

Kira S Makarova

List of PR Articles by Year in descending order

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169

PR articles

35,896

PR citations

3133

81

PR h-index

2912

169

g-index

193

documents

46605

doc citations

3246

88

h-index

32812

citing authors

#	ARTICLE	IF	PR CITATIONS
1	COG database update 2024. <i>Nucleic Acids Research</i> , 2025, 53, D356-D363.	15.7	81
2	Tail-tape-fused virion and non-virion RNA polymerases of a thermophilic virus with an extremely long tail. <i>Nature Communications</i> , 2024, 15, .	13.9	8
3	Computational analysis of genes with lethal knockout phenotype and prediction of essential genes in archaea. <i>MBio</i> , 2024, 15, .	4.4	3
4	Diversity, origin, and evolution of the ESCRT systems. <i>MBio</i> , 2024, 15, .	4.4	20
5	Widespread photosynthesis reaction centre barrel proteins are necessary for haloarchaeal cell division. <i>Nature Microbiology</i> , 2024, 9, 712-726.	16.5	13
6	tRNA anticodon cleavage by target-activated CRISPR-Cas13a effector. <i>Science Advances</i> , 2024, 10, .	11.0	25
7	Regulatory sequence-based discovery of anti-defense genes in archaeal viruses. <i>Nature Communications</i> , 2024, 15, .	13.9	6
8	Long range segmentation of prokaryotic genomes by gene age and functionality. <i>Nucleic Acids Research</i> , 2024, 52, 11045-11059.	15.7	5
9	Cellular differentiation into hyphae and spores in halophilic archaea. <i>Nature Communications</i> , 2023, 14, .	13.9	12
10	Compensatory relationship between low-complexity regions and gene paralogy in the evolution of prokaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.6	12
11	Search for Origins of Anti-CRISPR Proteins by Structure Comparison. <i>CRISPR Journal</i> , 2023, 6, 222-231.	3.5	10
12	Widespread CRISPR-derived RNA regulatory elements in CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2023, 51, 8150-8168.	15.7	23
13	Uncovering the functional diversity of rare CRISPR-Cas systems with deep terascale clustering. <i>Science</i> , 2023, 382, .	36.4	121
14	Diversity, evolution, and classification of the RNA-guided nucleases TnpB and Cas12. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.6	59
15	Cellular homologs of the double jelly-roll major capsid proteins clarify the origins of an ancient virus kingdom. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.6	46
16	Small-Molecule Mn Antioxidants in <i>Caenorhabditis elegans</i> and <i>Deinococcus radiodurans</i> Supplant MnSOD Enzymes during Aging and Irradiation. <i>MBio</i> , 2022, 13, .	4.4	22
17	Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis. <i>Biology Direct</i> , 2022, 17, .	4.5	12
18	The tRNA discriminator base defines the mutual orthogonality of two distinct pyrrolysyl-tRNA synthetase/tRNAPyl pairs in the same organism. <i>Nucleic Acids Research</i> , 2022, 50, 4601-4615.	15.7	11

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19	Prokaryotic innate immunity through pattern recognition of conserved viral proteins. <i>Science</i> , 2022, 377, .	36.4	221
20	Structure of the OMEGA nickase IsrB in complex with γ -RNA and target DNA. <i>Nature</i> , 2022, 610, 575-581.	38.7	32
21	RNA-triggered protein cleavage and cell growth arrest by the type III-E CRISPR nuclease-protease. <i>Science</i> , 2022, 378, 882-889.	36.4	53
22	Structure of the IscB γ -RNA ribonucleoprotein complex, the likely ancestor of CRISPR-Cas9. <i>Nature Communications</i> , 2022, 13, .	13.9	40
23	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.	15.7	825
24	CRISPRidentify: identification of CRISPR arrays using machine learning approach. <i>Nucleic Acids Research</i> , 2021, 49, e20-e20.	15.7	79
25	Expanded diversity of Asgard archaea and their relationships with eukaryotes. <i>Nature</i> , 2021, 593, 553-557.	38.7	273
26	Exposure to 1-Butanol Exemplifies the Response of the Thermoacidophilic Archaeon <i>Sulfolobus acidocaldarius</i> to Solvent Stress. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.5	15
27	Structural Basis for a Dual Function ATP Grasp Ligase That Installs Single and Bicyclic γ -Ester Macrocycles in a New Multicore RiPP Natural Product. <i>Journal of the American Chemical Society</i> , 2021, 143, 8056-8068.	15.0	31
28	A Unique Gene Module in Thermococcales Archaea Centered on a Hypervariable Protein Containing Immunoglobulin Domains. <i>Frontiers in Microbiology</i> , 2021, 12, .	3.9	2
29	CRISPRclassify: Repeat-Based Classification of CRISPR Loci. <i>CRISPR Journal</i> , 2021, 4, 558-574.	3.5	27
30	Compact RNA editors with small Cas13 proteins. <i>Nature Biotechnology</i> , 2021, 40, 194-197.	32.2	149
31	Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of <i>Acidithiobacillus</i> . <i>CRISPR Journal</i> , 2021, 4, 656-672.	3.5	38
32	Programmable RNA targeting with the single-protein CRISPR effector Cas7-11. <i>Nature</i> , 2021, 597, 720-725.	38.7	239
33	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , 2021, 374, 57-65.	36.4	348
34	The bone-degrading enzyme machinery: From multi-component understanding to the treatment of residues from the meat industry. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 6328-6342.	4.0	3
35	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020, 11, .	13.9	84
36	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020, 48, 8828-8847.	15.7	108

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37	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020, 369, 1077-1084.	36.4	585
38	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , 2020, 3, 156-163.	3.5	22
39	Structure and function of virion RNA polymerase of a crAss-like phage. <i>Nature</i> , 2020, 589, 306-309.	38.7	36
40	CRISPR Arrays Away from <i>cas</i> Genes. <i>CRISPR Journal</i> , 2020, 3, 535-549.	3.5	32
41	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 435-448.	3.4	58
42	Identification of Dephospho-Coenzyme A (Dephospho-CoA) Kinase in <i>Thermococcus kodakarensis</i> and Elucidation of the Entire CoA Biosynthesis Pathway in Archaea. <i>MBio</i> , 2019, 10, .	4.4	18
43	Engineering of CRISPR-Cas12b for human genome editing. <i>Nature Communications</i> , 2019, 10, .	13.9	325
44	RNA-guided DNA insertion with CRISPR-associated transposases. <i>Science</i> , 2019, 365, 48-53.	36.4	635
45	CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , 2019, 17, 513-525.	85.9	273
46	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019, 10, .	4.4	56
47	Predicted highly derived class 1 CRISPR-Cas system in Haloarchaea containing diverged Cas5 and Cas7 homologs but no CRISPR array. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.9	16
48	Unexpected connections between type VI-B CRISPR-Cas systems, bacterial natural competence, ubiquitin signaling network and DNA modification through a distinct family of membrane proteins. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.9	19
49	Origins and evolution of CRISPR-Cas systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180087.	3.8	424
50	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019, 47, 389-398.	4.1	49
51	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019, 21, 2056-2078.	3.8	50
52	CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , 2019, 431, 3-20.	4.2	94
53	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019, 20, 1063-1070.	6.7	278
54	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2019, 18, 67-83.	85.9	2,180

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55	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018, 3, 461-469.	16.5	132
56	Evolution of Genome Architecture in Archaea: Spontaneous Generation of a New Chromosome in <i>Haloflex volcanii</i> . <i>Molecular Biology and Evolution</i> , 2018, 35, 1855-1868.	4.7	30
57	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	2.9	55
58	Cas13d Is a Compact RNA-Targeting Type VI CRISPR Effector Positively Modulated by a WYL-Domain-Containing Accessory Protein. <i>Molecular Cell</i> , 2018, 70, 327-339.e5.	13.4	443
59	DNA silencing by prokaryotic Argonaute proteins adds a new layer of defense against invading nucleic acids. <i>FEMS Microbiology Reviews</i> , 2018, 42, 376-387.	10.9	64
60	A Reverse Transcriptase-Cas1 Fusion Protein Contains a Cas6 Domain Required for Both CRISPR RNA Biogenesis and RNA Spacer Acquisition. <i>Molecular Cell</i> , 2018, 72, 700-714.e8.	13.4	27
61	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. <i>CRISPR Journal</i> , 2018, 1, 325-336.	3.5	272
62	Systematic prediction of genes functionally linked to CRISPR-Cas systems by gene neighborhood analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, .	7.6	165
63	<i>Escherichia coli</i> ItaT is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA ^{Leu} . <i>Nucleic Acids Research</i> , 2018, 46, 7873-7885.	15.7	39
64	Proteomic Analysis of <i>Methanohalobium thermophilum</i> AMET1, a Representative of a Putative New Class of Euryarchaeota, <i>Genes</i> , 2018, 9, 28.	2.6	12
65	Myosin-driven transport network in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, .	7.6	73
66	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017, 15, 169-182.	85.9	983
67	SnapShot: Class 2 CRISPR-Cas Systems. <i>Cell</i> , 2017, 168, 328-328.e1.	34.1	164
68	SnapShot: Class 1 CRISPR-Cas Systems. <i>Cell</i> , 2017, 168, 946-946.e1.	34.1	148
69	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. <i>Journal of Physiology</i> , 2017, 595, 4611-4630.	3.4	11
70	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, .	16.5	252
71	Diversity, classification and evolution of CRISPR-Cas systems. <i>Current Opinion in Microbiology</i> , 2017, 37, 67-78.	7.0	1,357
72	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , 2017, 17, .	3.1	64

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73	Cas13b Is a Type VI-B CRISPR-Associated RNA-Guided RNase Differentially Regulated by Accessory Proteins Csx27 and Csx28. <i>Molecular Cell</i> , 2017, 65, 618-630.e7.	13.4	549
74	Mobile Genetic Elements and Evolution of CRISPR-Cas Systems: All the Way There and Back. <i>Genome Biology and Evolution</i> , 2017, 9, 2812-2825.	2.4	166
75	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , 2017, 8, .	4.4	209
76	Recruitment of CRISPR-Cas systems by Tn7-like transposons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, .	7.6	281
77	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017, 8, .	4.4	63
78	â€˜ARMANâ€™™ archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, .	13.9	136
79	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 233-261.	9.2	338
80	Proposed Role for KaiC-Like ATPases as Major Signal Transduction Hubs in Archaea. <i>MBio</i> , 2017, 8, .	4.4	16
81	Extreme Deviations from Expected Evolutionary Rates in Archaeal Protein Families. <i>Genome Biology and Evolution</i> , 2017, 9, 2791-2811.	2.4	11
82	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , 2017, 17, .	3.1	76
83	Diversity and Evolution of Type IV pili Systems in Archaea. <i>Frontiers in Microbiology</i> , 2016, 7, .	3.9	120
84	The genome of AR9, a giant transducing Bacillus phage encoding two multisubunit RNA polymerases. <i>Virology</i> , 2016, 495, 185-196.	2.3	95
85	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	34.1	731
86	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. <i>Science</i> , 2016, 353, .	36.4	619
87	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , 2016, 353, .	36.4	2,154
88	Recent Mobility of Casposons, Self-Synthesizing Transposons at the Origin of the CRISPR-Cas Immunity. <i>Genome Biology and Evolution</i> , 2016, 8, 375-386.	2.4	36
89	ISC, a Novel Group of Bacterial and Archaeal DNA Transposons That Encode Cas9 Homologs. <i>Journal of Bacteriology</i> , 2016, 198, 797-807.	2.9	107
90	Evolution of plant Î¹1-pyrroline-5-carboxylate reductases from phylogenetic and structural perspectives. <i>Frontiers in Plant Science</i> , 2015, 6, .	4.1	22

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91	Archaeal Clusters of Orthologous Genes (arCOGs): An Update and Application for Analysis of Shared Features between Thermococcales, Methanococcales, and Methanobacteriales. <i>Life</i> , 2015, 5, 818-840.	2.8	260
92	A non-canonical multisubunit RNA polymerase encoded by a giant bacteriophage. <i>Nucleic Acids Research</i> , 2015, , gkv1095.	15.7	53
93	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015, 43, D261-D269.	15.7	1,638
94	Comparative genomic analysis of evolutionarily conserved but functionally uncharacterized membrane proteins in archaea: Prediction of novel components of secretion, membrane remodeling and glycosylation systems. <i>Biochimie</i> , 2015, 118, 302-312.	2.9	15
95	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <i>Nature Communications</i> , 2015, 6, .	13.9	23
96	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	2.2	100
97	<i>Babela massiliensis</i> , a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. <i>Biology Direct</i> , 2015, 10, .	4.5	77
98	In vivo genome editing using <i>Staphylococcus aureus</i> Cas9. <i>Nature</i> , 2015, 520, 186-191.	38.7	2,577
99	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	85.9	2,476
100	Cpf1 Is a Single RNA-Guided Endonuclease of a Class 2 CRISPR-Cas System. <i>Cell</i> , 2015, 163, 759-771.	34.1	4,498
101	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015, 60, 385-397.	13.4	1,181
102	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014, 5, .	2.4	188
103	Evolution of replicative DNA polymerases in archaea and their contributions to the eukaryotic replication machinery. <i>Frontiers in Microbiology</i> , 2014, 5, .	3.9	76
104	Enzymatic Synthesis of Bioinformatically Predicted Microcin C-Like Compounds Encoded by Diverse Bacteria. <i>MBio</i> , 2014, 5, .	4.4	35
105	Classification and evolution of type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2014, 42, 6091-6105.	15.7	487
106	Phylogeny of Cas9 determines functional exchangeability of dual-RNA and Cas9 among orthologous type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2014, 42, 2577-2590.	15.7	344
107	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. <i>Extremophiles</i> , 2014, 18, 877-893.	2.2	50
108	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 743-753.	8.7	527

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109	Casposons: a new superfamily of self-synthesizing DNA transposons at the origin of prokaryotic CRISPR-Cas immunity. <i>BMC Biology</i> , 2014, 12, .	4.0	178
110	Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. <i>Biology Direct</i> , 2013, 8, .	4.5	260
111	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. <i>Biology Direct</i> , 2013, 8, .	4.5	109
112	Archaeology of Eukaryotic DNA Replication. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012963-a012963.	7.3	78
113	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , 2013, 41, 4360-4377.	15.7	431
114	CRISPR-Cas. <i>RNA Biology</i> , 2013, 10, 679-686.	3.4	185
115	Displacement of the canonical single-stranded DNA-binding protein in the Thermoproteales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, .	7.6	34
116	Nature and Intensity of Selection Pressure on CRISPR-Associated Genes. <i>Journal of Bacteriology</i> , 2012, 194, 1216-1225.	2.9	96
117	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012, 7, .	4.5	136
118	Updated clusters of orthologous genes for Archaea: a complex ancestor of the Archaea and the byways of horizontal gene transfer. <i>Biology Direct</i> , 2012, 7, 46.	4.5	153
119	The CMG (CDC45/RecJ, MCM, GINS) complex is a conserved component of the DNA replication system in all archaea and eukaryotes. <i>Biology Direct</i> , 2012, 7, 7.	4.5	84
120	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2011, 9, 467-477.	85.9	2,373
121	The Complete Genome Sequence of <i>Thermoproteus tenax</i> : A Physiologically Versatile Member of the Crenarchaeota. <i>PLoS ONE</i> , 2011, 6, e24222.	2.4	55
122	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. <i>Biology Direct</i> , 2011, 6, .	4.5	411
123	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. <i>Journal of Bacteriology</i> , 2011, 193, 6039-6056.	2.9	511
124	Evolution of diverse cell division and vesicle formation systems in Archaea. <i>Nature Reviews Microbiology</i> , 2010, 8, 731-741.	85.9	224
125	Archaeal Ubiquitin-Like Proteins: Functional Versatility and Putative Ancestral Involvement in tRNA Modification Revealed by Comparative Genomic Analysis. <i>Archaea</i> , 2010, 2010, 1-10.	1.0	29
126	Abundance of type I toxin-antitoxin systems in bacteria: searches for new candidates and discovery of novel families. <i>Nucleic Acids Research</i> , 2010, 38, 3743-3759.	15.7	257

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127	Comprehensive comparative-genomic analysis of Type 2 toxin-antitoxin systems and related mobile stress response systems in prokaryotes. <i>Biology Direct</i> , 2009, 4, .	4.5	419
128	Prokaryotic homologs of Argonaute proteins are predicted to function as key components of a novel system of defense against mobile genetic elements. <i>Biology Direct</i> , 2009, 4, .	4.5	287
129	CRISPR-Cas: an adaptive immunity system in prokaryotes. <i>F1000 Biology Reports</i> , 2009, 1, .	2.5	107
130	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008, 3, .	4.5	155
131	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, <i>Methylacidiphilum infernum</i> , a representative of the bacterial phylum Verrucomicrobia. <i>Biology Direct</i> , 2008, 3, .	4.5	236
132	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, .	8.2	106
133	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , 2008, 9, R161.	12.8	72
134	A Novel Family of Sequence-specific Endoribonucleases Associated with the Clustered Regularly Interspaced Short Palindromic Repeats. <i>Journal of Biological Chemistry</i> , 2008, 283, 20361-20371.	2.2	187
135	Role of Hypermutability in the Evolution of the Genus <i>Oenococcus</i> . <i>Journal of Bacteriology</i> , 2008, 190, 564-570.	2.9	77
136	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8102-8107.	7.6	277
137	The Deep Archaeal Roots of Eukaryotes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1619-1630.	4.7	160
138	Evolutionary Genomics of Lactic Acid Bacteria. <i>Journal of Bacteriology</i> , 2007, 189, 1199-1208.	2.9	263
139	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. <i>Biology Direct</i> , 2007, 2, .	4.5	174
140	<i>Deinococcus geothermalis</i> : The Pool of Extreme Radiation Resistance Genes Shrinks. <i>PLoS ONE</i> , 2007, 2, e955.	2.4	231
141	The cyanobacterial genome core and the origin of photosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13126-13131.	7.6	297
142	GINs, a central nexus in the archaeal DNA replication fork. <i>EMBO Reports</i> , 2006, 7, 539-545.	5.2	125
143	Title is missing!. <i>Biology Direct</i> , 2006, 1, 7.	4.5	1,048
144	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. <i>Bioinformatics</i> , 2006, 22, 1297-1301.	4.8	41

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145	The HicAB cassette, a putative novel, RNA-targeting toxin-antitoxin system in archaea and bacteria. <i>Bioinformatics</i> , 2006, 22, 2581-2584.	4.8	112
146	Kinase Activity of Overexpressed HipA Is Required for Growth Arrest and Multidrug Tolerance in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2006, 188, 8360-8367.	2.9	191
147	Genomic analysis of <i>Oenococcus oeni</i> -PSU-1 and its relevance to winemaking. <i>FEMS Microbiology Reviews</i> , 2005, 29, 465-475.	10.9	17
148	Title is missing!. <i>BMC Evolutionary Biology</i> , 2005, 5, 57.	3.1	164
149	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. <i>Nucleic Acids Research</i> , 2005, 33, 4626-4638.	15.7	182
150	Evolutionary and functional genomics of the Archaea. <i>Current Opinion in Microbiology</i> , 2005, 8, 586-594.	7.0	42
151	Identification and Functional Verification of Archaeal-Type Phosphoenolpyruvate Carboxylase, a Missing Link in Archaeal Central Carbohydrate Metabolism. <i>Journal of Bacteriology</i> , 2004, 186, 7754-7762.	2.9	35
152	Comparative genomics of the FtsK-HerA superfamily of pumping ATPases: implications for the origins of chromosome segregation, cell division and viral capsid packaging. <i>Nucleic Acids Research</i> , 2004, 32, 5260-5279.	15.7	306
153	Potential genomic determinants of hyperthermophily. <i>Trends in Genetics</i> , 2003, 19, 172-176.	9.9	74
154	Filling a gap in the central metabolism of archaea: prediction of a novel aconitase by comparative-genomic analysis. <i>FEMS Microbiology Letters</i> , 2003, 227, 17-23.	1.9	37
155	Transcriptome dynamics of <i>Deinococcus radiodurans</i> recovering from ionizing radiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4191-4196.	7.6	363
156	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. <i>Nucleic Acids Research</i> , 2002, 30, 482-496.	15.7	365
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