

Kira S Makarova

List of Publications by Year in descending order

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179
papers

43,844
citations

3531

90
h-index

4015

176
g-index

190
all docs

190
docs citations

190
times ranked

28453
citing authors

#	ARTICLE	IF	CITATIONS
1	Cpf1 Is a Single RNA-Guided Endonuclease of a Class 2 CRISPR-Cas System. <i>Cell</i> , 2015, 163, 759-771.	28.9	3,558
2	In vivo genome editing using <i>Staphylococcus aureus</i> Cas9. <i>Nature</i> , 2015, 520, 186-191.	27.8	2,237
3	Small CRISPR RNAs Guide Antiviral Defense in Prokaryotes. <i>Science</i> , 2008, 321, 960-964.	12.6	2,138
4	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	28.6	2,081
5	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2011, 9, 467-477.	28.6	2,078
6	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , 2016, 353, aaf5573.	12.6	1,647
7	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	28.6	1,427
8	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015, 43, D261-D269.	14.5	1,345
9	Diversity, classification and evolution of CRISPR-Cas systems. <i>Current Opinion in Microbiology</i> , 2017, 37, 67-78.	5.1	1,076
10	Horizontal Gene Transfer in Prokaryotes: Quantification and Classification. <i>Annual Review of Microbiology</i> , 2001, 55, 709-742.	7.3	1,024
11	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015, 60, 385-397.	9.7	971
12	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. <i>Biology Direct</i> , 2006, 1, 7.	4.6	961
13	Genome Sequence of the Radioresistant Bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , 1999, 286, 1571-1577.	12.6	879
14	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017, 15, 169-182.	28.6	792
15	Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium <i>Clostridium acetobutylicum</i> . <i>Journal of Bacteriology</i> , 2001, 183, 4823-4838.	2.2	725
16	Genome of the Extremely Radiation-Resistant Bacterium <i>Deinococcus radiodurans</i> Viewed from the Perspective of Comparative Genomics. <i>Microbiology and Molecular Biology Reviews</i> , 2001, 65, 44-79.	6.6	619
17	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016, 165, 949-962.	28.9	552
18	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. <i>Science</i> , 2016, 353, aad5147.	12.6	523

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19	RNA-guided DNA insertion with CRISPR-associated transposases. <i>Science</i> , 2019, 365, 48-53.	12.6	448
20	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.	9.7	445
21	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021, 49, D274-D281.	14.5	441
22	Classification and evolution of type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2014, 42, 6091-6105.	14.5	401
23	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 743-753.	8.2	400
24	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.	4.6	390
25	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.	4.6	379
26	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , 2013, 41, 4360-4377.	14.5	365
27	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. <i>Journal of Bacteriology</i> , 2011, 193, 6039-6056.	2.2	358
28	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.	9.7	356
29	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.	7.1	345
30	Functionally diverse type V CRISPR-Cas systems. <i>Science</i> , 2019, 363, 88-91.	12.6	342
31	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. <i>Nucleic Acids Research</i> , 2002, 30, 482-496.	14.5	331
32	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.	14.5	315
33	Annotation and Classification of CRISPR-Cas Systems. <i>Methods in Molecular Biology</i> , 2015, 1311, 47-75.	0.9	304
34	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020, 369, 1077-1084.	12.6	302
35	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.	14.5	284
36	The complete genome of hyperthermophile <i>Methanopyrus kandleri</i> AV19 and monophyly of archaeal methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4644-4649.	7.1	283

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37	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.	7.1	277
38	Origins and evolution of CRISPR-Cas systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180087.	4.0	258
39	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 233-261.	7.3	256
40	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.	7.1	253
41	Engineering of CRISPR-Cas12b for human genome editing. <i>Nature Communications</i> , 2019, 10, 212.	12.8	249
42	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , 2018, 3, 38-46.	13.3	245
43	Evolutionary Genomics of Lactic Acid Bacteria. <i>Journal of Bacteriology</i> , 2007, 189, 1199-1208.	2.2	242
44	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.	14.5	237
45	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.	4.6	232
46	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. <i>CRISPR Journal</i> , 2018, 1, 325-336.	2.9	232
47	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.	4.6	221
48	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.	4.6	216
49	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.	2.4	216
50	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, 17081.	13.3	213
51	Evolution of diverse cell division and vesicle formation systems in Archaea. <i>Nature Reviews Microbiology</i> , 2010, 8, 731-741.	28.6	212
52	<i>Deinococcus geothermalis</i> : The Pool of Extreme Radiation Resistance Genes Shrinks. <i>PLoS ONE</i> , 2007, 2, e955.	2.5	212
53	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.	7.1	210
54	CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , 2019, 17, 513-525.	28.6	205

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55	How radiation kills cells: Survival of and under oxidative stress. FEMS Microbiology Reviews, 2005, 29, 361-375.	8.6	197
56	Microbial genome analysis: the COG approach. Briefings in Bioinformatics, 2019, 20, 1063-1070.	6.5	186
57	Kinase Activity of Overexpressed HipA Is Required for Growth Arrest and Multidrug Tolerance in <i>Escherichia coli</i> . Journal of Bacteriology, 2006, 188, 8360-8367.	2.2	181
58	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. MBio, 2017, 8, .	4.1	181
59	A Novel Family of Sequence-specific Endoribonucleases Associated with the Clustered Regularly Interspaced Short Palindromic Repeats. Journal of Biological Chemistry, 2008, 283, 20361-20371.	3.4	177
60	Connected gene neighborhoods in prokaryotic genomes. Nucleic Acids Research, 2002, 30, 2212-2223.	14.5	167
61	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. Nucleic Acids Research, 2005, 33, 4626-4638.	14.5	165
62	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. Biology Direct, 2007, 2, 33.	4.6	164
63	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. Frontiers in Genetics, 2014, 5, 102.	2.3	164
64	A superfamily of archaeal, bacterial, and eukaryotic proteins homologous to animal transglutaminases. Protein Science, 1999, 8, 1714-1719.	7.6	161
65	Expanded diversity of Asgard archaea and their relationships with eukaryotes. Nature, 2021, 593, 553-557.	27.8	161
66	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. Nature Reviews Genetics, 2020, 21, 119-131.	16.3	159
67	CRISPR-Cas. RNA Biology, 2013, 10, 679-686.	3.1	158
68	The basic building blocks and evolution of CRISPR-Cas systems. Biochemical Society Transactions, 2013, 41, 1392-1400.	3.4	157
69	Casposons: a new superfamily of self-synthesizing DNA transposons at the origin of prokaryotic CRISPR-Cas immunity. BMC Biology, 2014, 12, 36.	3.8	156
70	Programmable RNA targeting with the single-protein CRISPR effector Cas7-11. Nature, 2021, 597, 720-725.	27.8	155
71	The Deep Archaeal Roots of Eukaryotes. Molecular Biology and Evolution, 2008, 25, 1619-1630.	8.9	153
72	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

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73	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , 2021, 374, 57-65.	12.6	152
74	Genomic analysis of PSU-1 and its relevance to winemaking. <i>FEMS Microbiology Reviews</i> , 2005, 29, 465-475.	8.6	146
75	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008, 3, 13.	4.6	144
76	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.	4.6	142
77	SnapShot: Class 2 CRISPR-Cas Systems. <i>Cell</i> , 2017, 168, 328-328.e1.	28.9	138
78	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.	7.1	138
79	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.	2.5	131
80	Physiologic Determinants of Radiation Resistance in <i>Deinococcus radiodurans</i> . <i>Applied and Environmental Microbiology</i> , 2000, 66, 2620-2626.	3.1	130
81	GINS, a central nexus in the archaeal DNA replication fork. <i>EMBO Reports</i> , 2006, 7, 539-545.	4.5	121
82	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012, 7, 40.	4.6	119
83	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018, 3, 461-469.	13.3	118
84	SnapShot: Class 1 CRISPR-Cas Systems. <i>Cell</i> , 2017, 168, 946-946.e1.	28.9	116
85	â€œARMANâ€™ archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, 60.	12.8	116
86	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. <i>Genome Research</i> , 2001, 11, 555-565.	5.5	110
87	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, R158.	8.8	104
88	Diversity and Evolution of Type IV pili Systems in Archaea. <i>Frontiers in Microbiology</i> , 2016, 7, 667.	3.5	103
89	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.	4.6	102
90	The HicAB cassette, a putative novel, RNA-targeting toxin-antitoxin system in archaea and bacteria. <i>Bioinformatics</i> , 2006, 22, 2581-2584.	4.1	97

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91	Nature and Intensity of Selection Pressure on CRISPR-Associated Genes. <i>Journal of Bacteriology</i> , 2012, 194, 1216-1225.	2.2	90
92	CRISPR-Cas: an adaptive immunity system in prokaryotes. <i>F1000 Biology Reports</i> , 2009, 1, 95.	4.0	87
93	Compact RNA editors with small Cas13 proteins. <i>Nature Biotechnology</i> , 2022, 40, 194-197.	17.5	86
94	The genome of AR9, a giant transducing <i>Bacillus</i> phage encoding two multisubunit RNA polymerases. <i>Virology</i> , 2016, 495, 185-196.	2.4	81
95	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.	4.6	80
96	Comparative genomics of Archaea: how much have we learned in six years, and what's next?. <i>Genome Biology</i> , 2003, 4, 115.	9.6	78
97	<i>Methanonatronarchaeum thermophilum</i> gen. nov., sp. nov. and 'Candidatus <i>Methanohalarchaeum thermophilum</i> ', extremely halo(natrono)philic methyl-reducing methanogens from hypersaline lakes comprising a new euryarchaeal class <i>Methanonatronarchaeia</i> classis nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 2199-2208.	1.7	78
98	Potential genomic determinants of hyperthermophily. <i>Trends in Genetics</i> , 2003, 19, 172-176.	6.7	74
99	CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , 2019, 431, 3-20.	4.2	73
100	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , 2008, 9, R161.	9.6	71
101	<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.	4.6	71
102	SWIM, a novel Zn-chelating domain present in bacteria, archaea and eukaryotes. <i>Trends in Biochemical Sciences</i> , 2002, 27, 384-386.	7.5	70
103	Role of Hypermutability in the Evolution of the Genus <i>Oenococcus</i> . <i>Journal of Bacteriology</i> , 2008, 190, 564-570.	2.2	70
104	Archaeology of Eukaryotic DNA Replication. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013, 5, a012963-a012963.	5.5	70
105	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	3.4	70
106	Evolution of replicative DNA polymerases in archaea and their contributions to the eukaryotic replication machinery. <i>Frontiers in Microbiology</i> , 2014, 5, 354.	3.5	66
107	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020, 48, 8828-8847.	14.5	66
108	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. <i>Cell Reports</i> , 2013, 4, 938-944.	6.4	64

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109	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020, 11, 3784.	12.8	64
110	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , 2017, 17, 232.	3.2	61
111	ISC, a Novel Group of Bacterial and Archaeal DNA Transposons That Encode Cas9 Homologs. <i>Journal of Bacteriology</i> , 2016, 198, 797-807.	2.2	60
112	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.	7.1	59
113	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017, 8, .	4.1	52
114	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.	8.6	52
115	The Complete Genome Sequence of <i>Thermoproteus tenax</i> : A Physiologically Versatile Member of the Crenarchaeota. <i>PLoS ONE</i> , 2011, 6, e24222.	2.5	51
116	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. <i>Extremophiles</i> , 2014, 18, 877-893.	2.3	48
117	Evolutionary plasticity and functional versatility of CRISPR systems. <i>PLoS Biology</i> , 2022, 20, e3001481.	5.6	47
118	The Structure and Evolution of Penelope in the virilis Species Group of <i>Drosophila</i> : An Ancient Lineage of Retroelements. <i>Journal of Molecular Evolution</i> , 2001, 52, 445-456.	1.8	46
119	A non-canonical multisubunit RNA polymerase encoded by a giant bacteriophage. <i>Nucleic Acids Research</i> , 2015, 43, gkv1095.	14.5	46
120	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , 2017, 17, 94.	3.2	46
121	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.	4.6	45
122	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.	4.6	45
123	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 435-448.	3.1	45
124	CRISPRidentify: identification of CRISPR arrays using machine learning approach. <i>Nucleic Acids Research</i> , 2021, 49, e20-e20.	14.5	44
125	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	41
126	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019, 10, .	4.1	41

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127	Evolutionary and functional genomics of the Archaea. <i>Current Opinion in Microbiology</i> , 2005, 8, 586-594.	5.1	40
128	Two fundamentally different classes of microbial genes. <i>Nature Microbiology</i> , 2017, 2, 16208.	13.3	39
129	Specific expansion of protein families in the radioresistant bacterium <i>Deinococcus radiodurans</i> . <i>Genetica</i> , 2000, 108, 25-34.	1.1	38
130	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019, 21, 2056-2078.	3.8	38
131	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.	1.8	35
132	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. <i>Bioinformatics</i> , 2006, 22, 1297-1301.	4.1	35
133	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019, 47, 389-398.	3.4	35
134	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.	7.1	34
135	Response to Comment on "œRNA-guided DNA insertion with CRISPR-associated transposases". <i>Science</i> , 2020, 368, .	12.6	34
136	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.	2.2	33
137	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.	3.4	33
138	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021, 29, 582-592.	7.7	33
139	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.	2.5	32
140	<i>Escherichia coli</i> ItaT is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA ^{Ile} . <i>Nucleic Acids Research</i> , 2018, 46, 7873-7885.	14.5	31
141	Structure and function of virion RNA polymerase of a crAss-like phage. <i>Nature</i> , 2021, 589, 306-309.	27.8	29
142	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
143	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, .	7.1	26
144	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.	9.7	25

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145	Enzymatic Synthesis of Bioinformatically Predicted Microcin C-Like Compounds Encoded by Diverse Bacteria. <i>MBio</i> , 2014, 5, e01059-14.	4.1	24
146	Short repeats and IS elements in the extremely radiation-resistant bacterium <i>Deinococcus radiodurans</i> and comparison to other bacterial species. <i>Research in Microbiology</i> , 1999, 150, 711-724.	2.1	22
147	Evolution of plant γ -pyrroline-5-carboxylate reductases from phylogenetic and structural perspectives. <i>Frontiers in Plant Science</i> , 2015, 6, 567.	3.6	21
148	Anti-CRISPRs on the march. <i>Science</i> , 2018, 362, 156-157.	12.6	21
149	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019, 14, 3013-3031.	12.0	21
150	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.	2.9	21
151	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.	2.3	20
152	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.	13.7	20
153	Evolution of Genome Architecture in Archaea: Spontaneous Generation of a New Chromosome in <i>Haloferax volcanii</i> . <i>Molecular Biology and Evolution</i> , 2018, 35, 1855-1868.	8.9	19
154	Thermolysin and mitochondrial processing peptidase: How far structure \rightarrow functional convergence goes. <i>Protein Science</i> , 1999, 8, 2537-2540.	7.6	18
155	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <i>Nature Communications</i> , 2015, 6, 7300.	12.8	18
156	CRISPR Arrays Away from <i>cas</i> Genes. <i>CRISPR Journal</i> , 2020, 3, 535-549.	2.9	18
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