Konstantin Severinov

List of Publications by Year
in descending order

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141 papers	14,958 citations	41323 49 h-index	20343 116 g-index
151 all docs	151 docs citations	151 times ranked	11223 citing authors

#	Article	IF	Citations
1	Efficient target cleavage by Type V Cas12a effectors programmed with split CRISPR RNA. Nucleic Acids Research, 2022, 50, 1162-1173.	6.5	18
2	Persistence of plasmids targeted by CRISPR interference in bacterial populations. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2114905119.	3.3	2
3	Cell-Free Mutant Analysis Combined with Structure Prediction of a Lasso Peptide Biosynthetic Protease B2. ACS Synthetic Biology, 2022, 11, 2022-2028.	1.9	8
4	New developments in RiPP discovery, enzymology and engineering. Natural Product Reports, 2021, 38, 130-239.	5.2	412
5	Natural Trojan horse inhibitors of aminoacyl-tRNA synthetases. RSC Chemical Biology, 2021, 2, 468-485.	2.0	22
6	Prespacers formed during primed adaptation associate with the Cas1â€“Cas2 adaptation complex and the Cas3 interference nucleaseâ€“helicase. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
7	Identification and characterization of andalusicin: N-terminally dimethylated class III lantibiotic from Bacillus thuringiensis sv. andalousiensis. IScience, 2021, 24, 102480.	1.9	18
8	Protospacer-Adjacent Motif Specificity during Clostridioides difficile Type I-B CRISPR-Cas Interference and Adaptation. MBio, 2021, 12, e0213621.	1.8	4
9	The comparison of ZFNs, TALENs, and SpCas9 by GUIDE-seq in HPV-targeted gene therapy. Molecular Therapy - Nucleic Acids, 2021, 26, 1466-1478.	2.3	18
10	Spacer acquisition by Type III CRISPRâ€“Cas system during bacteriophage infection of Thermus thermophilus. Nucleic Acids Research, 2020, 48, 9787-9803.	6.5	24
11	Position of Deltaproteobacteria Cas12e nuclease cleavage sites depends on spacer length of guide RNA. RNA Biology, 2020, 17, 1472-1479.	1.5	10
12	Translation-Targeting RiPPs and Where to Find Them. Frontiers in Genetics, 2020, 11, 226.	1.1	11
13	DNA targeting by Clostridium cellulolyticum CRISPRâ€“Cas9 Type II-C system. Nucleic Acids Research, 2020, 48, 2026-2034.	6.5	20
14	In vitro and in vivo growth inhibition of human cervical cancer cells via human papillomavirus E6/E7 mRNAsâ€™ cleavage by CRISPR/Cas13a system. Antiviral Research, 2020, 178, 104794.	1.9	27
15	Detection of CRISPR adaptation. Biochemical Society Transactions, 2020, 48, 257-269.	1.6	11
16	Defining the seed sequence of the Cas12b CRISPR-Cas effector complex. RNA Biology, 2019, 16, 413-422.	1.5	22
17	Structure of ribosome-bound azole-modified peptide phazolicin rationalizes its species-specific mode of bacterial translation inhibition. Nature Communications, 2019, 10, 4563.	5.8	45
18	Detection of spacer precursors formed in vivo during primed CRISPR adaptation. Nature Communications, 2019, 10, 4603.	5.8	23

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19	Genome Maintenance Proteins Modulate Autoimmunity Mediated Primed Adaptation by the Escherichia coli Type I-E CRISPR-Cas System. Genes, 2019, 10, 872.	1.0	8
20	Using an Endogenous CRISPR-Cas System for Genome Editing in the Human Pathogen Clostridium difficile. Applied and Environmental Microbiology, 2019, 85, .	1.4	39
21	Biosynthesis of the RiPP trojan horse nucleotide antibiotic microcin C is directed by the <i>N</i>-formyl of the peptide precursor. Chemical Science, 2019, 10, 2391-2395.	3.7	16
22	Structural Basis of Leader Peptide Recognition in Lasso Peptide Biosynthesis Pathway. ACS Chemical Biology, 2019, 14, 1619-1627.	1.6	40
23	Systematic analysis of Type Iâ€E <i>Escherichia coli</i> CRISPRâ€Cas PAM sequences ability to promote interference and primed adaptation. Molecular Microbiology, 2019, 111, 1558-1570.	1.2	27
24	Xenogeneic Regulation of the Bacterial Transcription Machinery. Journal of Molecular Biology, 2019, 431, 4078-4092.	2.0	21
25	BREX system of<i>Escherichia coli</i>distinguishes self from non-self by methylation of a specific DNA site. Nucleic Acids Research, 2019, 47, 253-265.	6.5	105
26	Architecture of Microcin B17 Synthetase: An Octameric Protein Complex Converting a Ribosomally Synthesized Peptide into a DNA Gyrase Poison. Molecular Cell, 2019, 73, 749-762.e5.	4.5	48
27	Primed CRISPR adaptation in Escherichia coli cells does not depend on conformational changes in the Cascade effector complex detected in Vitro. Nucleic Acids Research, 2018, 46, 4087-4098.	6.5	19
28	Avoidance of Trinucleotide Corresponding to Consensus Protospacer Adjacent Motif Controls the Efficiency of Prespacer Selection during Primed Adaptation. MBio, 2018, 9, .	1.8	11
29	Controller protein of restrictionâ€“modification system Kpn2I affects transcription of its gene by acting as a transcription elongation roadblock. Nucleic Acids Research, 2018, 46, 10810-10826.	6.5	10
30	New Insights Into Functions and Possible Applications of Clostridium difficile CRISPR-Cas System. Frontiers in Microbiology, 2018, 9, 1740.	1.5	11
31	Diversity and evolution of class 2 CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2017, 15, 169-182.	13.6	792
32	Acinetodin and Klebsidin, RNA Polymerase Targeting Lasso Peptides Produced by Human Isolates of <i>Acinetobacter gyllenbergii</i> and <i>Klebsiella pneumoniae</i>. ACS Chemical Biology, 2017, 12, 814-824.	1.6	54
33	Spacer-length DNA intermediates are associated with Cas1 in cells undergoing primed CRISPR adaptation. Nucleic Acids Research, 2017, 45, 3297-3307.	6.5	19
34	Multiplex gene editing by CRISPRâ€“Cpf1 using a single crRNA array. Nature Biotechnology, 2017, 35, 31-34.	9.4	736
35	Dynamics of <i>Escherichia coli</i> type Iâ€E CRISPR spacers over 42Â000Âyears. Molecular Ecology, 2017, 26, 2019-2026.	2.0	29
36	The Origins of Specificity in the Microcin-Processing Protease TldD/E. Structure, 2017, 25, 1549-1561.e5.	1.6	34

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37	Interdependencies Between the Adaptation and Interference Modules Guide Efficient CRISPR-Cas Immunity. , 2017, , 51-62.		1
38	The action of<i>Escherichia coli</i>CRISPRâ€"Cas system on lytic bacteriophages with different lifestyles and development strategies. Nucleic Acids Research, 2017, 45, gkx042.	6.5	62
39	Klebsazolicin inhibits 70S ribosome by obstructing the peptide exit tunnel. Nature Chemical Biology, 2017, 13, 1129-1136.	3.9	50
40	Features of CRISPR-Cas Regulation Key to Highly Efficient and Temporally-Specific crRNA Production. Frontiers in Microbiology, 2017, 8, 2139.	1.5	5
41	Optimal number of spacers in CRISPR arrays. PLoS Computational Biology, 2017, 13, e1005891.	1.5	48
42	Metagenomic Analysis of Bacterial Communities of Antarctic Surface Snow. Frontiers in Microbiology, 2016, 7, 398.	1.5	58
43	The Influence of Copy-Number of Targeted Extrachromosomal Genetic Elements on the Outcome of CRISPR-Cas Defense. Frontiers in Molecular Biosciences, 2016, 3, 45.	1.6	26
44	A Trojan-Horse Peptide-Carboxymethyl-Cytidine Antibiotic from <i>Bacillus amyloliquefaciens</i>. Journal of the American Chemical Society, 2016, 138, 15690-15698.	6.6	27
45	Altered stoichiometry<i>Escherichia coli</i>Cascade complexes with shortened CRISPR RNA spacers are capable of interference and primed adaptation. Nucleic Acids Research, 2016, 44, 10849-10861.	6.5	37
46	Highly efficient primed spacer acquisition from targets destroyed by the <i>Escherichia coli</i> type I-E CRISPR-Cas interfering complex. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7626-7631.	3.3	83
47	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science, 2016, 353, aaf5573.	6.0	1,647
48	Kinetics of the CRISPR-Cas9 effector complex assembly and the role of 3â€²-terminal segment of guide RNA. Nucleic Acids Research, 2016, 44, 2837-2845.	6.5	71
49	A non-canonical multisubunit RNA polymerase encoded by a giant bacteriophage. Nucleic Acids Research, 2015, 43, gkv1095.	6.5	46
50	Foreign DNA acquisition by the I-FÂCRISPRâ€"Cas system requires all components of the interference machinery. Nucleic Acids Research, 2015, 43, 10848-10860.	6.5	88
51	The Cas6e ribonuclease is not required for interference and adaptation by the<i>E. coli</i>type I-E CRISPR-Cas system. Nucleic Acids Research, 2015, 43, 6049-6061.	6.5	21
52	CRISPR interference and priming varies with individual spacer sequences. Nucleic Acids Research, 2015, 43, 10831-10847.	6.5	95
53	Structure, Bioactivity, and Resistance Mechanism of Streptomonomicin, an Unusual Lasso Peptide from an Understudied Halophilic Actinomycete. Chemistry and Biology, 2015, 22, 241-250.	6.2	78
54	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. Molecular Cell, 2015, 60, 385-397.	4.5	971

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55	Function of the CRISPR-Cas System of the Human Pathogen Clostridium difficile. MBio, 2015, 6, e01112-15.	1.8	57
56	Rapid Multiplex Creation of Escherichia coli Strains Capable of Interfering with Phage Infection Through CRISPR. Methods in Molecular Biology, 2015, 1311, 147-159.	0.4	8
57	CRISPR RNA binding and DNA target recognition by purified Cascade complexes from Escherichia coli. Nucleic Acids Research, 2015, 43, 530-543.	6.5	22
58	Structural basis for promoter specificity switching of RNA polymerase by a phage factor. Genes and Development, 2014, 28, 521-531.	2.7	31
59	A bacteriophage transcription regulator inhibits bacterial transcription initiation by Ïƒ-factor displacement. Nucleic Acids Research, 2014, 42, 4294-4305.	6.5	27
60	The sabotage of the bacterial transcription machinery by a small bacteriophage protein. Bacteriophage, 2014, 4, e28520.	1.9	7
61	Pervasive generation of oppositely oriented spacers during CRISPR adaptation. Nucleic Acids Research, 2014, 42, 5907-5916.	6.5	65
62	CRISPR-Cas: Outstanding questions remain. Physics of Life Reviews, 2014, 11, 146-148.	1.5	2
63	Molecular basis of RNA polymerase promoter specificity switch revealed through studies of<i>Thermus</i>bacteriophage transcription regulator. Bacteriophage, 2014, 4, e29399.	1.9	3
64	Ribosomally synthesized and post-translationally modified peptide natural products: overview and recommendations for a universal nomenclature. Natural Product Reports, 2013, 30, 108-160.	5.2	1,692
65	High-throughput analysis of type I-E CRISPR/Cas spacer acquisition in<i>E. coli</i>. RNA Biology, 2013, 10, 716-725.	1.5	98
66	Type I-E CRISPR-Cas Systems Discriminate Target from Non-Target DNA through Base Pairing-Independent PAM Recognition. PLoS Genetics, 2013, 9, e1003742.	1.5	187
67	Genome-Wide Identification of Regulatory RNAs in the Human Pathogen Clostridium difficile. PLoS Genetics, 2013, 9, e1003493.	1.5	239
68	Structure of Microcin B-Like Compounds Produced by Pseudomonas syringae and Species Specificity of Their Antibacterial Action. Journal of Bacteriology, 2013, 195, 4129-4137.	1.0	47
69	A novel phage-encoded transcription antiterminator acts by suppressing bacterial RNA polymerase pausing. Nucleic Acids Research, 2012, 40, 4052-4063.	6.5	22
70	CRISPR transcript processing: a mechanism for generating a large number of small interfering RNAs. Biology Direct, 2012, 7, 24.	1.9	22
71	Molecular memory of prior infections activates the CRISPR/Cas adaptive bacterial immunity system. Nature Communications, 2012, 3, 945.	5.8	490
72	CRISPR Immunity Relies on the Consecutive Binding and Degradation of Negatively Supercoiled Invader DNA by Cascade and Cas3. Molecular Cell, 2012, 46, 595-605.	4.5	475

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73	Use of Semi-quantitative Northern Blot Analysis to Determine Relative Quantities of Bacterial CRISPR Transcripts. , 2012, 905, 73-86.		4
74	CRISPR Transcript Processing: An Unusual Mechanism for Rapid Production of Desired Molecules. Lecture Notes in Computer Science, 2012, , 31-34.	1.0	0
75	Class I Microcins: Their Structures, Activities, and Mechanisms of Resistance. , 2011, , 289-308.		8
76	Temporal Regulation of Gene Expression of the Thermus thermophilus Bacteriophage P23-45. Journal of Molecular Biology, 2011, 405, 125-142.	2.0	33
77	The Antibacterial Threaded-lasso Peptide Capistruin Inhibits Bacterial RNA Polymerase. Journal of Molecular Biology, 2011, 412, 842-848.	2.0	82
78	Extended targeting potential and improved synthesis of Microcin C analogs as antibacterials. Bioorganic and Medicinal Chemistry, 2011, 19, 5462-5467.	1.4	23
79	Interference by clustered regularly interspaced short palindromic repeat (CRISPR) RNA is governed by a seed sequence. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10098-10103.	3.3	665
80	Interaction of Escherichia coli RNA Polymerase Ïƒ70 Subunit with Promoter Elements in the Context of Free Ïƒ70, RNA Polymerase Holoenzyme, and the Î²â€²-Ïƒ70 Complex. Journal of Biological Chemistry, 2011, 286, 270-279.	1.6	34
81	A new basal promoter element recognized by RNA polymerase core enzyme. EMBO Journal, 2011, 30, 3766-3775.	3.5	38
82	Transcription, processing and function of CRISPR cassettes in <i>Escherichia coli</i>. Molecular Microbiology, 2010, 77, 1367-1379.	1.2	203
83	Synthetic Microcin C Analogs Targeting Different Aminoacyl-tRNA Synthetases. Journal of Bacteriology, 2009, 191, 6273-6280.	1.0	53
84	Early Transcriptional Arrest at Escherichia coli rplN and ompX Promoters. Journal of Biological Chemistry, 2009, 284, 35702-35713.	1.6	20
85	Analysis of CRISPR system function in plant pathogen<i>Xanthomonas oryzae</i>. FEMS Microbiology Letters, 2009, 296, 110-116.	0.7	73
86	The Ile¹³residue of microcin J25 is essential for recognition by the receptor FhuA, but not by the inner membrane transporter SbmA. FEMS Microbiology Letters, 2009, 301, 124-129.	0.7	11
87	Recombinant bacterial RNA polymerase: Preparation and applications. Methods, 2009, 47, 44-52.	1.9	8
88	Potential Applicability of Chymotrypsin-Susceptible Microcin J25 Derivatives to Food Preservation. Applied and Environmental Microbiology, 2009, 75, 5734-5738.	1.4	30
89	<i>Modus operandi</i> of the bacterial RNA polymerase containing the Ïƒ⁵⁴ promoterâ€specificity factor. Molecular Microbiology, 2008, 68, 538-546.	1.2	118
90	Mapping of RNA Polymerase Residues that Interact with Bacteriophage Xp10 Transcription Antitermination Factor p7. Journal of Molecular Biology, 2008, 375, 29-35.	2.0	16

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91	Systematic Structure-Activity Analysis of Microcin J25. Journal of Biological Chemistry, 2008, 283, 25589-25595.	1.6	112
92	Structural Modules of RNA Polymerase Required for Transcription from Promoters Containing Downstream Basal Promoter Element GGGA. Journal of Biological Chemistry, 2008, 283, 22482-22489.	1.6	17
93	Analysis of Promoter Targets for<i>Escherichia coli</i>Transcription Elongation Factor GreA In Vivo and In Vitro. Journal of Bacteriology, 2007, 189, 8772-8785.	1.0	73
94	Lowâ€molecularâ€weight postâ€translationally modified microcins. Molecular Microbiology, 2007, 65, 1380-1394.	1.2	132
95	Recombinant Thermus aquaticus RNA Polymerase for Structural Studies. Journal of Molecular Biology, 2006, 359, 110-121.	2.0	19
96	Interplay between the Î²â€² Clamp and the Î²â€² Jaw Domains during DNA Opening by the Bacterial RNA Polymerase at Ïƒ54-dependent Promoters. Journal of Molecular Biology, 2006, 359, 1182-1195.	2.0	11
97	The Role of the Largest RNA Polymerase Subunit Lid Element in Preventing the Formation of Extended RNA-DNA Hybrid. Journal of Molecular Biology, 2006, 361, 634-643.	2.0	42
98	Mutational Analysis of Ïƒ70 Region 4 Needed for Appropriation by the Bacteriophage T4 Transcription Factors AsiA and MotA. Journal of Molecular Biology, 2006, 363, 931-944.	2.0	28
99	Microcin J25 Uptake: His 5 of the MccJ25 Lariat Ring Is Involved in Interaction with the Inner Membrane MccJ25 Transporter Protein SbmA. Journal of Bacteriology, 2006, 188, 3324-3328.	1.0	30
100	Aspartyl-tRNA Synthetase Is the Target of Peptide Nucleotide Antibiotic Microcin C. Journal of Biological Chemistry, 2006, 281, 18033-18042.	1.6	137
101	Structural, functional, and genetic analysis of sorangicin inhibition of bacterial RNA polymerase. EMBO Journal, 2005, 24, 674-682.	3.5	137
102	The interaction between Â70 and the Â-flap of Escherichia coli RNA polymerase inhibits extension of nascent RNA during early elongation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4488-4493.	3.3	82
103	Stable DNA Opening within Open Promoter Complexes Is Mediated by the RNA Polymerase Î²â€²-Jaw Domain. Journal of Biological Chemistry, 2005, 280, 36176-36184.	1.6	20
104	Structure-Activity Analysis of Microcin J25: Distinct Parts of the Threaded Lasso Molecule Are Responsible for Interaction with Bacterial RNA Polymerase. Journal of Bacteriology, 2005, 187, 3859-3863.	1.0	46
105	The involvement of the aspartate triad of the active center in all catalytic activities of multisubunit RNA polymerase. Nucleic Acids Research, 2005, 33, 4202-4211.	6.5	56
106	Remodeling of the Ïƒ70 Subunit Non-template DNA Strand Contacts During the Final Step of Transcription Initiation. Journal of Molecular Biology, 2005, 350, 930-937.	2.0	21
107	Transcription regulation by bacteriophage T4 AsiA. Protein Expression and Purification, 2005, 41, 1-8.	0.6	12
108	Reorganisation of an RNA polymeraseâ€"promoter DNA complex for DNA melting. EMBO Journal, 2004, 23, 4253-4263.	3.5	33

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109	Molecular Mechanism of Transcription Inhibition by Peptide Antibiotic Microcin J25. Molecular Cell, 2004, 14, 753-762.	4.5	165
110	Regulation of RNA Polymerase Promoter Selectivity by Covalent Modification of DNA. Journal of Molecular Biology, 2004, 335, 103-111.	2.0	16
111	A Conserved Zinc Binding Domain in the Largest Subunit of DNA-dependent RNA Polymerase Modulates Intrinsic Transcription Termination and Antitermination but does not Stabilize the Elongation Complex. Journal of Molecular Biology, 2004, 342, 1143-1154.	2.0	31
112	Bacteriophage-Induced Modifications of Host RNA Polymerase. Annual Review of Microbiology, 2003, 57, 301-322.	2.9	76
113	Interaction of T4 AsiA with its Target Sites in the RNA Polymerase Ïƒ70 Subunit Leads to Distinct and Opposite Effects on Transcription. Journal of Molecular Biology, 2003, 326, 679-690.	2.0	24
114	Structure of Microcin J25, a Peptide Inhibitor of Bacterial RNA Polymerase, is a Lassoed Tail. Journal of the American Chemical Society, 2003, 125, 12475-12483.	6.6	227
115	Preparation and Characterization of Recombinant Thermus aquaticus RNA Polymerase. Methods in Enzymology, 2003, 370, 94-108.	0.4	28
116	Multiple Roles of the RNA Polymerase Î² Subunit Flap Domain in Ï‚54-Dependent Transcription. Journal of Biological Chemistry, 2003, 278, 3455-3465.	1.6	20
117	Role of Second-Largest RNA Polymerase I Subunit Zn-Binding Domain in Enzyme Assembly. Eukaryotic Cell, 2003, 2, 1046-1052.	3.4	6
118	On the Role of the Escherichia coli RNA Polymerase Ïƒ70 Region 4.2 and Î±-Subunit C-terminal Domains in Promoter Complex Formation on the Extended â€“10 galP1 Promoter. Journal of Biological Chemistry, 2003, 278, 29710-29718.	1.6	40
119	Mapping Ïƒ54-RNA Polymerase Interactions at the â€“24 Consensus Promoter Element. Journal of Biological Chemistry, 2003, 278, 29728-29743.	1.6	28
120	Mutations of Bacterial RNA Polymerase Leading to Resistance to Microcin J25. Journal of Biological Chemistry, 2002, 277, 50867-50875.	1.6	134
121	A Role for Interaction of the RNA Polymerase Flap Domain with the sigma Subunit in Promoter Recognition. Science, 2002, 295, 855-857.	6.0	169
122	Î² Subunit Residues 186â€“433 and 436â€“445 are Commonly Used by EÏƒ54 and EÏƒ70 RNA Polymerase for Open Promoter Complex Formation. Journal of Molecular Biology, 2002, 319, 1067-1083.	2.0	9
123	A Novel Bacteriophage-encoded RNA Polymerase Binding Protein Inhibits Transcription Initiation and Abolishes Transcription Termination by Host RNA Polymerase. Journal of Molecular Biology, 2002, 320, 11-22.	2.0	27
124	Role of the RNA polymerase sigma subunit in transcription initiation. Research in Microbiology, 2002, 153, 557-562.	1.0	68
125	Structure-based analysis of RNA polymerase function: the largest subunit's rudder contributes critically to elongation complex stability and is not involved in the maintenance of RNA-DNA hybrid length. EMBO Journal, 2002, 21, 1369-1378.	3.5	59
126	Mapping the molecular interface between the Ïƒ70 subunit of E. coli RNA polymerase and T4 AsiA. Journal of Molecular Biology, 2001, 306, 631-642.	2.0	42

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127	Binding of the Initiation Factor Ïƒ70 to Core RNA Polymerase Is a Multistep Process. Molecular Cell, 2001, 8, 21-31.	4.5	61
128	The Î²â€² Subunit of Escherichia coli RNA Polymerase Is Not Required for Interaction with Initiating Nucleotide but Is Necessary for Interaction with Rifampicin. Journal of Biological Chemistry, 2001, 276, 13308-13313.	1.6	25
129	Recombinant Thermus aquaticus RNA Polymerase, a New Tool for Structure-Based Analysis of Transcription. Journal of Bacteriology, 2001, 183, 71-76.	1.0	48
130	Inter- and Intrasubunit Interactions during the Formation of RNA Polymerase Assembly Intermediate. Journal of Biological Chemistry, 2000, 275, 31183-31190.	1.6	9
131	Dissection of Two Hallmarks of the Open Promoter Complex by Mutation in an RNA Polymerase Core Subunit. Journal of Biological Chemistry, 2000, 275, 25516-25522.	1.6	32
132	RNA polymerase structureâ€“function: insights into points of transcriptional regulation. Current Opinion in Microbiology, 2000, 3, 118-125.	2.3	52
133	Crystal Structure of Thermus aquaticus Core RNA Polymerase at 3.3 Ã… Resolution. Cell, 1999, 98, 811-824.	13.5	766
134	Inhibition of Escherichia coli RNA polymerase by bacteriophage T4 AsiA 1 1Edited by E. Ebright. Journal of Molecular Biology, 1998, 279, 9-18.	2.0	88
135	Expressed Protein Ligation, a Novel Method for Studying Protein-Protein Interactions in Transcription. Journal of Biological Chemistry, 1998, 273, 16205-16209.	1.6	178
136	Tethering of the Large Subunits of Escherichia coli RNA Polymerase. Journal of Biological Chemistry, 1997, 272, 24137-24140.	1.6	50
137	Determinants for Escherichia coli RNA polymerase assembly within the Î² subunit. Journal of Molecular Biology, 1997, 270, 648-662.	2.0	36
138	Histidine-tagged RNA polymerase of Escherichia coli and transcription in solid phase. Methods in Enzymology, 1996, 274, 326-334.	0.4	79
139	Domain Organization of theEscherichia coliRNA Polymerase Ïƒ70Subunit. Journal of Molecular Biology, 1996, 263, 637-647.	2.0	133
140	The Î² Subunit Rif-cluster I Is Only Angstroms Away from the Active Center of Escherichia coli RNA Polymerase. Journal of Biological Chemistry, 1995, 270, 29428-29432.	1.6	55
141	RifR mutations in the beginning of the Escherichia coli rpoB gene. Molecular Genetics and Genomics, 1994, 244, 120-126.	2.4	65