

# Kira S Makarova

## List of Publications by Citations

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184  
papers

30,336  
citations

80  
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190  
ext. papers

38,187  
ext. citations

13.4  
avg, IF

7.41  
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#	Paper	IF	Citations
184	Cpf1 is a single RNA-guided endonuclease of a class 2 CRISPR-Cas system. <i>Cell</i> , <b>2015</b> , 163, 759-71	56.2	2414
183	In vivo genome editing using <i>Staphylococcus aureus</i> Cas9. <i>Nature</i> , <b>2015</b> , 520, 186-91	50.4	1700
182	Small CRISPR RNAs guide antiviral defense in prokaryotes. <i>Science</i> , <b>2008</b> , 321, 960-4	33.3	1698
181	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , <b>2011</b> , 9, 467-77	22.2	1604
180	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , <b>2015</b> , 13, 722-36	22.2	1434
179	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , <b>2016</b> , 353, aaf5573	33.3	1037
178	Horizontal gene transfer in prokaryotes: quantification and classification. <i>Annual Review of Microbiology</i> , <b>2001</b> , 55, 709-42	17.5	859
177	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D261-9	20.1	818
176	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> , <b>2006</b> , 1, 7	7.2	803
175	Genome sequence of the radioresistant bacterium <i>Deinococcus radiodurans</i> R1. <i>Science</i> , <b>1999</b> , 286, 1571-73	37.3	760
174	Diversity, classification and evolution of CRISPR-Cas systems. <i>Current Opinion in Microbiology</i> , <b>2017</b> , 37, 67-78	7.9	720
173	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , <b>2015</b> , 60, 385-97	17.6	670
172	Genome sequence and comparative analysis of the solvent-producing bacterium <i>Clostridium acetobutylicum</i> . <i>Journal of Bacteriology</i> , <b>2001</b> , 183, 4823-38	3.5	656
171	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , <b>2020</b> , 18, 67-83	22.2	545
170	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , <b>2017</b> , 15, 169-182	22.2	516
169	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> , <b>2001</b> , 65, 44-79	13.2	512
168	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. <i>Science</i> , <b>2016</b> , 353, aad5147	33.3	378

167	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , <b>2016</b> , 165, 949-62	56.2	362
166	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. <i>Biology Direct</i> , <b>2011</b> , 6, 38	7.2	324
165	Comprehensive comparative-genomic analysis of type 2 toxin-antitoxin systems and related mobile stress response systems in prokaryotes. <i>Biology Direct</i> , <b>2009</b> , 4, 19	7.2	315
164	Cas13b Is a Type VI-B CRISPR-Associated RNA-Guided RNase Differentially Regulated by Accessory Proteins Csx27 and Csx28. <i>Molecular Cell</i> , <b>2017</b> , 65, 618-630.e7	17.6	294
163	Classification and evolution of type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 6091-105	20.1	288
162	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> , <b>2003</b> , 100, 4191-6	11.5	288
161	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 482-96	20.1	273
160	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> , <b>2002</b> , 99, 4644-9	11.5	263
159	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 4360-77	20.1	255
158	Phylogeny of Cas9 determines functional exchangeability of dual-RNA and Cas9 among orthologous type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 2577-90	20.1	251
157	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 743-53	17.6	240
156	The cyanobacterial genome core and the origin of photosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 13126-31	11.5	236
155	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> , <b>2004</b> , 32, 5260-79	20.1	234
154	RNA-guided DNA insertion with CRISPR-associated transposases. <i>Science</i> , <b>2019</b> , 365, 48-53	33.3	232
153	Cas13d Is a Compact RNA-Targeting Type VI CRISPR Effector Positively Modulated by a WYL-Domain-Containing Accessory Protein. <i>Molecular Cell</i> , <b>2018</b> , 70, 327-339.e5	17.6	215
152	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> , <b>2008</b> , 105, 8102-7	11.5	214
151	Defense islands in bacterial and archaeal genomes and prediction of novel defense systems. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 6039-56	3.5	209
150	Evolutionary genomics of lactic acid bacteria. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 1199-208	3.5	209

149	Abundance of type I toxin-antitoxin systems in bacteria: searches for new candidates and discovery of novel families. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 3743-59	20.1	205
148	<i>Deinococcus geothermalis</i> : the pool of extreme radiation resistance genes shrinks. <i>PLoS ONE</i> , <b>2007</b> , 2, e955	3.7	179
147	How radiation kills cells: survival of <i>Deinococcus radiodurans</i> and <i>Shewanella oneidensis</i> under oxidative stress. <i>FEMS Microbiology Reviews</i> , <b>2005</b> , 29, 361-75	15.1	171
146	Functionally diverse type V CRISPR-Cas systems. <i>Science</i> , <b>2019</b> , 363, 88-91	33.3	169
145	Annotation and Classification of CRISPR-Cas Systems. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1311, 47-75	1.4	168
144	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> , <b>2008</b> , 3, 26	7.2	168
143	Evolution of diverse cell division and vesicle formation systems in Archaea. <i>Nature Reviews Microbiology</i> , <b>2010</b> , 8, 731-41	22.2	165
142	Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. <i>Biology Direct</i> , <b>2013</b> , 8, 15	7.2	156
141	A novel family of sequence-specific endoribonucleases associated with the clustered regularly interspaced short palindromic repeats. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 20361-71	5.4	156
140	Kinase activity of overexpressed HipA is required for growth arrest and multidrug tolerance in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 8360-7	3.5	153
139	Engineering of CRISPR-Cas12b for human genome editing. <i>Nature Communications</i> , <b>2019</b> , 10, 212	17.4	149
138	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , <b>2017</b> , 71, 233-261	17.5	149
137	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , <b>2018</b> , 3, 38-46	26.6	148
136	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. <i>Biology Direct</i> , <b>2007</b> , 2, 33	7.2	146
135	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> , <b>2009</b> , 4, 29	7.2	143
134	The deep archaeal roots of eukaryotes. <i>Molecular Biology and Evolution</i> , <b>2008</b> , 25, 1619-30	8.3	143
133	A superfamily of archaeal, bacterial, and eukaryotic proteins homologous to animal transglutaminases. <i>Protein Science</i> , <b>1999</b> , 8, 1714-9	6.3	142
132	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. <i>CRISPR Journal</i> , <b>2018</b> , 1, 325-336	2.5	140

131	Comparative genomics of <i>Thermus thermophilus</i> and <i>Deinococcus radiodurans</i> : divergent routes of adaptation to thermophily and radiation resistance. <i>BMC Evolutionary Biology</i> , <b>2005</b> , 5, 57	3	138
130	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 4626-38	20.1	134
129	Connected gene neighborhoods in prokaryotic genomes. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 2212-23	20.1	131
128	CRISPR-Cas: evolution of an RNA-based adaptive immunity system in prokaryotes. <i>RNA Biology</i> , <b>2013</b> , 10, 679-86	4.8	127
127	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17081	26.6	126
126	Origins and evolution of CRISPR-Cas systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2019</b> , 374, 20180087	5.8	126
125	Genomic analysis of <i>Oenococcus oeni</i> PSU-1 and its relevance to winemaking. <i>FEMS Microbiology Reviews</i> , <b>2005</b> , 29, 465-75	15.1	126
124	Archaeal Clusters of Orthologous Genes (arCOGs): An Update and Application for Analysis of Shared Features between Thermococcales, Methanococcales, and Methanobacteriales. <i>Life</i> , <b>2015</b> , 5, 818-40	3	125
123	Casposons: a new superfamily of self-synthesizing DNA transposons at the origin of prokaryotic CRISPR-Cas immunity. <i>BMC Biology</i> , <b>2014</b> , 12, 36	7.3	122
122	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , <b>2017</b> , 8,	7.8	122
121	Updated clusters of orthologous genes for Archaea: a complex ancestor of the Archaea and the byways of horizontal gene transfer. <i>Biology Direct</i> , <b>2012</b> , 7, 46	7.2	120
120	The basic building blocks and evolution of CRISPR-CAS systems. <i>Biochemical Society Transactions</i> , <b>2013</b> , 41, 1392-400	5.1	120
119	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 102	4.5	118
118	GIN5, a central nexus in the archaeal DNA replication fork. <i>EMBO Reports</i> , <b>2006</b> , 7, 539-45	6.5	112
117	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , <b>2008</b> , 3, 13	7.2	109
116	Recruitment of CRISPR-Cas systems by Tn7-like transposons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E7358-E7366	11.5	106
115	Physiologic determinants of radiation resistance in <i>Deinococcus radiodurans</i> . <i>Applied and Environmental Microbiology</i> , <b>2000</b> , 66, 2620-6	4.8	106
114	CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , <b>2019</b> , 17, 513-525	22.2	105

113	Snapshot: Class 2 CRISPR-Cas Systems. <i>Cell</i> , <b>2017</b> , 168, 328-328.e1	56.2	97
112	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , <b>2008</b> , 9, R158	18.3	92
111	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , <b>2018</b> , 3, 461-469	26.6	87
110	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , <b>2012</b> , 7, 40	7.2	86
109	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D274-D281	20.1	84
108	Mobile Genetic Elements and Evolution of CRISPR-Cas Systems: All the Way There and Back. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 2812-2825	3.9	83
107	The HicAB cassette, a putative novel, RNA-targeting toxin-antitoxin system in archaea and bacteria. <i>Bioinformatics</i> , <b>2006</b> , 22, 2581-4	7.2	83
106	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> , <b>2013</b> , 8, 9	7.2	80
105	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1063-1070	13.4	80
104	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> , <b>2018</b> , 115, E5307-E5316	11.5	80
103	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , <b>2020</b> , 369, 1077-1084	33.3	78
102	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. <i>Nature Reviews Genetics</i> , <b>2020</b> , 21, 119-131	30.1	77
101	Snapshot: Class 1 CRISPR-Cas Systems. <i>Cell</i> , <b>2017</b> , 168, 946-946.e1	56.2	75
100	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. <i>Genome Research</i> , <b>2001</b> , 11, 555-565	5.7	75
99	Comparative genomics of Archaea: how much have we learned in six years, and what's next?. <i>Genome Biology</i> , <b>2003</b> , 4, 115	18.3	73
98	Nature and intensity of selection pressure on CRISPR-associated genes. <i>Journal of Bacteriology</i> , <b>2012</b> , 194, 1216-25	3.5	69
97	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> , <b>2012</b> , 7, 7	7.2	68
96	Potential genomic determinants of hyperthermophily. <i>Trends in Genetics</i> , <b>2003</b> , 19, 172-6	8.5	66

95	Diversity and Evolution of Type IV pili Systems in Archaea. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 667	5.7	65
94	Role of hypermutability in the evolution of the genus <i>Oenococcus</i> . <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 564-70	3.5	62
93	CRISPR-Cas: an adaptive immunity system in prokaryotes. <i>F1000 Biology Reports</i> , <b>2009</b> , 1, 95		62
92	SWIM, a novel Zn-chelating domain present in bacteria, archaea and eukaryotes. <i>Trends in Biochemical Sciences</i> , <b>2002</b> , 27, 384-6	10.3	61
91	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , <b>2008</b> , 9, R161	18.3	58
90	ARMANArchaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , <b>2017</b> , 8, 60	17.4	56
89	Archaeology of eukaryotic DNA replication. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2013</b> , 5, a012963	10.2	56
88	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> : BIOCHEMICAL, STRUCTURAL, AND EVOLUTIONARY INSIGHTS. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 18678-98	5.4	52
87	Evolution of replicative DNA polymerases in archaea and their contributions to the eukaryotic replication machinery. <i>Frontiers in Microbiology</i> , <b>2014</b> , 5, 354	5.7	51
86	Differential translation tunes uneven production of operon-encoded proteins. <i>Cell Reports</i> , <b>2013</b> , 4, 938-46	4.6	48
85	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. <i>Extremophiles</i> , <b>2014</b> , 18, 877-93	3	43
84	<i>Methanonatronarchaeum thermophilum</i> gen. nov., sp. nov. and <i>Candidatus Methanohalarchaeum thermophilum</i> , extremely halo(natrono)philic methyl-reducing methanogens from hypersaline lakes comprising a new euryarchaeal class <i>Methanonatronarchaeia classis nov.</i> <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2016</b> , 62, 2182-2200	2.2	43
83	The genome of AR9, a giant transducing <i>Bacillus</i> phage encoding two multisubunit RNA polymerases. <i>Virology</i> , <b>2016</b> , 495, 185-96	3.6	42
82	The complete genome sequence of <i>Thermoproteus tenax</i> : a physiologically versatile member of the Crenarchaeota. <i>PLoS ONE</i> , <b>2011</b> , 6, e24222	3.7	41
81	Expanded diversity of Asgard archaea and their relationships with eukaryotes. <i>Nature</i> , <b>2021</b> , 593, 553-557	70.4	41
80	CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 3-20	6.5	41
79	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> , <b>2001</b> , 52, 445-56	3.1	39
78	Evolutionary and functional genomics of the Archaea. <i>Current Opinion in Microbiology</i> , <b>2005</b> , 8, 586-94	7.9	38



77	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , <b>2017</b> , 17, 232	3	36
76	Myosin-driven transport network in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E1385-E1394	11.5	35
75	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , <b>2017</b> , 8,	7.8	34
74	Two new families of the FtsZ-tubulin protein superfamily implicated in membrane remodeling in diverse bacteria and archaea. <i>Biology Direct</i> , <b>2010</b> , 5, 33	7.2	33
73	Babela massiliensis, a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. <i>Biology Direct</i> , <b>2015</b> , 10, 13	7.2	31
72	Identification and functional verification of archaeal-type phosphoenolpyruvate carboxylase, a missing link in archaeal central carbohydrate metabolism. <i>Journal of Bacteriology</i> , <b>2004</b> , 186, 7754-62	3.5	31
71	The complex domain architecture of SAMD9 family proteins, predicted STAND-like NTPases, suggests new links to inflammation and apoptosis. <i>Biology Direct</i> , <b>2017</b> , 12, 13	7.2	30
70	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , <b>2018</b> , 200,	3.5	29
69	A non-canonical multisubunit RNA polymerase encoded by a giant bacteriophage. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 10411-20	20.1	29
68	Specific expansion of protein families in the radioresistant bacterium <i>Deinococcus radiodurans</i> . <i>Genetica</i> , <b>2000</b> , 108, 25-34	1.5	29
67	Filling a gap in the central metabolism of archaea: prediction of a novel aconitase by comparative-genomic analysis. <i>FEMS Microbiology Letters</i> , <b>2003</b> , 227, 17-23	2.9	28
66	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , <b>2017</b> , 17, 94	3	27
65	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> , <b>2012</b> , 109, E398-405	11.5	27
64	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. <i>Bioinformatics</i> , <b>2006</b> , 22, 1297-301	7.2	27
63	Programmable RNA targeting with the single-protein CRISPR effector Cas7-11. <i>Nature</i> , <b>2021</b> , 597, 720-735	35.4	27
62	Recent Mobility of Casposons, Self-Synthesizing Transposons at the Origin of the CRISPR-Cas Immunity. <i>Genome Biology and Evolution</i> , <b>2016</b> , 8, 375-86	3.9	26
61	ISC, a Novel Group of Bacterial and Archaeal DNA Transposons That Encode Cas9 Homologs. <i>Journal of Bacteriology</i> , <b>2015</b> , 198, 797-807	3.5	26
60	Two fundamentally different classes of microbial genes. <i>Nature Microbiology</i> , <b>2016</b> , 2, 16208	26.6	26



59	Discovery of Oligonucleotide Signaling Mediated by CRISPR-Associated Polymerases Solves Two Puzzles but Leaves an Enigma. <i>ACS Chemical Biology</i> , <b>2018</b> , 13, 309-312	4.9	25
58	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , <b>2021</b> , 374, 57-65	33.3	25
57	Archaeal ubiquitin-like proteins: functional versatility and putative ancestral involvement in tRNA modification revealed by comparative genomic analysis. <i>Archaea</i> , <b>2010</b> , 2010,	2	24
56	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonsel Self Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , <b>2019</b> , 10,	7.8	23
55	DNA silencing by prokaryotic Argonaute proteins adds a new layer of defense against invading nucleic acids. <i>FEMS Microbiology Reviews</i> , <b>2018</b> , 42, 376-387	15.1	21
54	Enzymatic synthesis of bioinformatically predicted microcin C-like compounds encoded by diverse bacteria. <i>MBio</i> , <b>2014</b> , 5, e01059-14	7.8	21
53	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , <b>2020</b> , 11, 3784	17.4	21
52	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 8828-8847	20.1	21
51	Escherichia coli ItaT is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA <sup>Ile</sup> . <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 7873-7885	20.1	21
50	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , <b>2019</b> , 16, 435-448	4.8	20
49	Short repeats and IS elements in the extremely radiation-resistant bacterium Deinococcus radiodurans and comparison to other bacterial species. <i>Research in Microbiology</i> , <b>1999</b> , 150, 711-24	4	20
48	Compact RNA editors with small Cas13 proteins. <i>Nature Biotechnology</i> , <b>2021</b> ,	44.5	20
47	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , <b>2019</b> , 21, 2056-2073	32	19
46	Thermolysin and mitochondrial processing peptidase: how far structure-functional convergence goes. <i>Protein Science</i> , <b>1999</b> , 8, 2537-40	6.3	17
45	Structure and function of virion RNA polymerase of a crAss-like phage. <i>Nature</i> , <b>2021</b> , 589, 306-309	50.4	17
44	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , <b>2019</b> , 47, 389-398	5.1	16
43	Evolution of plant (1)-pyrroline-5-carboxylate reductases from phylogenetic and structural perspectives. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 567	6.2	16
42	Functional curation of the Sulfolobus solfataricus P2 and S. acidocaldarius 98-3 complete genome sequences. <i>Extremophiles</i> , <b>2011</b> , 15, 711-2	3	16

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36	Evolution of Genome Architecture in Archaea: Spontaneous Generation of a New Chromosome in <i>Haloferax volcanii</i> . <i>Molecular Biology and Evolution</i> , <b>2018</b> , 35, 1855-1868	8.3	12
35	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , <b>2021</b> , 29, 582-592	12.4	12
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33	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector		10
32	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. <i>Journal of Physiology</i> , <b>2017</b> , 595, 4611-4630	3.9	9
31	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> , <b>2019</b> , 366,	2.9	9
30	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> , <b>2019</b> , 366,	2.9	9
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27	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , <b>2020</b> , 3, 156-163	2.5	8
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25	Evolutionary plasticity and functional versatility of CRISPR systems.. <i>PLoS Biology</i> , <b>2022</b> , 20, e3001481	9.7	8
24	High-quality genome sequence of the radioresistant bacterium KS 0460. <i>Standards in Genomic Sciences</i> , <b>2017</b> , 12, 46		7

23	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> , <b>2019</b> , 10,	7.8	7
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17	The CRISPR spacer space is dominated by sequences from the species-specific mobilome		4
16	Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of. <i>CRISPR Journal</i> , <b>2021</b> , 4, 656-672	2.5	4
15	Comparative Genomics of Stress Response Systems in <i>Deinococcus</i> Bacteria <b>2014</b> , 445-457		3
14	Exposure to 1-Butanol Exemplifies the Response of the Thermoacidophilic Archaeon <i>Sulfolobus acidocaldarius</i> to Solvent Stress. <i>Applied and Environmental Microbiology</i> , <b>2021</b> , 87,	4.8	3
13	Reply to $\beta$ Evolutionary placement of <i>Methanonatronarchaeia</i> <i>Nature Microbiology</i> , <b>2019</b> , 4, 560-561	26.6	2
12	Small-Molecule Mn Antioxidants in <i>Caenorhabditis elegans</i> and <i>Deinococcus radiodurans</i> Supplant MnSOD Enzymes during Aging and Irradiation.. <i>MBio</i> , <b>2022</b> , e0339421	7.8	2
11	Recruitment of CRISPR-Cas systems by Tn7-like transposons		2
10	CRISPRidentify: identification of CRISPR arrays using machine learning approach		2
9	KaiC-like ATPases as Signal Transduction Hubs in Archaea <b>2017</b> , 175-194		1
8	CRISPR-Cas Systems and Cas Protein Families <b>2013</b> , 341-381		1
7	A putative RNA-interference-based immune system in prokaryotes: the epitome of prokaryotic genomic diversity39-64		1
6	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> , <b>2021</b> , 19, 6328-6342	6.8	1

5	Towards comprehensive characterization of CRISPR-linked genes		1
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