

Kira S Makarova

List of Publications by Year in descending order

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Version: 2024-02-01

179
papers

43,844
citations

4103

90
h-index

4622

176
g-index

190
all docs

190
docs citations

190
times ranked

31573
citing authors

#	ARTICLE	IF	CITATIONS
1	Compact RNA editors with small Cas13 proteins. <i>Nature Biotechnology</i> , 2022, 40, 194-197.	9.4	86
2	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, .	3.3	26
3	Evolutionary plasticity and functional versatility of CRISPR systems. <i>PLoS Biology</i> , 2022, 20, e3001481.	2.6	47
4	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, e0339421.	1.8	12
5	Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis. <i>Biology Direct</i> , 2022, 17, 7.	1.9	9
6	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.	6.5	7
7	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.	6.5	441
8	Structure and function of virion RNA polymerase of a crAss-like phage. <i>Nature</i> , 2021, 589, 306-309.	13.7	29
9	CRISPRidentify: identification of CRISPR arrays using machine learning approach. <i>Nucleic Acids Research</i> , 2021, 49, e20-e20.	6.5	44
10	Expanded diversity of Asgard archaea and their relationships with eukaryotes. <i>Nature</i> , 2021, 593, 553-557.	13.7	161
11	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, .	1.4	8
12	Structural Basis for a Dual Function ATP Grasp Ligase That Installs Single and Bicyclic β -Ester Macrocycles in a New Multicore RiPP Natural Product. <i>Journal of the American Chemical Society</i> , 2021, 143, 8056-8068.	6.6	20
13	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021, 29, 582-592.	3.5	33
14	A Unique Gene Module in Thermococcales Archaea Centered on a Hypervariable Protein Containing Immunoglobulin Domains. <i>Frontiers in Microbiology</i> , 2021, 12, 721392.	1.5	1
15	CRISPRclassify: Repeat-Based Classification of CRISPR Loci. <i>CRISPR Journal</i> , 2021, 4, 558-574.	1.4	12
16	Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of <i>Acidithiobacillia</i> . <i>CRISPR Journal</i> , 2021, 4, 656-672.	1.4	21
17	Programmable RNA targeting with the single-protein CRISPR effector Cas7-11. <i>Nature</i> , 2021, 597, 720-725.	13.7	155
18	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , 2021, 374, 57-65.	6.0	152

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19	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.	1.9	2
20	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. <i>Nature Reviews Genetics</i> , 2020, 21, 119-131.	7.7	159
21	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	13.6	1,427
22	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020, 11, 3784.	5.8	64
23	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020, 48, 8828-8847.	6.5	66
24	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020, 369, 1077-1084.	6.0	302
25	Response to Comment on "CRISPR-guided DNA insertion with CRISPR-associated transposases". <i>Science</i> , 2020, 368, .	6.0	34
26	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , 2020, 3, 156-163.	1.4	17
27	CRISPR Arrays Away from <i>cas</i> Genes. <i>CRISPR Journal</i> , 2020, 3, 535-549.	1.4	18
28	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 435-448.	1.5	45
29	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, .	1.8	11
30	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019, 14, 3013-3031.	5.5	21
31	Engineering of CRISPR-Cas12b for human genome editing. <i>Nature Communications</i> , 2019, 10, 212.	5.8	249
32	RNA-guided DNA insertion with CRISPR-associated transposases. <i>Science</i> , 2019, 365, 48-53.	6.0	448
33	CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , 2019, 17, 513-525.	13.6	205
34	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019, 10, .	1.8	41
35	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, .	0.7	10
36	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, .	0.7	13

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37	Origins and evolution of CRISPR-Cas systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180087.	1.8	258
38	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019, 47, 389-398.	1.6	35
39	Reply to "Evolutionary placement of Methanonatronarchaeia". <i>Nature Microbiology</i> , 2019, 4, 560-561.	5.9	7
40	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019, 21, 2056-2078.	1.8	38
41	CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , 2019, 431, 3-20.	2.0	73
42	Functionally diverse type V CRISPR-Cas systems. <i>Science</i> , 2019, 363, 88-91.	6.0	342
43	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019, 20, 1063-1070.	3.2	186
44	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018, 3, 461-469.	5.9	118
45	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.	3.5	19
46	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	41
47	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.	4.5	356
48	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.	3.9	52
49	Discovery of Oligonucleotide Signaling Mediated by CRISPR-Associated Polymerases Solves Two Puzzles but Leaves an Enigma. <i>ACS Chemical Biology</i> , 2018, 13, 309-312.	1.6	33
50	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , 2018, 3, 38-46.	5.9	245
51	Anti-CRISPRs on the march. <i>Science</i> , 2018, 362, 156-157.	6.0	21
52	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.	4.5	25
53	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. <i>CRISPR Journal</i> , 2018, 1, 325-336.	1.4	232
54	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, E5307-E5316.	3.3	138

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55	Escherichia coli ItaT is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA ^{Leu} . <i>Nucleic Acids Research</i> , 2018, 46, 7873-7885.	6.5	31
56	Proteomic Analysis of Methanonatronarchaeum thermophilum AMET1, a Representative of a Putative New Class of Euryarchaeota, <i>Genes</i> , 2018, 9, 28.	1.0	8
57	Methanonatronarchaeum thermophilum gen. nov., sp. nov. and 'Candidatus Methanohalarchaeum thermophilum', extremely halo(natrono)philic methyl-reducing methanogens from hypersaline lakes comprising a new euryarchaeal class Methanonatronarchaeia classis nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2199-2208.	0.8	78
58	Myosin-driven transport network in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1385-E1394.	3.3	59
59	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017, 15, 169-182.	13.6	792
60	SnapShot: Class 2 CRISPR-Cas Systems. <i>Cell</i> , 2017, 168, 328-328.e1.	13.5	138
61	SnapShot: Class 1 CRISPR-Cas Systems. <i>Cell</i> , 2017, 168, 946-946.e1.	13.5	116
62	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. <i>Journal of Physiology</i> , 2017, 595, 4611-4630.	1.3	11
63	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, 17081.	5.9	213
64	Diversity, classification and evolution of CRISPR-Cas systems. <i>Current Opinion in Microbiology</i> , 2017, 37, 67-78.	2.3	1,076
65	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , 2017, 17, 94.	3.2	46
66	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.	4.5	445
67	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.	1.1	131
68	KaiC-like ATPases as Signal Transduction Hubs in Archaea. , 2017, , 175-194.		1
69	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , 2017, 8, .	1.8	181
70	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, E7358-E7366.	3.3	210
71	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017, 8, .	1.8	52
72	ARMAN™ archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, 60.	5.8	116

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73	The complex domain architecture of SAMD9 family proteins, predicted STAND-like NTPases, suggests new links to inflammation and apoptosis. <i>Biology Direct</i> , 2017, 12, 13.	1.9	45
74	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 233-261.	2.9	256
75	Two fundamentally different classes of microbial genes. <i>Nature Microbiology</i> , 2017, 2, 16208.	5.9	39
76	Proposed Role for KaiC-Like ATPases as Major Signal Transduction Hubs in Archaea. <i>MBio</i> , 2017, 8, .	1.8	12
77	Extreme Deviations from Expected Evolutionary Rates in Archaeal Protein Families. <i>Genome Biology and Evolution</i> , 2017, 9, 2791-2811.	1.1	11
78	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , 2017, 17, 232.	3.2	61
79	High-quality genome sequence of the radioresistant bacterium <i>Deinococcus ficus</i> KS 0460. <i>Standards in Genomic Sciences</i> , 2017, 12, 46.	1.5	10
80	Diversity and Evolution of Type IV pili Systems in Archaea. <i>Frontiers in Microbiology</i> , 2016, 7, 667.	1.5	103
81	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
82	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	13.5	552
83	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. <i>Science</i> , 2016, 353, aad5147.	6.0	523
84	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , 2016, 353, aaf5573.	6.0	1,647
85	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.	1.1	32
86	ISC, a Novel Group of Bacterial and Archaeal DNA Transposons That Encode Cas9 Homologs. <i>Journal of Bacteriology</i> , 2016, 198, 797-807.	1.0	60
87	Evolution of plant γ -pyrroline-5-carboxylate reductases from phylogenetic and structural perspectives. <i>Frontiers in Plant Science</i> , 2015, 6, 567.	1.7	21
88	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.	1.1	216
89	A non-canonical multisubunit RNA polymerase encoded by a giant bacteriophage. <i>Nucleic Acids Research</i> , 2015, 43, gkv1095.	6.5	46
90	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015, 43, D261-D269.	6.5	1,345

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91	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.	1.3	11
92	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <i>Nature Communications</i> , 2015, 6, 7300.	5.8	18
93	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	1.6	70
94	<i>Babela massiliensis</i> , a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. <i>Biology Direct</i> , 2015, 10, 13.	1.9	71
95	In vivo genome editing using <i>Staphylococcus aureus</i> Cas9. <i>Nature</i> , 2015, 520, 186-191.	13.7	2,237
96	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	13.6	2,081
97	Annotation and Classification of CRISPR-Cas Systems. <i>Methods in Molecular Biology</i> , 2015, 1311, 47-75.	0.4	304
98	Cpf1 Is a Single RNA-Guided Endonuclease of a Class 2 CRISPR-Cas System. <i>Cell</i> , 2015, 163, 759-771.	13.5	3,558
99	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015, 60, 385-397.	4.5	971
100	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014, 5, 102.	1.1	164
101	Evolution of replicative DNA polymerases in archaea and their contributions to the eukaryotic replication machinery. <i>Frontiers in Microbiology</i> , 2014, 5, 354.	1.5	66
102	Enzymatic Synthesis of Bioinformatically Predicted Microcin C-Like Compounds Encoded by Diverse Bacteria. <i>MBio</i> , 2014, 5, e01059-14.	1.8	24
103	Classification and evolution of type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2014, 42, 6091-6105.	6.5	401
104	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.	6.5	315
105	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. <i>Extremophiles</i> , 2014, 18, 877-893.	0.9	48
106	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 743-753.	3.6	400
107	Casposons: a new superfamily of self-synthesizing DNA transposons at the origin of prokaryotic CRISPR-Cas immunity. <i>BMC Biology</i> , 2014, 12, 36.	1.7	156
108	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, 15.	1.9	221

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109	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, 9.	1.9	102
110	Evolution and Classification of CRISPR-Cas Systems and Cas Protein Families. , 2013, , 61-91.		6
111	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. <i>Cell Reports</i> , 2013, 4, 938-944.	2.9	64
112	The basic building blocks and evolution of CRISPR-Cas systems. <i>Biochemical Society Transactions</i> , 2013, 41, 1392-1400.	1.6	157
113	Archaeology of Eukaryotic DNA Replication. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012963-a012963.	2.3	70
114	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , 2013, 41, 4360-4377.	6.5	365
115	CRISPR-Cas. <i>RNA Biology</i> , 2013, 10, 679-686.	1.5	158
116	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, E398-405.	3.3	34
117	Nature and Intensity of Selection Pressure on CRISPR-Associated Genes. <i>Journal of Bacteriology</i> , 2012, 194, 1216-1225.	1.0	90
118	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012, 7, 40.	1.9	119
119	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.	1.9	142
120	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.	1.9	80
121	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2011, 9, 467-477.	13.6	2,078
122	The Complete Genome Sequence of <i>Thermoproteus tenax</i> : A Physiologically Versatile Member of the Crenarchaeota. <i>PLoS ONE</i> , 2011, 6, e24222.	1.1	51
123	Functional curation of the <i>Sulfolobus solfataricus</i> P2 and <i>S. acidocaldarius</i> 98-3 complete genome sequences. <i>Extremophiles</i> , 2011, 15, 711-712.	0.9	20
124	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. <i>Biology Direct</i> , 2011, 6, 38.	1.9	379
125	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. <i>Journal of Bacteriology</i> , 2011, 193, 6039-6056.	1.0	358
126	Two new families of the FtsZ-tubulin protein superfamily implicated in membrane remodeling in diverse bacteria and archaea. <i>Biology Direct</i> , 2010, 5, 33.	1.9	45

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127	Evolution of diverse cell division and vesicle formation systems in Archaea. <i>Nature Reviews Microbiology</i> , 2010, 8, 731-741.	13.6	212
128	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.	2.3	26
129	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.	6.5	237
130	Comprehensive comparative-genomic analysis of Type 2 toxin-antitoxin systems and related mobile stress response systems in prokaryotes. <i>Biology Direct</i> , 2009, 4, 19.	1.9	390
131	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, 29.	1.9	232
132	CRISPR-Cas: an adaptive immunity system in prokaryotes. <i>F1000 Biology Reports</i> , 2009, 1, 95.	4.0	87
133	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008, 3, 13.	1.9	144
134	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, <i>Methylacidiphilum infernorum</i> , a representative of the bacterial phylum Verrucomicrobia. <i>Biology Direct</i> , 2008, 3, 26.	1.9	216
135	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, R158.	3.8	104
136	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , 2008, 9, R161.	13.9	71
137	Small CRISPR RNAs Guide Antiviral Defense in Prokaryotes. <i>Science</i> , 2008, 321, 960-964.	6.0	2,138
138	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.	1.6	177
139	Role of Hypermutability in the Evolution of the Genus <i>Oenococcus</i> . <i>Journal of Bacteriology</i> , 2008, 190, 564-570.	1.0	70
140	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.	3.3	253
141	The Deep Archaeal Roots of Eukaryotes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1619-1630.	3.5	153
142	Evolutionary Genomics of Lactic Acid Bacteria. <i>Journal of Bacteriology</i> , 2007, 189, 1199-1208.	1.0	242
143	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. <i>Biology Direct</i> , 2007, 2, 33.	1.9	164
144	<i>Deinococcus geothermalis</i> : The Pool of Extreme Radiation Resistance Genes Shrinks. <i>PLoS ONE</i> , 2007, 2, e955.	1.1	212

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145	The cyanobacterial genome core and the origin of photosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13126-13131.	3.3	277
146	GINs, a central nexus in the archaeal DNA replication fork. EMBO Reports, 2006, 7, 539-545.	2.0	121
147	A putative RNA-interference-based immune system in prokaryotes: computational analysis of the predicted enzymatic machinery, functional analogies with eukaryotic RNAi, and hypothetical mechanisms of action. Biology Direct, 2006, 1, 7.	1.9	961
148	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. Bioinformatics, 2006, 22, 1297-1301.	1.8	35
149	The HicAB cassette, a putative novel, RNA-targeting toxin-antitoxin system in archaea and bacteria. Bioinformatics, 2006, 22, 2581-2584.	1.8	97
150	Kinase Activity of Overexpressed HipA Is Required for Growth Arrest and Multidrug Tolerance in Escherichia coli. Journal of Bacteriology, 2006, 188, 8360-8367.	1.0	181
151	Genomic analysis of <i>Oenococcus oeni</i> PSU-1 and its relevance to winemaking. FEMS Microbiology Reviews, 2005, 29, 465-475.	3.9	16
152	How radiation kills cells: Survival of and under oxidative stress. FEMS Microbiology Reviews, 2005, 29, 361-375.	3.9	197
153	Genomic analysis of PSU-1 and its relevance to winemaking. FEMS Microbiology Reviews, 2005, 29, 465-475.	3.9	146
154	Comparative genomics of <i>Thermus thermophilus</i> and <i>Deinococcus radiodurans</i> : divergent routes of adaptation to thermophily and radiation resistance. BMC Evolutionary Biology, 2005, 5, 57.	3.2	152
155	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. Nucleic Acids Research, 2005, 33, 4626-4638.	6.5	165
156	Evolutionary and functional genomics of the Archaea. Current Opinion in Microbiology, 2005, 8, 586-594.	2.3	40
157	Identification and Functional Verification of Archaeal-Type Phosphoenolpyruvate Carboxylase, a Missing Link in Archaeal Central Carbohydrate Metabolism. Journal of Bacteriology, 2004, 186, 7754-7762.	1.0	33
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