequence Determinants for RNA 5' Capping with NAD <sup>+</sup> . <i>Molecular Cell</i> , 2018, 70, 553-564.e9.	9.7	64

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91	Highly efficient 5' capping of mitochondrial RNA with NAD <sup>+</sup> and NADH by yeast and human mitochondrial RNA polymerase. <i>ELife</i> , 2018, 7, .	6.0	64
92	Multiplexed protein-DNA cross-linking: Scrunching in transcription start site selection. <i>Science</i> , 2016, 351, 1090-1093.	12.6	62
93	The RNA Polymerase II General Transcription Factors: Past, Present, and Future. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998, 63, 83-105.	1.1	61
94	Transcription Factor B Contacts Promoter DNA Near the Transcription Start Site of the Archaeal Transcription Initiation Complex. <i>Journal of Biological Chemistry</i> , 2004, 279, 2825-2831.	3.4	59
95	High-specificity DNA cleavage agent: design and application to kilobase and megabase DNA substrates. <i>Science</i> , 1994, 265, 959-962.	12.6	57
96	Indirect readout of DNA sequence at the primary-kink site in the CAP-DNA complex: alteration of DNA binding specificity through alteration of DNA kinking. <i>Journal of Molecular Biology</i> , 2001, 314, 75-82.	4.2	57
97	Mutational analysis of a transcriptional activation region of the VP16 protein of herpes simplex virus [published erratum appears in <i>Nucleic Acids Res</i> 1998 Dec 1;26(23):537-8]. <i>Nucleic Acids Research</i> , 1998, 26, 4487-4496.	14.5	56
98	Evidence for a contact between glutamine-18 of lac repressor and base pair 7 of lac operator.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 303-307.	7.1	55
99	Identification of a contact between arginine-180 of the catabolite gene activator protein (CAP) and base pair 5 of the DNA site in the CAP-DNA complex.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 4717-4721.	7.1	55
100	Mean DNA Bend Angle and Distribution of DNA Bend Angles in the CAP-DNA Complex in Solution. <i>Journal of Molecular Biology</i> , 2001, 312, 453-468.	4.2	55
101	S-[2-(4-Azidosalicylamido)ethylthio]-2-thiopyridine:â€‰ Radioiodinatable, Cleavable, Photoactivatable Cross-Linking Agent. <i>Bioconjugate Chemistry</i> , 1996, 7, 380-384.	3.6	53
102	Indirect readout of DNA sequence at the primary-kink site in the CAP-DNA complex: DNA binding specificity based on energetics of DNA kinking. <i>Journal of Molecular Biology</i> , 2001, 314, 63-74.	4.2	52
103	Determination of the orientation of a DNA binding motif in a protein-DNA complex by photocrosslinking.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 10287-10291.	7.1	51
104	Orientation of OmpR monomers within an OmpR:DNA complex determined by DNA affinity cleaving 1 Edited by K. Yamamoto. <i>Journal of Molecular Biology</i> , 1999, 285, 555-566.	4.2	49
105	Derivatives of CAP Having No Solvent-Accessible Cysteine Residues, or Having a Unique Solvent-Accessible Cysteine Residue at Amino Acid 2 of the Helix-Turn-Helix Motif. <i>Journal of Biomolecular Structure and Dynamics</i> , 1991, 9, 463-473.	3.5	46
106	Distance-Restrained Docking of Rifampicin and Rifamycin SV to RNA Polymerase Using Systematic FRET Measurements: Developing Benchmarks of Model Quality and Reliability. <i>Biophysical Journal</i> , 2005, 88, 925-938.	0.5	46
107	Salinamide F, new depsipeptide antibiotic and inhibitor of bacterial RNA polymerase from a marine-derived <i>Streptomyces</i> sp.. <i>Journal of Antibiotics</i> , 2015, 68, 206-209.	2.0	45
108	The RNA polymerase clamp interconverts dynamically among three states and is stabilized in a partly closed state by ppGpp. <i>Nucleic Acids Research</i> , 2018, 46, 7284-7295.	14.5	45



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109	Transcription activation at the Escherichia coli uhpT promoter by the catabolite gene activator protein. Journal of Bacteriology, 1995, 177, 1712-1718.	2.2	44
110	Indirect Readout of DNA Sequence at the Primary-kink Site in the CAP-DNA Complex: Recognition of Pyrimidine-Purine and Purine-Purine Steps. Journal of Molecular Biology, 2006, 357, 173-183.	4.2	43
111	Use of Loss-of-Contact-Substitutions to Identify Residues Involved in an Amino Acid-Base Pair Contact: Effect of Substitution of Gln18 of Lac Repressor by Gly, Ser, and Leu. Journal of Biomolecular Structure and Dynamics, 1985, 3, 281-297.	3.5	42
112	Analysis of the Pseudouridimycin Biosynthetic Pathway Provides Insights into the Formation of C-nucleoside Antibiotics. Cell Chemical Biology, 2018, 25, 540-549.e4.	5.2	42
113	Pause sequences facilitate entry into long-lived paused states by reducing RNA polymerase transcription rates. Nature Communications, 2018, 9, 2930.	12.8	42
114	Activation mutants in yeast RNA polymerase II subunit RPB3 provide evidence for a structurally conserved surface required for activation in eukaryotes and bacteria. Genes and Development, 2000, 14, 339-348.	5.9	42
115	Mechanism for transcriptional action of cyclic AMP in Escherichia coli: entry into DNA to disrupt DNA secondary structure.. Proceedings of the National Academy of Sciences of the United States of America, 1981, 78, 4011-4015.	7.1	39
116	[10] Escherichia coli RNA polymerase holoenzyme: Rapid reconstitution from recombinant $\hat{\sigma}$ , $\hat{\sigma}^2$ , and $\hat{\sigma}^3$ subunits. Methods in Enzymology, 1996, 273, 130-134.	1.0	39
117	Fluorescence Resonance Energy Transfer (FRET) in Analysis of Transcription-Complex Structure and Function. Methods in Enzymology, 2003, 371, 144-159.	1.0	39
118	Roles of the Histone H2A-H2B Dimers and the (H3-H4) <sub>2</sub> Tetramer in Nucleosome Remodeling by the SWI-SNF Complex. Journal of Biological Chemistry, 2000, 275, 11545-11552.	3.4	38
119	[30] Identification of amino acid-base pair contacts by genetic methods. Methods in Enzymology, 1991, 208, 620-640.	1.0	37
120	Structural basis of ECF- $\sigma$ -factor-dependent transcription initiation. Nature Communications, 2019, 10, 710.	12.8	37
121	Interactions between RNA polymerase and the core recognition element are a determinant of transcription start site selection. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2899-905.	7.1	36
122	Structural basis of Q-dependent antitermination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18384-18390.	7.1	35
123	DNA affinity cleaving analysis of homeodomain-DNA interaction: identification of homeodomain consensus sites in genomic DNA.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 118-122.	7.1	32
124	Upstream promoter sequences and $\hat{\sigma}$ -CTD mediate stable DNA wrapping within the RNA polymerase-promoter open complex. EMBO Reports, 2007, 8, 271-278.	4.5	32
125	RNA extension drives a stepwise displacement of an initiation-factor structural module in initial transcription. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5801-5809.	7.1	27
126	Closing and opening of the RNA polymerase trigger loop. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15642-15649.	7.1	27



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127	Structural Basis of Transcription Inhibition by CBR Hydroxamides and CBR Pyrazoles. <i>Structure</i> , 2015, 23, 1470-1481.	3.3	25
128	Frequency, Spectrum, and Nonzero Fitness Costs of Resistance to Myxopyronin in <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6250-6255.	3.2	24
129	Single-Molecule DNA Nanomanipulation: Detection of Promoter-Unwinding Events by RNA Polymerase. <i>Methods in Enzymology</i> , 2003, 370, 577-598.	1.0	23
130	An Open Letter to Elias Zerhouni. <i>Science</i> , 2005, 307, 1409c-1410c.	12.6	23
131	The fight over flu. <i>Nature</i> , 2012, 481, 257-259.	27.8	23
132	The mechanism of variability in transcription start site selection. <i>ELife</i> , 2017, 6, .	6.0	23
133	Phenyl-azide-mediated Photocrosslinking Analysis of Cro-DNA Interaction. <i>Journal of Molecular Biology</i> , 1993, 230, 453-460.	4.2	22
134	Structure of the LexA Repressor~DNA Complex Probed by Affinity Cleavage and Affinity Photo-Cross-Linking. <i>Biochemistry</i> , 1996, 35, 4279-4286.	2.5	22
135	Artificial Sequence-Specific DNA Binding Peptides: A Branched-Chain Basic Regions. <i>Journal of the American Chemical Society</i> , 1996, 118, 5831-5835.	13.7	22
136	Mechanisms of Viral Activators. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998, 63, 243-252.	1.1	22
137	Requirement for two copies of RNA polymerase alpha subunit C-terminal domain for synergistic transcription activation at complex bacterial promoters. <i>Genes and Development</i> , 2002, 16, 2557-2565.	5.9	20
138	Discovery, properties, and biosynthesis of pseudouridimycin, an antibacterial nucleoside-analog inhibitor of bacterial RNA polymerase. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 335-343.	3.0	20
139	XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for Initial-Transcription Pausing. <i>Molecular Cell</i> , 2020, 79, 797-811.e8.	9.7	20
140	RNA Polymerase-DNA Interaction: Structures of Intermediate, Open, and Elongation Complexes. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1998, 63, 11-20.	1.1	19
141	Azide-Specific Labeling of Biomolecules by Staudinger~Bertozzi Ligation. <i>Methods in Enzymology</i> , 2010, 472, 19-30.	1.0	18
142	Site-Specific Protein-DNA Photocrosslinking: Analysis of Bacterial Transcription Initiation Complexes. , 2001, 148, 337-361.		17
143	An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2. <i>Lancet</i> , The, 2021, 398, 1402-1404.	13.7	17
144	Orientation of the Lac repressor DNA binding domain in complex with the left operator half site characterized by affinity cleaving. <i>Nucleic Acids Research</i> , 1991, 19, 5233-5236.	14.5	16

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145	Synthesis and Evaluation of Novel Analogues of Ripostatins. Chemistry - A European Journal, 2014, 20, 12310-12319.	3.3	16
146	Lysine 188 of the catabolite gene activator protein (CAP) plays no role in specificity at base pair 7 of the DNA half site. Nucleic Acids Research, 1990, 18, 1457-1464.	14.5	15
147	Identification of the Subunit of cAMP Receptor Protein (CRP) That Functionally Interacts with CytR in CRP-CytR-mediated Transcriptional Repression. Journal of Biological Chemistry, 2000, 275, 11951-11956.	3.4	15
148	Affinity Selectionâ€“Mass Spectrometry Identifies a Novel Antibacterial RNA Polymerase Inhibitor. ACS Chemical Biology, 2017, 12, 1346-1352.	3.4	15
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