

Richard H Ebright

List of Publications by Year in descending order

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179
papers

17,266
citations

9234

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124
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all docs

209
docs citations

209
times ranked

9935
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and mechanistic basis of reiterative transcription initiation. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	5
2	Design, Synthesis, and Characterization of TNP-2198, a Dual-Targeted Rifamycin-Nitroimidazole Conjugate with Potent Activity against Microaerophilic and Anaerobic Bacterial Pathogens. Journal of Medicinal Chemistry, 2022, 65, 4481-4495.	2.9	13
3	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
4	RNA polymerase clamp conformational dynamics: long-lived states and modulation by crowding, cations, and nonspecific DNA binding. Nucleic Acids Research, 2021, 49, 2790-2802.	6.5	13
5	Blocks in the pseudouridimycin pathway unlock hidden metabolites in the Streptomyces producer strain. Scientific Reports, 2021, 11, 5827.	1.6	8
6	Promoter-sequence determinants and structural basis of primer-dependent transcription initiation in <i>Escherichia coli</i> . Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	4
7	An appeal for an objective, open, and transparent scientific debate about the origin of SARS-CoV-2. Lancet, The, 2021, 398, 1402-1404.	6.3	17
8	Transcription initiation at a consensus bacterial promoter proceeds via a "bind-unwind-load-and-lock" mechanism. ELife, 2021, 10, .	2.8	11
9	CHAPTER 1. The Transition from Transcription Initiation to Transcription Elongation: Start-site Selection, Initial Transcription, and Promoter Escape. Chemical Biology, 2021, , 1-24.	0.1	7
10	XACT-Seq Comprehensively Defines the Promoter-Position and Promoter-Sequence Determinants for Initial-Transcription Pausing. Molecular Cell, 2020, 79, 797-811.e8.	4.5	20
11	Structural basis of transcription-translation coupling. Science, 2020, 369, 1359-1365.	6.0	101
12	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.	3.3	27
13	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.	3.3	27
14	RNA Polymerase Reaches 60: Transcription Initiation, Elongation, Termination, and Regulation in Prokaryotes. Journal of Molecular Biology, 2019, 431, 3945-3946.	2.0	3
15	Structural basis of Q-dependent antitermination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18384-18390.	3.3	35
16	The Infectious Diseases Society of America's 10 \AA - \AA 20 Initiative (10 New Systemic Antibacterial Agents US) Tj ETQq0 0 0 rgBT / 2019, 69, 1-11.	2.9	120
17	Functionalised bicyclic tetramates derived from cysteine as antibacterial agents. Organic and Biomolecular Chemistry, 2019, 17, 5615-5632.	1.5	11
18	Determining Dynamics of RNA Polymerase Elongation and Pausing using Nanopore Tweezers. Biophysical Journal, 2019, 116, 209a.	0.2	0

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19	Structural basis of ECF- σ -factor-dependent transcription initiation. <i>Nature Communications</i> , 2019, 10, 710.	5.8	37
20	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.	1.4	20
21	Fractional nucleotide translocation in sequence-dependent pausing by RNA polymerase: Single-molecule picometer-resolution nanopore tweezers (SPRNT). <i>FASEB Journal</i> , 2019, 33, 221.1.	0.2	0
22	CapZyme-Seq Comprehensively Defines Promoter-Sequence Determinants for RNA 5' Capping with NAD ⁺ . <i>Molecular Cell</i> , 2018, 70, 553-564.e9.	4.5	64
23	Analysis of the Pseudouridimycin Biosynthetic Pathway Provides Insights into the Formation of C-nucleoside Antibiotics. <i>Cell Chemical Biology</i> , 2018, 25, 540-549.e4.	2.5	42
24	Structural Basis of Transcription Inhibition by Fidaxomicin (Lipiarmycin A3). <i>Molecular Cell</i> , 2018, 70, 60-71.e15.	4.5	81
25	New Insights into Transcriptional Pausing using Ultra-high Resolution Optical Tweezers and Novel Analysis Algorithms. <i>Biophysical Journal</i> , 2018, 114, 394a-395a.	0.2	0
26	Reply to Paul and Leibovici. <i>Journal of Infectious Diseases</i> , 2018, 217, 509-510.	1.9	1
27	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.	6.5	45
28	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
29	Highly efficient 5' capping of mitochondrial RNA with NAD ⁺ and NADH by yeast and human mitochondrial RNA polymerase. <i>ELife</i> , 2018, 7, .	2.8	64
30	RNA Polymerase Transcription Elongation Pausing and Termination Investigated at Super Resolution with the Mspa Nanopore. <i>Biophysical Journal</i> , 2017, 112, 212a.	0.2	0
31	White Paper: Developing Antimicrobial Drugs for Resistant Pathogens, Narrow-Spectrum Indications, and Unmet Needs. <i>Journal of Infectious Diseases</i> , 2017, 216, 228-236.	1.9	83
32	Antibacterial Nucleoside-Analog Inhibitor of Bacterial RNA Polymerase. <i>Cell</i> , 2017, 169, 1240-1248.e23.	13.5	121
33	RNA Polymerase Translocation in Processive Transcription Elongation and Pausing: Dynamics, Force-Dependence, and Modulation by Sequence-Specific RNAP-DNA Interactions. <i>Biophysical Journal</i> , 2017, 112, 211a.	0.2	1
34	Single-Molecule Picometer Resolution Nanopore Tweezers Resolution. <i>Biophysical Journal</i> , 2017, 112, 517a.	0.2	0
35	Structural Basis of Mycobacterium tuberculosis Transcription and Transcription Inhibition. <i>Molecular Cell</i> , 2017, 66, 169-179.e8.	4.5	130
36	Affinity Selection-Mass Spectrometry Identifies a Novel Antibacterial RNA Polymerase Inhibitor. <i>ACS Chemical Biology</i> , 2017, 12, 1346-1352.	1.6	15

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37	RNA Capping by Transcription Initiation with Non-canonical Initiating Nucleotides (NCINs): Determination of Relative Efficiencies of Transcription Initiation with NCINs and NTPs. <i>Bio-protocol</i> , 2017, 7, .	0.2	7
38	The mechanism of variability in transcription start site selection. <i>ELife</i> , 2017, 6, .	2.8	23
39	The mechanism of RNA 5' capping with NAD ⁺ , NADH and desphospho-CoA. <i>Nature</i> , 2016, 535, 444-447.	13.7	181
40	Interactions between RNA polymerase and the core recognition element are a determinant of transcription start site selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2899-905.	3.3	36
41	Structural basis of transcription activation. <i>Science</i> , 2016, 352, 1330-1333.	6.0	92
42	Multiplexed protein-DNA cross-linking: Scrunching in transcription start site selection. <i>Science</i> , 2016, 351, 1090-1093.	6.0	62
43	Sequence-Specific RNAP-DNA Interactions in Transcription Initiation and Elongation: Core Recognition Element (CRE). <i>Biophysical Journal</i> , 2015, 108, 535a.	0.2	0
44	Massively Systematic Transcript End Readout, "MASTER" Transcription Start Site Selection, Transcriptional Slippage, and Transcript Yields. <i>Molecular Cell</i> , 2015, 60, 953-965.	4.5	72
45	Structural Basis of Transcription Inhibition by CBR Hydroxamidines and CBR Pyrazoles. <i>Structure</i> , 2015, 23, 1470-1481.	1.6	25
46	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.	1.0	45
47	Site-Specific Incorporation of Probes into RNA Polymerase by Unnatural-Amino-Acid Mutagenesis and Staudinger-Bertozzi Ligation. <i>Methods in Molecular Biology</i> , 2015, 1276, 101-131.	0.4	12
48	Transcription inhibition by the depsipeptide antibiotic salinamide A. <i>ELife</i> , 2014, 3, e02451.	2.8	71
49	Structure of the DNA-Binding and RNA-Polymerase-Binding Region of Transcription Antitermination Factor Φ Q. <i>Structure</i> , 2014, 22, 488-495.	1.6	14
50	Synthesis and Evaluation of Novel Analogues of Ripostatins. <i>Chemistry - A European Journal</i> , 2014, 20, 12310-12319.	1.7	16
51	Sequence-Specific RNAP-DNA Interactions in Transcription Initiation and Elongation: Core Recognition Element (CRE). <i>Biophysical Journal</i> , 2014, 106, 488a.	0.2	0
52	Interactions between RNA polymerase and the "core recognition element" counteract pausing. <i>Science</i> , 2014, 344, 1285-1289.	6.0	158
53	GE23077 binds to the RNA polymerase σ^{70} and σ^{32} sites and prevents the binding of initiating nucleotides. <i>ELife</i> , 2014, 3, e02450.	2.8	68
54	The Transcription Bubble of the RNA Polymerase "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.	2.0	77

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55	Flexibility in Transcription Start-Site Selection by RNA Polymerase Involves Transcription-Bubble Expansion (â€œScrunchingâ€œ) or Contraction (â€œUnscrunchingâ€œ). <i>Biophysical Journal</i> , 2013, 104, 585a-586a.	0.2	0
56	The fight over flu. <i>Nature</i> , 2012, 481, 257-259.	13.7	23
57	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.	1.4	24
58	Structural Basis of Transcription Initiation. <i>Science</i> , 2012, 338, 1076-1080.	6.0	333
59	Opening and Closing of the Bacterial RNA Polymerase Clamp. <i>Science</i> , 2012, 337, 591-595.	6.0	210
60	Antibiotic Production by Myxobacteria Plays a Role in Predation. <i>Journal of Bacteriology</i> , 2011, 193, 4626-4633.	1.0	150
61	New target for inhibition of bacterial RNA polymerase: â€œswitch regionâ€œ™. <i>Current Opinion in Microbiology</i> , 2011, 14, 532-543.	2.3	176
62	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.	4.5	136
63	The Antibacterial Threaded-Iasso Peptide Capistruin Inhibits Bacterial RNA Polymerase. <i>Journal of Molecular Biology</i> , 2011, 412, 842-848.	2.0	82
64	Azide-Specific Labeling of Biomolecules by Staudingerâ€™Bertozzi Ligation. <i>Methods in Enzymology</i> , 2010, 472, 19-30.	0.4	18
65	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.	3.3	197
66	Direct Detection of Abortive RNA Transcripts in Vivo. <i>Science</i> , 2009, 324, 927-928.	6.0	96
67	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.	3.3	76
68	Structures of RNA polymeraseâ€™antibiotic complexes. <i>Current Opinion in Structural Biology</i> , 2009, 19, 715-723.	2.6	132
69	Single-Molecule Analysis of Transcription. <i>Biophysical Journal</i> , 2009, 96, 202a.	0.2	0
70	Static and Kinetic Site-Specific Protein-DNA Photocrosslinking: Analysis of Bacterial Transcription Initiation Complexes. <i>Methods in Molecular Biology</i> , 2009, 543, 403-437.	0.4	5
71	The RNA Polymerase â€œSwitch Regionâ€œIs a Target for Inhibitors. <i>Cell</i> , 2008, 135, 295-307.	13.5	234
72	Systematic Structure-Activity Analysis of Microcin J25. <i>Journal of Biological Chemistry</i> , 2008, 283, 25589-25595.	1.6	112

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73	Nonradioactive, ultrasensitive site-specific protein-protein photocrosslinking: interactions of σ -helix 2 of TATA-binding protein with general transcription factor TFIIA and transcriptional repressor NC2. <i>Nucleic Acids Research</i> , 2008, 36, 6143-6154.	6.5	5
74	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.	3.3	90
75	Upstream promoter sequences and σ -CTD mediate stable DNA wrapping within the RNA polymerase-promoter open complex. <i>EMBO Reports</i> , 2007, 8, 271-278.	2.0	32
76	Abortive Initiation and Productive Initiation by RNA Polymerase Involve DNA Scrunching. <i>Science</i> , 2006, 314, 1139-1143.	6.0	346
77	Initial Transcription by RNA Polymerase Proceeds Through a DNA-Scrunching Mechanism. <i>Science</i> , 2006, 314, 1144-1147.	6.0	400
78	Direct Observation of Abortive Initiation and Promoter Escape within Single Immobilized Transcription Complexes. <i>Biophysical Journal</i> , 2006, 90, 1419-1431.	0.2	136
79	Indirect Readout of DNA Sequence at the Primary-kink Site in the CAP-DNA Complex: Recognition of Pyrimidine-Purine and Purine-Purine Steps. <i>Journal of Molecular Biology</i> , 2006, 357, 173-183.	2.0	43
80	Dynamically driven protein allostery. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 831-838.	3.6	574
81	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.	3.3	98
82	Single-molecule DNA nanomanipulation: Improved resolution through use of shorter DNA fragments. <i>Nature Methods</i> , 2005, 2, 127-138.	9.0	69
83	An Open Letter to Elias Zerhouni. <i>Science</i> , 2005, 307, 1409c-1410c.	6.0	23
84	Response of RNA polymerase to ppGpp: requirement for the σ subunit and relief of this requirement by DksA. <i>Genes and Development</i> , 2005, 19, 2378-2387.	2.7	91
85	The interaction between σ 70 and the σ -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.	3.3	82
86	Retention of Transcription Initiation Factor σ 70 in Transcription Elongation: Single-Molecule Analysis. <i>Molecular Cell</i> , 2005, 20, 347-356.	4.5	132
87	Inhibition of Bacterial RNA Polymerase by Streptolydigin: Stabilization of a Straight-Bridge-Helix Active-Center Conformation. <i>Cell</i> , 2005, 122, 541-552.	13.5	183
88	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.	0.2	46
89	Accurate FRET Measurements within Single Diffusing Biomolecules Using Alternating-Laser Excitation. <i>Biophysical Journal</i> , 2005, 88, 2939-2953.	0.2	440
90	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.	1.6	59

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91	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.	3.3	157
92	The β 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.	3.6	78
93	Catabolite activator protein: DNA binding and transcription activation. <i>Current Opinion in Structural Biology</i> , 2004, 14, 10-20.	2.6	291
94	Antibacterial Peptide Microcin J25 Inhibits Transcription by Binding within and Obstructing the RNA Polymerase Secondary Channel. <i>Molecular Cell</i> , 2004, 14, 739-751.	4.5	206
95	Structure of Antibacterial Peptide Microcin J25: A 21-Residue Lariat Protoknot. <i>Journal of the American Chemical Society</i> , 2003, 125, 12382-12383.	6.6	203
96	Functional Interaction between RNA Polymerase β Subunit C-Terminal Domain and β 70 in UP-Element- and Activator-Dependent Transcription. <i>Molecular Cell</i> , 2003, 11, 1621-1633.	4.5	77
97	Fluorescence Resonance Energy Transfer (FRET) in Analysis of Transcription-Complex Structure and Function. <i>Methods in Enzymology</i> , 2003, 371, 144-159.	0.4	39
98	Single-Molecule DNA Nanomanipulation: Detection of Promoter-Unwinding Events by RNA Polymerase. <i>Methods in Enzymology</i> , 2003, 370, 577-598.	0.4	23
99	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.	2.7	20
100	Determinants of the C-Terminal Domain of the Escherichia coli RNA Polymerase β Subunit Important for Transcription at Class I Cyclic AMP Receptor Protein-Dependent Promoters. <i>Journal of Bacteriology</i> , 2002, 184, 2273-2280.	1.0	64
101	Structural Basis of Transcription Activation: The CAP-alpha CTD-DNA Complex. <i>Science</i> , 2002, 297, 1562-1566.	6.0	234
102	Structural Organization of Bacterial RNA Polymerase Holoenzyme and the RNA Polymerase-Promoter Open Complex. <i>Cell</i> , 2002, 108, 599-614.	13.5	279
103	Bioweapon agents: more access means more risk. <i>Nature</i> , 2002, 415, 364-364.	13.7	6
104	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.	2.0	55
105	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.	2.0	52
106	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.	2.0	57
107	Translocation of β 70 with RNA Polymerase during Transcription. <i>Cell</i> , 2001, 106, 453-463.	13.5	181
108	Site-Specific Incorporation of Fluorescent Probes into Protein: A Hexahistidine-Tag-Mediated Fluorescent Labeling with (Ni ²⁺ :Nitrilotriacetic Acid) ⁿ ~Fluorochrome Conjugates. <i>Journal of the American Chemical Society</i> , 2001, 123, 12123-12125.	6.6	182

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109	Bacterial RNA polymerase subunit $\hat{\text{A}}$ and eukaryotic RNA polymerase subunit RPB6 are sequence, structural, and functional homologs and promote RNA polymerase assembly. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 892-897.	3.3	197
110	Site-Specific Protein-DNA Photocrosslinking: Analysis of Bacterial Transcription Initiation Complexes. , 2001, 148, 337-361.		17
111	Roles of the Histone H2A-H2B Dimers and the (H3-H4) ₂ Tetramer in Nucleosome Remodeling by the SWI-SNF Complex. Journal of Biological Chemistry, 2000, 275, 11545-11552.	1.6	38
112	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.	1.6	15
113	RNA Polymerase: Structural Similarities Between Bacterial RNA Polymerase and Eukaryotic RNA Polymerase II. Journal of Molecular Biology, 2000, 304, 687-698.	2.0	223
114	Structural Organization of the RNA Polymerase-Promoter Open Complex. Cell, 2000, 101, 601-611.	13.5	177
115	Mechanism of ATP-Dependent Promoter Melting by Transcription Factor IIH. Science, 2000, 288, 1418-1421.	6.0	236
116	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.	2.7	42
117	Orientation of OmpR monomers within an OmpR:DNA complex determined by DNA affinity cleaving 1 Edited by K. Yamamoto. Journal of Molecular Biology, 1999, 285, 555-566.	2.0	49
118	Transcription activation by catabolite activator protein (CAP). Journal of Molecular Biology, 1999, 293, 199-213.	2.0	709
119	Bacterial promoter architecture: subsite structure of UP elements and interactions with the carboxy-terminal domain of the RNA polymerase alpha subunit. Genes and Development, 1999, 13, 2134-2147.	2.7	185
120	Transcription activation at Class II CRP-dependent promoters: identification of determinants in the C-terminal domain of the RNA polymerase alpha subunit. EMBO Journal, 1998, 17, 3439-3447.	3.5	133
121	New core promoter element in RNA polymerase II-dependent transcription: sequence-specific DNA binding by transcription factor $\hat{\text{A}}$. Genes and Development, 1998, 12, 34-44.	2.7	336
122	Mutational analysis of a transcriptional activation region of the VP16 protein of herpes simplex virus [published erratum appears in Nucleic Acids Res 1998 Dec 1;26(23):537-8]. Nucleic Acids Research, 1998, 26, 4487-4496.	6.5	56
123	RNA Polymerase-DNA Interaction: Structures of Intermediate, Open, and Elongation Complexes. Cold Spring Harbor Symposia on Quantitative Biology, 1998, 63, 11-20.	2.0	19
124	Mechanisms of Viral Activators. Cold Spring Harbor Symposia on Quantitative Biology, 1998, 63, 243-252.	2.0	22
125	The RNA Polymerase II General Transcription Factors: Past, Present, and Future. Cold Spring Harbor Symposia on Quantitative Biology, 1998, 63, 83-105.	2.0	61
126	RNA Polymerase $\hat{\text{A}}$ Subunit: A Target of DNA Binding-Independent Activation. Science, 1997, 275, 1655-1657.	6.0	71

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127	Trajectory of DNA in the RNA polymerase II transcription preinitiation complex. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12268-12273.	3.3	113
128	Transcription activation at Class II CAP-dependent promoters. Molecular Microbiology, 1997, 23, 853-859.	1.2	193
129	Structure of the LexA Repressor-DNA Complex Probed by Affinity Cleavage and Affinity Photo-Cross-Linking. Biochemistry, 1996, 35, 4279-4286.	1.2	22
130	Artificial Sequence-Specific DNA Binding Peptides: A Branched-Chain Basic Regions. Journal of the American Chemical Society, 1996, 118, 5831-5835.	6.6	22
131	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.	2.0	262
132	Transcription Activation at Class II CAP-Dependent Promoters: Two Interactions between CAP and RNA Polymerase. Cell, 1996, 87, 1123-1134.	13.5	279
133	Fluorescence anisotropy: Rapid, quantitative assay for protein-DNA and protein-protein interaction. Methods in Enzymology, 1996, 274, 492-503.	0.4	137
134	High-resolution mapping of nucleoprotein complexes by site-specific protein-DNA photocrosslinking: organization of the human TBP-TFIIA-TFIIB-DNA quaternary complex.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 10620-10625.	3.3	106
135	Protein-protein interactions in eukaryotic transcription initiation: structure of the preinitiation complex.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 1119-1124.	3.3	100
136	Determinants of RNA polymerase alpha subunit for interaction with beta, beta', and sigma subunits: hydroxyl-radical protein footprinting.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 10162-10166.	3.3	81
137	A single substitution in the putative helix-turn-helix motif of the pleiotropic activator PrfA attenuates Listeria monocytogenes virulence. Molecular Microbiology, 1996, 20, 785-797.	1.2	67
138	Aromatic hydrogen bond in sequence-specific protein DNA recognition. Nature Structural and Molecular Biology, 1996, 3, 837-841.	3.6	66
139	DNA-binding determinants of the alpha subunit of RNA polymerase: novel DNA-binding domain architecture.. Genes and Development, 1996, 10, 16-26.	2.7	188
140	S-[2-(4-Azidosalicylamido)ethylthio]-2-thiopyridine: a Radioiodinatable, Cleavable, Photoactivatable Cross-Linking Agent. Bioconjugate Chemistry, 1996, 7, 380-384.	1.8	53
141	[10] Escherichia coli RNA polymerase holoenzyme: Rapid reconstitution from recombinant $\hat{1}$, $\hat{1}^2$, $\hat{1}^2\hat{1}$, and $\hat{1}^2\hat{1}^2$ subunits. Methods in Enzymology, 1996, 273, 130-134.	0.4	39
142	Rapid RNA polymerase genetics: one-day, no-column preparation of reconstituted recombinant Escherichia coli RNA polymerase.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 4902-4906.	3.3	121
143	Transcription activation at the Escherichia coli uhpT promoter by the catabolite gene activator protein. Journal of Bacteriology, 1995, 177, 1712-1718.	1.0	44
144	Letters: Affirmative Action: A Quota System. Academe, 1995, 81, 4.	0.3	1

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145	The Escherichia coli RNA polymerase β subunit: structure and function. <i>Current Opinion in Genetics and Development</i> , 1995, 5, 197-203.	1.5	151
146	High-specificity DNA cleavage agent: design and application to kilobase and megabase DNA substrates. <i>Science</i> , 1994, 265, 959-962.	6.0	57
147	Location, structure, and function of the target of a transcriptional activator protein.. <i>Genes and Development</i> , 1994, 8, 3058-3067.	2.7	111
148	Domain organization of RNA polymerase β subunit: C-terminal 85 amino acids constitute a domain capable of dimerization and DNA binding. <i>Cell</i> , 1994, 78, 889-896.	13.5	251
149	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.	2.0	80
150	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.	2.0	99
151	Promoter structure, promoter recognition, and transcription activation in prokaryotes. <i>Cell</i> , 1994, 79, 743-746.	13.5	432
152	Identification of the target of a transcription activator protein by protein-protein photocrosslinking. <i>Science</i> , 1994, 265, 90-92.	6.0	178
153	DNA affinity cleaving analysis of homeodomain-DNA interaction: identification of homeodomain consensus sites in genomic DNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 118-122.	3.3	32
154	CAP interacts with RNA polymerase in solution in the absence of promoter DNA. <i>Nature</i> , 1993, 364, 548-549.	13.7	90
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