

Kira S Makarova

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

184
papers

30,336
citations

80
h-index

174
g-index

190
ext. papers

38,187
ext. citations

13.4
avg, IF

7.41
L-index

#	Paper	IF	Citations
184	Evolutionary plasticity and functional versatility of CRISPR systems.. <i>PLoS Biology</i> , 2022 , 20, e3001481	9.7	8
183	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 , e0339421	7.8	2
182	Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis.. <i>Biology Direct</i> , 2022 , 17, 7	7.2	0
181	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	6.8	1
180	Expanded diversity of Asgard archaea and their relationships with eukaryotes. <i>Nature</i> , 2021 , 593, 553-557	30.4	41
179	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,	4.8	3
178	Structural Basis for a Dual Function ATP Grasp Ligase That Installs Single and Bicyclic Ester Macrocycles in a New Multicore RiPP Natural Product. <i>Journal of the American Chemical Society</i> , 2021 , 143, 8056-8068	16.4	5
177	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021 , 49, D274-D281	20.1	84
176	Structure and function of virion RNA polymerase of a crAss-like phage. <i>Nature</i> , 2021 , 589, 306-309	50.4	17
175	CRISPRidentify: identification of CRISPR arrays using machine learning approach. <i>Nucleic Acids Research</i> , 2021 , 49, e20	20.1	11
174	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021 , 29, 582-592	12.4	12
173	A Unique Gene Module in Archaea Centered on a Hypervariable Protein Containing Immunoglobulin Domains. <i>Frontiers in Microbiology</i> , 2021 , 12, 721392	5.7	0
172	CRISPRclassify: Repeat-Based Classification of CRISPR Loci. <i>CRISPR Journal</i> , 2021 , 4, 558-574	2.5	1
171	Compact RNA editors with small Cas13 proteins. <i>Nature Biotechnology</i> , 2021 ,	44.5	20
170	Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of. <i>CRISPR Journal</i> , 2021 , 4, 656-672	2.5	4
169	Programmable RNA targeting with the single-protein CRISPR effector Cas7-11. <i>Nature</i> , 2021 , 597, 720-725	35.4	27
168	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. <i>Science</i> , 2021 , 374, 57-65	33.3	25

167	Response to Comment on "RNA-guided DNA insertion with CRISPR-associated transposases". <i>Science</i> , 2020 , 368,	33.3	14
166	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , 2020 , 3, 156-163	2.5	8
165	CRISPR Arrays Away from Genes. <i>CRISPR Journal</i> , 2020 , 3, 535-549	2.5	7
164	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020 , 18, 67-83	22.2	545
163	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020 , 11, 3784	17.4	21
162	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020 , 48, 8828-8847	20.1	21
161	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020 , 369, 1077-1084	33.3	78
160	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. <i>Nature Reviews Genetics</i> , 2020 , 21, 119-131	30.1	77
159	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019 , 14, 3013-3031	18.8	12
158	Engineering of CRISPR-Cas12b for human genome editing. <i>Nature Communications</i> , 2019 , 10, 212	17.4	149
157	RNA-guided DNA insertion with CRISPR-associated transposases. <i>Science</i> , 2019 , 365, 48-53	33.3	232
156	CRISPR-Cas in mobile genetic elements: counter-defence and beyond. <i>Nature Reviews Microbiology</i> , 2019 , 17, 513-525	22.2	105
155	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonsel Self Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019 , 10,	7.8	23
154	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,	2.9	9
153	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,	2.9	9
152	Origins and evolution of CRISPR-Cas systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019 , 374, 20180087	5.8	126
151	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019 , 47, 389-398	5.1	16
150	Reply to Evolutionary placement of MethanonatronarchaeiaR <i>Nature Microbiology</i> , 2019 , 4, 560-561	26.6	2

149	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019 , 16, 435-448	4.8	20
148	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,	7.8	7
147	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019 , 21, 2056-2073	8.2	19
146	CRISPR-Cas: Complex Functional Networks and Multiple Roles beyond Adaptive Immunity. <i>Journal of Molecular Biology</i> , 2019 , 431, 3-20	6.5	41
145	Functionally diverse type V CRISPR-Cas systems. <i>Science</i> , 2019 , 363, 88-91	33.3	169
144	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1063-1070	13.4	80
143	Anti-CRISPR proteins encoded by archaeal lytic viruses inhibit subtype I-D immunity. <i>Nature Microbiology</i> , 2018 , 3, 461-469	26.6	87
142	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	8.3	12
141	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	29
140	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	17.6	215
139	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	15.1	21
138	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	4.9	25
137	Proteomic Analysis of <i>Methanonatronarchaeum thermophilum</i> AMET1, a Representative of a Putative New Class of Euryarchaeota, "Methanonatronarchaeia". <i>Genes</i> , 2018 , 9,	4.2	5
136	<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</i> classis nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 2199-2208	2.2	43
135	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. <i>Nature Microbiology</i> , 2018 , 3, 38-46	26.6	148
134	Anti-CRISPRs on the march. <i>Science</i> , 2018 , 362, 156-157	33.3	16
133	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	17.6	16
132	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. <i>CRISPR Journal</i> , 2018 , 1, 325-336	2.5	140

131	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	11.5	80
130	<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	20.1	21
129	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	11.5	35
128	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017 , 15, 169-182	22.2	516
127	SnapShot: Class 2 CRISPR-Cas Systems. <i>Cell</i> , 2017 , 168, 328-328.e1	56.2	97
126	SnapShot: Class 1 CRISPR-Cas Systems. <i>Cell</i> , 2017 , 168, 946-946.e1	56.2	75
125	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. <i>Journal of Physiology</i> , 2017 , 595, 4611-4630	3.9	9
124	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017 , 2, 17081	26.6	126
123	Diversity, classification and evolution of CRISPR-Cas systems. <i>Current Opinion in Microbiology</i> , 2017 , 37, 67-78	7.9	720
122	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , 2017 , 17, 94	3	27
121	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	17.6	294
120	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	3.9	83
119	KaiC-like ATPases as Signal Transduction Hubs in Archaea 2017 , 175-194		1
118	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , 2017 , 17, 232	3	36
117	High-quality genome sequence of the radioresistant bacterium KS 0460. <i>Standards in Genomic Sciences</i> , 2017 , 12, 46		7
116	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , 2017 , 8,	7.8	122
115	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	11.5	106
114	On the Origin of Reverse Transcriptase-Using CRISPR-Cas Systems and Their Hyperdiverse, Enigmatic Spacer Repertoires. <i>MBio</i> , 2017 , 8,	7.8	34

113	ARMAN Archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017 , 8, 60	17.4	56
112	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	7.2	30
111	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017 , 71, 233-261	17.5	149
110	Proposed Role for KaiC-Like ATPases as Major Signal Transduction Hubs in Archaea. <i>MBio</i> , 2017 , 8,	7.8	9
109	Extreme Deviations from Expected Evolutionary Rates in Archaeal Protein Families. <i>Genome Biology and Evolution</i> , 2017 , 9, 2791-2811	3.9	6
108	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , 2016 , 353, aaf5573	33.3	1037
107	Recent Mobility of Casposons, Self-Synthesizing Transposons at the Origin of the CRISPR-Cas Immunity. <i>Genome Biology and Evolution</i> , 2016 , 8, 375-86	3.9	26
106	Two fundamentally different classes of microbial genes. <i>Nature Microbiology</i> , 2016 , 2, 16208	26.6	26
105	Diversity and Evolution of Type IV pili Systems in Archaea. <i>Frontiers in Microbiology</i> , 2016 , 7, 667	5.7	65
104	The genome of AR9, a giant transducing Bacillus phage encoding two multisubunit RNA polymerases. <i>Virology</i> , 2016 , 495, 185-96	3.6	42
103	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016 , 165, 949-62	56.2	362
102	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. <i>Science</i> , 2016 , 353, aad5147	33.3	378
101	A primase subunit essential for efficient primer synthesis by an archaeal eukaryotic-type primase. <i>Nature Communications</i> , 2015 , 6, 7300	17.4	13
100	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> : BIOCHEMICAL, STRUCTURAL, AND EVOLUTIONARY INSIGHTS. <i>Journal of Biological Chemistry</i> , 2015 , 290, 18678-98	5.4	52
99	Babela massiliensis, a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. <i>Biology Direct</i> , 2015 , 10, 13	7.2	31
98	In vivo genome editing using <i>Staphylococcus aureus</i> Cas9. <i>Nature</i> , 2015 , 520, 186-91	50.4	1700
97	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015 , 13, 722-36	22.2	1434
96	Annotation and Classification of CRISPR-Cas Systems. <i>Methods in Molecular Biology</i> , 2015 , 1311, 47-75	1.4	168

95	Cpf1 is a single RNA-guided endonuclease of a class 2 CRISPR-Cas system. <i>Cell</i> , 2015 , 163, 759-71	56.2	2414
94	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015 , 60, 385-97	17.6	670
93	ISC, a Novel Group of Bacterial and Archaeal DNA Transposons That Encode Cas9 Homologs. <i>Journal of Bacteriology</i> , 2015 , 198, 797-807	3.5	26
92	Evolution of plant (1)-pyrroline-5-carboxylate reductases from phylogenetic and structural perspectives. <i>Frontiers in Plant Science</i> , 2015 , 6, 567	6.2	16
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, 818-40	3	125
90	A non-canonical multisubunit RNA polymerase encoded by a giant bacteriophage. <i>Nucleic Acids Research</i> , 2015 , 43, 10411-20	20.1	29
89	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015 , 43, D261-9	20.1	818
88	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, 302-12	4.6	9
87	Enzymatic synthesis of bioinformatically predicted microcin C-like compounds encoded by diverse bacteria. <i>MBio</i> , 2014 , 5, e01059-14	7.8	21
86	Classification and evolution of type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2014 , 42, 6091-105	20.1	288
85	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, 2577-90	20.1	251
84	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. <i>Extremophiles</i> , 2014 , 18, 877-93	3	43
83	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 743-53	17.6	240
82	Casposons: a new superfamily of self-synthesizing DNA transposons at the origin of prokaryotic CRISPR-Cas immunity. <i>BMC Biology</i> , 2014 , 12, 36	7.3	122
81	Comparative Genomics of Stress Response Systems in Deinococcus Bacteria 2014 , 445-457		3
80	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014 , 5, 102	4.5	118
79	Evolution of replicative DNA polymerases in archaea and their contributions to the eukaryotic replication machinery. <i>Frontiers in Microbiology</i> , 2014 , 5, 354	5.7	51
78	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	7.2	156

77	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	7.2	80
76	Evolution and Classification of CRISPR-Cas Systems and Cas Protein Families 2013 , 61-91		5
75	Differential translation tunes uneven production of operon-encoded proteins. <i>Cell Reports</i> , 2013 , 4, 938-446	4.6	48
74	The basic building blocks and evolution of CRISPR-CAS systems. <i>Biochemical Society Transactions</i> , 2013 , 41, 1392-400	5.1	120
73	CRISPR-Cas Systems and Cas Protein Families 2013 , 341-381		1
72	Archaeology of eukaryotic DNA replication. <i>Cold Spring Harbor Perspectives in Biology</i> , 2013 , 5, a012963	10.2	56
71	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , 2013 , 41, 4360-77	20.1	255
70	CRISPR-Cas: evolution of an RNA-based adaptive immunity system in prokaryotes. <i>RNA Biology</i> , 2013 , 10, 679-86	4.8	127
69	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	7.2	68
68	Nature and intensity of selection pressure on CRISPR-associated genes. <i>Journal of Bacteriology</i> , 2012 , 194, 1216-25	3.5	69
67	Live virus-free or die: coupling of antiviral immunity and programmed suicide or dormancy in prokaryotes. <i>Biology Direct</i> , 2012 , 7, 40	7.2	86
66	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	7.2	120
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> , 2012 , 109, E398-405	11.5	27
64	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2011 , 9, 467-77	22.2	1604
63	The complete genome sequence of <i>Thermoproteus tenax</i> : a physiologically versatile member of the Crenarchaeota. <i>PLoS ONE</i> , 2011 , 6, e24222	3.7	41
62	Functional curation of the <i>Sulfolobus solfataricus</i> P2 and <i>S. acidocaldarius</i> 98-3 complete genome sequences. <i>Extremophiles</i> , 2011 , 15, 711-2	3	16
61	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	7.2	324
60	Defense islands in bacterial and archaeal genomes and prediction of novel defense systems. <i>Journal of Bacteriology</i> , 2011 , 193, 6039-56	3.5	209

59	Evolution of diverse cell division and vesicle formation systems in Archaea. <i>Nature Reviews Microbiology</i> , 2010 , 8, 731-41	22.2	165
58	Archaeal ubiquitin-like proteins: functional versatility and putative ancestral involvement in tRNA modification revealed by comparative genomic analysis. <i>Archaea</i> , 2010 , 2010,	2	24
57	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, 3743-59	20.1	205
56	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	7.2	33
55	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	7.2	315
54	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	7.2	143
53	CRISPR-Cas: an adaptive immunity system in prokaryotes. <i>F1000 Biology Reports</i> , 2009 , 1, 95		62
52	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008 , 3, 13	7.2	109
51	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, <i>Methylophilum infernum</i> , a representative of the bacterial phylum Verrucomicrobia. <i>Biology Direct</i> , 2008 , 3, 26	7.2	168
50	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008 , 9, R158	18.3	92
49	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium <i>Anoxybacillus flavithermus</i> WK1. <i>Genome Biology</i> , 2008 , 9, R161	18.3	58
48	Small CRISPR RNAs guide antiviral defense in prokaryotes. <i>Science</i> , 2008 , 321, 960-4	33.3	1698
47	A novel family of sequence-specific endoribonucleases associated with the clustered regularly interspaced short palindromic repeats. <i>Journal of Biological Chemistry</i> , 2008 , 283, 20361-71	5.4	156
46	Role of hypermutability in the evolution of the genus <i>Oenococcus</i> . <i>Journal of Bacteriology</i> , 2008 , 190, 564-70	3.5	62
45	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, 8102-7	11.5	214
44	The deep archaeal roots of eukaryotes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1619-30	8.3	143
43	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. <i>Biology Direct</i> , 2007 , 2, 33	7.2	146
42	Evolutionary genomics of lactic acid bacteria. <i>Journal of Bacteriology</i> , 2007 , 189, 1199-208	3.5	209

41	Deinococcus geothermalis: the pool of extreme radiation resistance genes shrinks. <i>PLoS ONE</i> , 2007 , 2, e955	3.7	179
40	Cyanobacterial response regulator PatA contains a conserved N-terminal domain (PATAN) with an alpha-helical insertion. <i>Bioinformatics</i> , 2006 , 22, 1297-301	7.2	27
39	The HicAB cassette, a putative novel, RNA-targeting toxin-antitoxin system in archaea and bacteria. <i>Bioinformatics</i> , 2006 , 22, 2581-4	7.2	83
38	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, 8360-7	3.5	153
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, 13126-31	11.5	236
36	GINS, a central nexus in the archaeal DNA replication fork. <i>EMBO Reports</i> , 2006 , 7, 539-45	6.5	112
35	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	7.2	803
34	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. <i>Nucleic Acids Research</i> , 2005 , 33, 4626-38	20.1	134
33	Evolutionary and functional genomics of the Archaea. <i>Current Opinion in Microbiology</i> , 2005 , 8, 586-94	7.9	38
32	Genomic analysis of <i>Oenococcus oeni</i> PSU-1 and its relevance to winemaking. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 465-475	15.1	8
31	How radiation kills cells: survival of <i>Deinococcus radiodurans</i> and <i>Shewanella oneidensis</i> under oxidative stress. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 361-75	15.1	171
30	Genomic analysis of <i>Oenococcus oeni</i> PSU-1 and its relevance to winemaking. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 465-75	15.1	126
29	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> , 2005 , 5, 57	3	138
28	Identification and functional verification of archaeal-type phosphoenolpyruvate carboxylase, a missing link in archaeal central carbohydrate metabolism. <i>Journal of Bacteriology</i> , 2004 , 186, 7754-62	3.5	31
27	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, 5260-79	20.1	234
26	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, 4191-6	11.5	288
25	Potential genomic determinants of hyperthermophily. <i>Trends in Genetics</i> , 2003 , 19, 172-6	8.5	66
24	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	2.9	28

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22	SWIM, a novel Zn-chelating domain present in bacteria, archaea and eukaryotes. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 384-6	10.3	61
21	Connected gene neighborhoods in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002 , 30, 2212-23	20.1	131
20	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. <i>Nucleic Acids Research</i> , 2002 , 30, 482-96	20.1	273
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18	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, 445-56	3.1	39
17	Horizontal gene transfer in prokaryotes: quantification and classification. <i>Annual Review of Microbiology</i> , 2001 , 55, 709-42	17.5	859
16	Genome sequence and comparative analysis of the solvent-producing bacterium <i>Clostridium acetobutylicum</i> . <i>Journal of Bacteriology</i> , 2001 , 183, 4823-38	3.5	656
15	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	13.2	512
14	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. <i>Genome Research</i> , 2001 , 11, 555-565	5.7	75
13	Specific expansion of protein families in the radioresistant bacterium <i>Deinococcus radiodurans</i> . <i>Genetica</i> , 2000 , 108, 25-34	1.5	29
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11	Thermolysin and mitochondrial processing peptidase: how far structure-functional convergence goes. <i>Protein Science</i> , 1999 , 8, 2537-40	6.3	17
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7	A putative RNA-interference-based immune system in prokaryotes: the epitome of prokaryotic genomic diversity	39-64	1
6	Towards comprehensive characterization of CRISPR-linked genes		1

5	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector	10
4	The CRISPR spacer space is dominated by sequences from the species-specific mobilome	4
3	Recruitment of CRISPR-Cas systems by Tn7-like transposons	2
2	Expanding diversity of Asgard archaea and the elusive ancestry of eukaryotes	1
1	CRISPRidentify: identification of CRISPR arrays using machine learning approach	2