

Konstantin V Severinov

List of Publications by Year in descending order

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166
papers

12,435
citations

53751

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30894

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178
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docs citations

178
times ranked

9904
citing authors

#	ARTICLE	IF	CITATIONS
1	Efficient target cleavage by Type V Cas12a effectors programmed with split CRISPR RNA. <i>Nucleic Acids Research</i> , 2022, 50, 1162-1173.	6.5	18
2	Uncertainty-aware and interpretable evaluation of Cas9 gRNA and Cas12a gRNA specificity for fully matched and partially mismatched targets with Deep Kernel Learning. <i>Nucleic Acids Research</i> , 2022, 50, e11-e11.	6.5	5
3	Bacteriostatic antibiotics promote CRISPR-Cas adaptive immunity by enabling increased spacer acquisition. <i>Cell Host and Microbe</i> , 2022, 30, 31-40.e5.	5.1	30
4	Regulation of Gene Expression of phiEco32-like Bacteriophage 7-11. <i>Viruses</i> , 2022, 14, 555.	1.5	0
5	Persistence of plasmids targeted by CRISPR interference in bacterial populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2114905119.	3.3	2
6	S51 Family Peptidases Provide Resistance to Peptidyl-Nucleotide Antibiotic McC. <i>MBio</i> , 2022, 13, e0080522.	1.8	0
7	GNAT toxins evolve toward narrow tRNA target specificities. <i>Nucleic Acids Research</i> , 2022, 50, 5807-5817.	6.5	2
8	Development of ONT-cappable-seq to unravel the transcriptional landscape of Pseudomonas phages. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2624-2638.	1.9	9
9	Structural basis of template strand deoxyuridine promoter recognition by a viral RNA polymerase. <i>Nature Communications</i> , 2022, 13, .	5.8	3
10	Cell-Free Mutant Analysis Combined with Structure Prediction of a Lasso Peptide Biosynthetic Protease B2. <i>ACS Synthetic Biology</i> , 2022, 11, 2022-2028.	1.9	8
11	Structure and function of virion RNA polymerase of a crAss-like phage. <i>Nature</i> , 2021, 589, 306-309.	13.7	29
12	Natural Trojan horse inhibitors of aminoacyl-tRNA synthetases. <i>RSC Chemical Biology</i> , 2021, 2, 468-485.	2.0	22
13	Microbial Arsenal of Antiviral Defenses – Part I. <i>Biochemistry (Moscow)</i> , 2021, 86, 319-337.	0.7	23
14	Diversity and Functions of Type II Topoisomerases. <i>Acta Naturae</i> , 2021, 13, 59-75.	1.7	11
15	Microbial Arsenal of Antiviral Defenses. Part II. <i>Biochemistry (Moscow)</i> , 2021, 86, 449-470.	0.7	32
16	Prespacers formed during primed adaptation associate with the Cas1-Cas2 adaptation complex and the Cas3 interference nuclease-helicase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
17	Identification and characterization of andalusicin: N-terminally dimethylated class III lantibiotic from <i>Bacillus thuringiensis</i> sv. <i>andalousiensis</i> . <i>Science</i> , 2021, 24, 102480.	1.9	18
18	Human short peptidoglycan recognition protein PGLYRP1/Tag7/PGRPα inhibits <i>Listeria monocytogenes</i> intracellular survival in macrophages. <i>FASEB Journal</i> , 2021, 35, .	0.2	0

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19	The bacteriophage LUZ24 ϕ lg ϕ -peptide inhibits the <i>Pseudomonas</i> DNA gyrase. <i>Cell Reports</i> , 2021, 36, 109567.	2.9	15
20	Protospacer-Adjacent Motif Specificity during <i>Clostridioides difficile</i> Type I-B CRISPR-Cas Interference and Adaptation. <i>MBio</i> , 2021, 12, e0213621.	1.8	4
21	Type III CRISPR-Cas Systems: Deciphering the Most Complex Prokaryotic Immune System. <i>Biochemistry (Moscow)</i> , 2021, 86, 1301-1314.	0.7	26
22	SCRAMBLER: A Tool for <i>De Novo</i> CRISPR Array Reconstruction and Its Application for Analysis of the Structure of Prokaryotic Populations. <i>CRISPR Journal</i> , 2021, 4, 673-685.	1.4	2
23	ϕ Drc TM , a structurally novel ssDNA-binding transcription regulator of N4-related bacterial viruses. <i>Nucleic Acids Research</i> , 2020, 48, 445-459.	6.5	23
24	Multisubunit RNA Polymerases of Jumbo Bacteriophages. <i>Viruses</i> , 2020, 12, 1064.	1.5	25
25	Liquid drop of DNA libraries reveals total genome information. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27300-27306.	3.3	4
26	Reproducible Antigen Recognition by the Type I-F CRISPR-Cas System. <i>CRISPR Journal</i> , 2020, 3, 378-387.	1.4	9
27	Novel <i>Escherichia coli</i> RNA Polymerase Binding Protein Encoded by Bacteriophage T5. <i>Viruses</i> , 2020, 12, 807.	1.5	7
28	The Phage-Encoded N-Acetyltransferase Rac Mediates Inactivation of <i>Pseudomonas aeruginosa</i> Transcription by Cleavage of the RNA Polymerase Alpha Subunit. <i>Viruses</i> , 2020, 12, 976.	1.5	11
29	Spacer acquisition by Type III CRISPR-Cas system during bacteriophage infection of <i>Thermus thermophilus</i> . <i>Nucleic Acids Research</i> , 2020, 48, 9787-9803.	6.5	24
30	PpCas9 from <i>Pasteurella pneumotropica</i> encodes a compact Type II-C Cas9 ortholog active in human cells. <i>Nucleic Acids Research</i> , 2020, 48, 12297-12309.	6.5	19
31	Position of Deltaproteobacteria Cas12e nuclease cleavage sites depends on spacer length of guide RNA. <i>RNA Biology</i> , 2020, 17, 1472-1479.	1.5	10
32	Mechanism of translation inhibition by type II GNAT toxin AtaT2. <i>Nucleic Acids Research</i> , 2020, 48, 8617-8625.	6.5	11
33	Mapping CRISPR spaceromes reveals vast host-specific viromes of prokaryotes. <i>Communications Biology</i> , 2020, 3, 321.	2.0	31
34	Translation-Targeting RiPPs and Where to Find Them. <i>Frontiers in Genetics</i> , 2020, 11, 226.	1.1	11
35	DNA targeting by <i>Clostridium cellulolyticum</i> CRISPR-Cas9 Type II-C system. <i>Nucleic Acids Research</i> , 2020, 48, 2026-2034.	6.5	20
36	Phage T7 DNA mimic protein Ocr is a potent inhibitor of BREX defence. <i>Nucleic Acids Research</i> , 2020, 48, 5397-5406.	6.5	53

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37	Quantification of the affinities of CRISPR-Cas9 nucleases for cognate protospacer adjacent motif (PAM) sequences. <i>Journal of Biological Chemistry</i> , 2020, 295, 6509-6517.	1.6	17
38	Histidine-Triad Hydrolases Provide Resistance to Peptide-Nucleotide Antibiotics. <i>MBio</i> , 2020, 11, .	1.8	5
39	Detection of CRISPR adaptation. <i>Biochemical Society Transactions</i> , 2020, 48, 257-269.	1.6	11
40	CRISPR Arrays Away from <i>cas</i> Genes. <i>CRISPR Journal</i> , 2020, 3, 535-549.	1.4	18
41	Human Short Peptidoglycan Recognition Protein PGLYRP1/Tag-7/PGRP-S Inhibits <i>Listeria monocytogenes</i> Intracellular Survival in Macrophages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 582803.	1.8	4
42	Defining the seed sequence of the Cas12b CRISPR-Cas effector complex. <i>RNA Biology</i> , 2019, 16, 413-422.	1.5	22
43	Structure of ribosome-bound azole-modified peptide phazolicin rationalizes its species-specific mode of bacterial translation inhibition. <i>Nature Communications</i> , 2019, 10, 4563.	5.8	45
44	Detection of spacer precursors formed in vivo during primed CRISPR adaptation. <i>Nature Communications</i> , 2019, 10, 4603.	5.8	23
45	Genome Maintenance Proteins Modulate Autoimmunity Mediated Primed Adaptation by the <i>Escherichia coli</i> Type I-E CRISPR-Cas System. <i>Genes</i> , 2019, 10, 872.	1.0	8
46	Using an Endogenous CRISPR-Cas System for Genome Editing in the Human Pathogen <i>Clostridium difficile</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	39
47	Efficient <i>in vivo</i> synthesis of lasso peptide pseudomycin proceeds in the absence of both the leader and the leader peptidase. <i>Chemical Science</i> , 2019, 10, 9699-9707.	3.7	25
48	Biosynthesis of the RiPP trojan horse nucleotide antibiotic microcin C is directed by the <i>N</i> -formyl of the peptide precursor. <i>Chemical Science</i> , 2019, 10, 2391-2395.	3.7	16
49	Structural Basis of Leader Peptide Recognition in Lasso Peptide Biosynthesis Pathway. <i>ACS Chemical Biology</i> , 2019, 14, 1619-1627.	1.6	40
50	Cytological Immunostaining of HMGA2, LRP1B, and TP63 as Potential Biomarkers for Triaging Human Papillomavirus-Positive Women. <i>Translational Oncology</i> , 2019, 12, 959-967.	1.7	12
51	Reiterative Synthesis by the Ribosome and Recognition of the N-Terminal Formyl Group by Biosynthetic Machinery Contribute to Evolutionary Conservation of the Length of Antibiotic Microcin C Peptide Precursor. <i>MBio</i> , 2019, 10, .	1.8	6
52	Natural diversity of CRISPR spacers of <i>Thermus</i> : evidence of local spacer acquisition and global spacer exchange. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180092.	1.8	21
53	Systematic analysis of Type I <i>Escherichia coli</i> CRISPR-Cas PAM sequences ability to promote interference and primed adaptation. <i>Molecular Microbiology</i> , 2019, 111, 1558-1570.	1.2	27
54	Effects of Population Dynamics on Establishment of a Restriction-Modification System in a Bacterial Host. <i>Molecules</i> , 2019, 24, 198.	1.7	1

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55	Cryo-EM structure and in vitro DNA packaging of a thermophilic virus with supersized T=7 capsids. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3556-3561.	3.3	54
56	Xenogeneic Regulation of the Bacterial Transcription Machinery. Journal of Molecular Biology, 2019, 431, 4078-4092.	2.0	21
57	Virus-borne mini-CRISPR arrays are involved in interval conflicts. Nature Communications, 2019, 10, 5204.	5.8	50
58	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
59	Single-nucleotide-resolution mapping of DNA gyrase cleavage sites across the <i>Escherichia coli</i> genome. Nucleic Acids Research, 2019, 47, 1373-1388.	6.5	50
60	Structure Studies of the CRISPR-Csm Complex Reveal Mechanism of Co-transcriptional Interference. Cell, 2019, 176, 239-253.e16.	13.5	110
61	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
62	CRISPR-Cas molecular beacons as tool for studies of assembly of CRISPR-Cas effector complexes and their interactions with DNA. Methods in Enzymology, 2019, 616, 337-363.	0.4	6
63	A <i>Thermus</i> phage protein inhibits host RNA polymerase by preventing template DNA strand loading during open promoter complex formation. Nucleic Acids Research, 2018, 46, 431-441.	6.5	8
64	Biosynthesis of Translation Inhibitor Klebsazolicin Proceeds through Heterocyclization and N-Terminal Amidine Formation Catalyzed by a Single YcaO Enzyme. Journal of the American Chemical Society, 2018, 140, 5625-5633.	6.6	25
65	Primed CRISPR adaptation in <i>Escherichia coli</i> 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
66	Avoidance of Trinucleotide Corresponding to Consensus Protospacer Adjacent Motif Controls the Efficiency of Pre-spacer Selection during Primed Adaptation. MBio, 2018, 9, .	1.8	11
67	Controller protein of restriction-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
68	Ultrahigh-throughput functional profiling of microbiota communities. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9551-9556.	3.3	79
69	Systematic prediction of genes functionally linked to CRISPR-Cas systems by gene neighborhood analysis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5307-E5316.	3.3	138
70	<i>Escherichia coli</i> ItaT is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA ^{Leu} . Nucleic Acids Research, 2018, 46, 7873-7885.	6.5	31
71	New Insights Into Functions and Possible Applications of <i>Clostridium difficile</i> CRISPR-Cas System. Frontiers in Microbiology, 2018, 9, 1740.	1.5	11
72	Diversity and evolution of class 2 CRISPR-Cas systems. Nature Reviews Microbiology, 2017, 15, 169-182.	13.6	792

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73	Transcription Profiling of <i>Bacillus subtilis</i> Cells Infected with AR9, a Giant Phage Encoding Two Multisubunit RNA Polymerases. <i>MBio</i> , 2017, 8, .	1.8	26
74	Peptide- ϵ -nucleotide antibiotic Microcin C is a potent inducer of stringent response and persistence in both sensitive and producing cells. <i>Molecular Microbiology</i> , 2017, 104, 463-471.	1.2	21
75	A non-canonical multisubunit RNA polymerase encoded by the AR9 phage recognizes the template strand of its uracil-containing promoters. <i>Nucleic Acids Research</i> , 2017, 45, 5958-5967.	6.5	22
76	Viral genome packaging terminase cleaves DNA using the canonical RuvC-like two-metal catalysis mechanism. <i>Nucleic Acids Research</i> , 2017, 45, gkw1354.	6.5	15
77	Spacer-length DNA intermediates are associated with Cas1 in cells undergoing primed CRISPR adaptation. <i>Nucleic Acids Research</i> , 2017, 45, 3297-3307.	6.5	19
78	Full shut-off of <i>Escherichia coli</i> RNA-polymerase by T7 phage requires a small phage-encoded DNA-binding protein. <i>Nucleic Acids Research</i> , 2017, 45, 7697-7707.	6.5	21
79	Mechanism of duplex DNA destabilization by RNA-guided Cas9 nuclease during target interrogation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5443-5448.	3.3	67
80	Multiplex gene editing by CRISPR- ϵ -Cpf1 using a single crRNA array. <i>Nature Biotechnology</i> , 2017, 35, 31-34.	9.4	736
81	The Origins of Specificity in the Microcin-Processing Protease TldD/E. <i>Structure</i> , 2017, 25, 1549-1561.e5.	1.6	34
82	The Product of <i>Yersinia pseudotuberculosis</i> mcc Operon Is a Peptide-Cytidine Antibiotic Activated Inside Producing Cells by the TldD/E Protease. <i>Journal of the American Chemical Society</i> , 2017, 139, 16178-16187.	6.6	27
83	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , 2017, 8, .	1.8	181
84	Interplay between λ region 3.2 and secondary channel factors during promoter escape by bacterial RNA polymerase. <i>Biochemical Journal</i> , 2017, 474, 4053-4064.	1.7	14
85	The action of <i>Escherichia coli</i> CRISPR- ϵ -Cas system on lytic bacteriophages with different lifestyles and development strategies. <i>Nucleic Acids Research</i> , 2017, 45, gkx042.	6.5	62
86	Features of CRISPR-Cas Regulation Key to Highly Efficient and Temporally-Specific crRNA Production. <i>Frontiers in Microbiology</i> , 2017, 8, 2139.	1.5	5
87	Novel Fri1-like Viruses Infecting <i>Acinetobacter baumannii</i> vB_AbaP_AS11 and vB_AbaP_AS12 Characterization, Comparative Genomic Analysis, and Host-Recognition Strategy. <i>Viruses</i> , 2017, 9, 188.	1.5	35
88	Optimal number of spacers in CRISPR arrays. <i>PLoS Computational Biology</i> , 2017, 13, e1005891.	1.5	48
89	Metagenomic Analysis of Bacterial Communities of Antarctic Surface Snow. <i>Frontiers in Microbiology</i> , 2016, 7, 398.	1.5	58
90	The Influence of Copy-Number of Targeted Extrachromosomal Genetic Elements on the Outcome of CRISPR-Cas Defense. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 45.	1.6	26

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91	Come Together: CRISPR-Cas Immunity Senses the Quorum. <i>Molecular Cell</i> , 2016, 64, 1013-1015.	4.5	10
92	The genome of AR9, a giant transducing <i>Bacillus</i> phage encoding two multisubunit RNA polymerases. <i>Virology</i> , 2016, 495, 185-196.	1.1	81
93	A Trojan-Horse Peptide-Carboxymethyl-Cytidine Antibiotic from <i>Bacillus amyloliquefaciens</i> . <i>Journal of the American Chemical Society</i> , 2016, 138, 15690-15698.	6.6	27
94	Altered stoichiometry of <i>Escherichia coli</i> Cascade complexes with shortened CRISPR RNA spacers are capable of interference and primed adaptation. <i>Nucleic Acids Research</i> , 2016, 44, 10849-10861.	6.5	37
95	Temporal dynamics of methyltransferase and restriction endonuclease accumulation in individual cells after introducing a restriction-modification system. <i>Nucleic Acids Research</i> , 2016, 44, 790-800.	6.5	28
96	Highly efficient primed spacer acquisition from targets destroyed by the <i>Escherichia coli</i> type I-E CRISPR-Cas interfering complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7626-7631.	3.3	83
97	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , 2016, 353, aaf5573.	6.0	1,647
98	Kinetics of the CRISPR-Cas9 effector complex assembly and the role of 3'-terminal segment of guide RNA. <i>Nucleic Acids Research</i> , 2016, 44, 2837-2845.	6.5	71
99	New Infestin-4 Mutants with Increased Selectivity against Factor XIIa. <i>PLoS ONE</i> , 2015, 10, e0144940.	1.1	17
100	The <i>Pseudomonas aeruginosa</i> PA14 ABC Transporter NppA1A2BCD Is Required for Uptake of Peptidyl Nucleoside Antibiotics. <i>Journal of Bacteriology</i> , 2015, 197, 2217-2228.	1.0	34
101	A non-canonical multisubunit RNA polymerase encoded by a giant bacteriophage. <i>Nucleic Acids Research</i> , 2015, 43, gkv1095.	6.5	46
102	Foreign DNA acquisition by the I-F CRISPR-Cas system requires all components of the interference machinery. <i>Nucleic Acids Research</i> , 2015, 43, 10848-10860.	6.5	88
103	The Cas6e ribonuclease is not required for interference and adaptation by the <i>E. coli</i> type I-E CRISPR-Cas system. <i>Nucleic Acids Research</i> , 2015, 43, 6049-6061.	6.5	21
104	Bacteriophage Xp10 anti-termination factor p7 induces forward translocation by host RNA polymerase. <i>Nucleic Acids Research</i> , 2015, 43, 6299-6308.	6.5	11
105	CRISPR interference and priming varies with individual spacer sequences. <i>Nucleic Acids Research</i> , 2015, 43, 10831-10847.	6.5	95
106	Distinct pathways of RNA polymerase regulation by a phage-encoded factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2017-2022.	3.3	18
107	Structure, Bioactivity, and Resistance Mechanism of Streptomycin, an Unusual Lasso Peptide from an Understudied Halophilic Actinomycete. <i>Chemistry and Biology</i> , 2015, 22, 241-250.	6.2	78
108	Enzymatic Synthesis and Functional Characterization of Bioactive Microcin C-Like Compounds with Altered Peptide Sequence and Length. <i>Journal of Bacteriology</i> , 2015, 197, 3133-3141.	1.0	14

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109	RNA polymerase molecular beacon as tool for studies of RNA polymerase–promoter interactions. <i>Methods</i> , 2015, 86, 19-26.	1.9	6
110	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015, 60, 385-397.	4.5	971
111	Function of the CRISPR-Cas System of the Human Pathogen <i>Clostridium difficile</i> . <i>MBio</i> , 2015, 6, e01112-15.	1.8	57
112	Rapid Multiplex Creation of <i>Escherichia coli</i> Strains Capable of Interfering with Phage Infection Through CRISPR. <i>Methods in Molecular Biology</i> , 2015, 1311, 147-159.	0.4	8
113	CRISPR RNA binding and DNA target recognition by purified Cascade complexes from <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2015, 43, 530-543.	6.5	22
114	The sabotage of the bacterial transcription machinery by a small bacteriophage protein. <i>Bacteriophage</i> , 2014, 4, e28520.	1.9	7
115	Pervasive generation of oppositely oriented spacers during CRISPR adaptation. <i>Nucleic Acids Research</i> , 2014, 42, 5907-5916.	6.5	65
116	Ribosome-controlled transcription termination is essential for the production of antibiotic microcin C. <i>Nucleic Acids Research</i> , 2014, 42, 11891-11902.	6.5	17
117	Coupling of Downstream RNA Polymerase–Promoter Interactions with Formation of Catalytically Competent Transcription Initiation Complex. <i>Journal of Molecular Biology</i> , 2014, 426, 3973-3984.	2.0	14
118	Molecular basis of RNA polymerase promoter specificity switch revealed through studies of <i>Thermus</i> bacteriophage transcription regulator. <i>Bacteriophage</i> , 2014, 4, e29399.	1.9	3
119	Systematic Identification of Hypothetical Bacteriophage Proteins Targeting Key Protein Complexes of <i>Pseudomonas aeruginosa</i> . <i>Journal of Proteome Research</i> , 2014, 13, 4446-4456.	1.8	54
120	The RimL Transacetylase Provides Resistance to Translation Inhibitor Microcin C. <i>Journal of Bacteriology</i> , 2014, 196, 3377-3385.	1.0	22
121	Development of Giant Bacteriophage ϕ KZ Is Independent of the Host Transcription Apparatus. <i>Journal of Virology</i> , 2014, 88, 10501-10510.	1.5	144
122	High-throughput analysis of type I-E CRISPR/Cas spacer acquisition in <i>E. coli</i> . <i>RNA Biology</i> , 2013, 10, 716-725.	1.5	98
123	Host RNA polymerase inhibitors encoded by ϕ KMV-like phages of <i>pseudomonas</i> . <i>Virology</i> , 2013, 436, 67-74.	1.1	21
124	Type I-E CRISPR-Cas Systems Discriminate Target from Non-Target DNA through Base Pairing-Independent PAM Recognition. <i>PLoS Genetics</i> , 2013, 9, e1003742.	1.5	187
125	The putative small terminase from the thermophilic dsDNA bacteriophage G20C is a nine-subunit oligomer. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 876-879.	0.7	7
126	12-Fold symmetry of the putative portal protein from the <i>Thermus thermophilus</i> bacteriophage G20C determined by X-ray analysis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1239-1241.	0.7	4

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127	Structure of Microcin B-Like Compounds Produced by <i>Pseudomonas syringae</i> and Species Specificity of Their Antibacterial Action. <i>Journal of Bacteriology</i> , 2013, 195, 4129-4137.	1.0	47
128	A novel phage-encoded transcription antiterminator acts by suppressing bacterial RNA polymerase pausing. <i>Nucleic Acids Research</i> , 2012, 40, 4052-4063.	6.5	22
129	Structural and Mechanistic Basis for the Inhibition of <i>Escherichia coli</i> RNA Polymerase by T7 Gp2. <i>Molecular Cell</i> , 2012, 47, 755-766.	4.5	39
130	Molecular memory of prior infections activates the CRISPR/Cas adaptive bacterial immunity system. <i>Nature Communications</i> , 2012, 3, 945.	5.8	490
131	Temporal Regulation of Gene Expression of the <i>Escherichia coli</i> Bacteriophage phiEco32. <i>Journal of Molecular Biology</i> , 2012, 416, 389-399.	2.0	21
132	CRISPR Immunity Relies on the Consecutive Binding and Degradation of Negatively Supercoiled Invader DNA by Cascade and Cas3. <i>Molecular Cell</i> , 2012, 46, 595-605.	4.5	475
133	Microcin C: biosynthesis and mechanisms of bacterial resistance. <i>Future Microbiology</i> , 2012, 7, 281-289.	1.0	51
134	Substitutions in the <i>Escherichia coli</i> RNA polymerase inhibitor T7 Gp2 that allow inhibition of transcription when the primary interaction interface between Gp2 and RNA polymerase becomes compromised. <i>Microbiology (United Kingdom)</i> , 2012, 158, 2753-2764.	0.7	12
135	Interference by clustered regularly interspaced short palindromic repeat (CRISPR) RNA is governed by a seed sequence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10098-10103.	3.3	665
136	Regulation of gene expression in restriction-modification system Eco29kl. <i>Nucleic Acids Research</i> , 2011, 39, 4653-4663.	6.5	13
137	Restriction-modification systems and bacteriophage invasion: Who wins?. <i>Journal of Theoretical Biology</i> , 2010, 266, 550-559.	0.8	30
138	Transcription, processing and function of CRISPR cassettes in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2010, 77, 1367-1379.	1.2	203
139	The Mechanism of Microcin C Resistance Provided by the MccF Peptidase. <i>Journal of Biological Chemistry</i> , 2010, 285, 37944-37952.	1.6	34
140	MccE Provides Resistance to Protein Synthesis Inhibitor Microcin C by Acetylating the Processed Form of the Antibiotic. <i>Journal of Biological Chemistry</i> , 2010, 285, 12662-12669.	1.6	35
141	Large-Scale Identification and Analysis of C-Proteins. <i>Methods in Molecular Biology</i> , 2010, 674, 269-282.	0.4	7
142	Self immunity and resistance mechanisms against trojan horse antibiotic Microcin C7. <i>FASEB Journal</i> , 2010, 24, lb201.	0.2	0
143	Transcription regulation of restriction-modification system Esp1396I. <i>Nucleic Acids Research</i> , 2009, 37, 3354-3366.	6.5	32
144	Transcription regulation of restriction-modification system Ecl18kl. <i>Nucleic Acids Research</i> , 2009, 37, 5322-5330.	6.5	35

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145	Systematic prediction of control proteins and their DNA binding sites. <i>Nucleic Acids Research</i> , 2009, 37, 441-451.	6.5	102
146	Genomic and Proteomic Analysis of phiEco32, a Novel <i>Escherichia coli</i> Bacteriophage. <i>Journal of Molecular Biology</i> , 2008, 377, 774-789.	2.0	61
147	Genome Comparison and Proteomic Characterization of <i>Thermus thermophilus</i> Bacteriophages P23-45 and P74-26: Siphoviruses with Triplex-forming Sequences and the Longest Known Tails. <i>Journal of Molecular Biology</i> , 2008, 378, 468-480.	2.0	56
148	Systematic Structure-Activity Analysis of Microcin J25. <i>Journal of Biological Chemistry</i> , 2008, 283, 25589-25595.	1.6	112
149	<i>Escherichia coli</i> Peptidase A, B, or N Can Process Translation Inhibitor Microcin C. <i>Journal of Bacteriology</i> , 2008, 190, 2607-2610.	1.0	73
150	Transcription regulation of the type II restriction-modification system AhdI. <i>Nucleic Acids Research</i> , 2008, 36, 1429-1442.	6.5	48
151	The <i>Escherichia coli</i> Yej Transporter Is Required for the Uptake of Translation Inhibitor Microcin C. <i>Journal of Bacteriology</i> , 2007, 189, 8361-8365.	1.0	108
152	Low-molecular-weight post-translationally modified microcins. <i>Molecular Microbiology</i> , 2007, 65, 1380-1394.	1.2	132
153	Low-molecular-weight post-translationally modified microcins. <i>Molecular Microbiology</i> , 2007, 66, 277-277.	1.2	1
154	<i>Thermus thermophilus</i> Bacteriophage ÎYS40 Genome and Proteomic Characterization of Virions. <i>Journal of Molecular Biology</i> , 2006, 364, 667-677.	2.0	60
155	Localization of the <i>Escherichia coli</i> RNA Polymerase Î² Subunit Residue Phosphorylated by Bacteriophage T7 Kinase Gp0.7. <i>Journal of Bacteriology</i> , 2006, 188, 3470-3476.	1.0	34
156	Aspartyl-tRNA Synthetase Is the Target of Peptide Nucleotide Antibiotic Microcin C. <i>Journal of Biological Chemistry</i> , 2006, 281, 18033-18042.	1.6	137
157	Transcription regulation of the EcoRV restriction-modification system. <i>Nucleic Acids Research</i> , 2005, 33, 6942-6951.	6.5	41
158	Regulation of RNA Polymerase Promoter Selectivity by Covalent Modification of DNA. <i>Journal of Molecular Biology</i> , 2004, 335, 103-111.	2.0	16
159	A new <i>Bacillus cereus</i> DNA-binding protein, HlyIIIR, negatively regulates expression of <i>B. cereus</i> haemolysin II. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3691-3701.	0.7	37
160	On the Role of the <i>Escherichia coli</i> RNA Polymerase Î70 Region 4.2 and Î±-Subunit C-terminal Domains in Promoter Complex Formation on the Extended Î10 galP1 Promoter. <i>Journal of Biological Chemistry</i> , 2003, 278, 29710-29718.	1.6	40
161	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. <i>EMBO Journal</i> , 2002, 21, 1369-1378.	3.5	59
162	<i>Helicobacter pylori</i> with separate beta- and beta'-subunits of RNA polymerase is viable and can colonize conventional mice. <i>Molecular Microbiology</i> , 1999, 32, 131-138.	1.2	19

#	ARTICLE	IF	CITATIONS
163	Crystal Structure of <i>Thermus aquaticus</i> Core RNA Polymerase at 3.3 Å... Resolution. <i>Cell</i> , 1999, 98, 811-824.	13.5	766
164	Expressed Protein Ligation, a Novel Method for Studying Protein-Protein Interactions in Transcription. <i>Journal of Biological Chemistry</i> , 1998, 273, 16205-16209.	1.6	178
165	Histidine-tagged RNA polymerase of <i>Escherichia coli</i> and transcription in solid phase. <i>Methods in Enzymology</i> , 1996, 274, 326-334.	0.4	79
166	Rif ^R mutations in the beginning of the <i>Escherichia coli</i> rpoB gene. <i>Molecular Genetics and Genomics</i> , 1994, 244, 120-126.	2.4	65