Yuri I Wolf

List of Publications by Year
in descending order

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277 papers	68,797 citations	1704 104 h-index	751 250 g-index
337 all docs	337 docs citations	337 times ranked	60581 citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	The COG database: an updated version includes eukaryotes. BMC Bioinformatics, 2003, 4, 41.	2.6	3,913
3	An updated evolutionary classification of CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2015, 13, 722-736.	28.6	2,081
4	Evolution and classification of the CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2011, 9, 467-477.	28.6	2,078
5	Evolutionary classification of CRISPRâ€“Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	28.6	1,427
6	Expanded microbial genome coverage and improved protein family annotation in the COG database. Nucleic Acids Research, 2015, 43, D261-D269.	14.5	1,345
7	Comparative genomics of the lactic acid bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15611-15616.	7.1	1,303
8	The Ecoresponsive Genome of <i>Daphnia pulex</i>. Science, 2011, 331, 555-561.	12.6	1,086
9	Classification and evolution of P-loop GTPases and related ATPases. Journal of Molecular Biology, 2002, 317, 41-72.	4.2	1,021
10	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. Molecular Cell, 2015, 60, 385-397.	9.7	971
11	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.	4.6	961
12	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. Genome Biology, 2004, 5, R7.	9.6	814
13	Diversity and evolution of class 2 CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2017, 15, 169-182.	28.6	792
14	Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium<i>Clostridium acetobutylicum</i>. Journal of Bacteriology, 2001, 183, 4823-4838.	2.2	725
15	Genomics of bacteria and archaea: the emerging dynamic view of the prokaryotic world. Nucleic Acids Research, 2008, 36, 6688-6719.	14.5	642
16	Selection in the evolution of gene duplications. Genome Biology, 2002, 3, research0008.1.	9.6	625
17	Genome of the Extremely Radiation-Resistant Bacterium <i>Deinococcus radiodurans</i> Viewed from the Perspective of Comparative Genomics. Microbiology and Molecular Biology Reviews, 2001, 65, 44-79.	6.6	619
18	The structure of the protein universe and genome evolution. Nature, 2002, 420, 218-223.	27.8	536

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19	Essential Genes Are More Evolutionarily Conserved Than Are Nonessential Genes in Bacteria. Genome Research, 2002, 12, 962-968.	5.5	491
20	Genome sequence of the cyanobacterium <i>Prochlorococcus marinus</i> SS120, a nearly minimal oxyphototrophic genome. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10020-10025.	7.1	442
21	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. Nucleic Acids Research, 2021, 49, D274-D281.	14.5	441
22	The Role of Lineage-Specific Gene Family Expansion in the Evolution of Eukaryotes. Genome Research, 2002, 12, 1048-1059.	5.5	416
23	Remarkable Interkingdom Conservation of Intron Positions and Massive, Lineage-Specific Intron Loss and Gain in Eukaryotic Evolution. Current Biology, 2003, 13, 1512-1517.	3.9	413
24	Comprehensive comparative-genomic analysis of Type 2 toxin-antitoxin systems and related mobile stress response systems in prokaryotes. Biology Direct, 2009, 4, 19.	4.6	390
25	Origins and Evolution of the Global RNA Virome. MBio, 2018, 9, .	4.1	383
26	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. Biology Direct, 2011, 6, 38.	4.6	379
27	Global Organization and Proposed Megataxonomy of the Virus World. Microbiology and Molecular Biology Reviews, 2020, 84, .	6.6	378
28	Gene Loss, Protein Sequence Divergence, Gene Dispensability, Expression Level, and Interactivity Are Correlated in Eukaryotic Evolution. Genome Research, 2003, 13, 2229-2235.	5.5	367
29	Comparative genomics of defense systems in archaea and bacteria. Nucleic Acids Research, 2013, 41, 4360-4377.	14.5	365
30	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. Journal of Bacteriology, 2011, 193, 6039-6056.	2.2	358
31	Small Proteins Can No Longer Be Ignored. Annual Review of Biochemistry, 2014, 83, 753-777.	11.1	346
32	Evolution of Aminoacyl-tRNA Synthetasesâ€"Analysis of Unique Domain Architectures and Phylogenetic Trees Reveals a Complex History of Horizontal Gene Transfer Events. Genome Research, 1999, 9, 689-710.	5.5	346
33	Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. Trends in Genetics, 1998, 14, 442-444.	6.7	337
34	A new superfamily of putative NTP-binding domains encoded by genomes of small DNA and RNA viruses. FEBS Letters, 1990, 262, 145-148.	2.8	336
35	Genome trees and the tree of life. Trends in Genetics, 2002, 18, 472-479.	6.7	336
36	Eukaryotic large nucleo-cytoplasmic DNA viruses: Clusters of orthologous genes and reconstruction of viral genome evolution. Virology Journal, 2009, 6, 223.	3.4	321

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37	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. Science, 2020, 369, 1077-1084.	12.6	302
38	The complete genome of hyperthermophile <i>Methanopyrus kandleri AV19</i> and monophyly of archaeal methanogens. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4644-4649.	7.1	283
39	A universal trend of amino acid gain and loss in protein evolution. Nature, 2005, 433, 633-638.	27.8	282
40	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.	7.1	277
41	Genome trees constructed using five different approaches suggest new major bacterial clades. BMC Evolutionary Biology, 2001, 1, 8.	3.2	272
42	Genome Alignment, Evolution of Prokaryotic Genome Organization, and Prediction of Gene Function Using Genomic Context. Genome Research, 2001, 11, 356-372.	5.5	270
43	Genome reduction as the dominant mode of evolution. BioEssays, 2013, 35, 829-837.	2.5	267
44	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. Annual Review of Microbiology, 2017, 71, 233-261.	7.3	256
45	A korarchaeal genome reveals insights into the evolution of the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8102-8107.	7.1	253
46	Genome-wide Analysis of Substrate Specificities of the Escherichia coli Haloacid Dehalogenase-like Phosphatase Family. Journal of Biological Chemistry, 2006, 281, 36149-36161.	3.4	249
47	The Big Bang of picorna-like virus evolution antedates the radiation of eukaryotic supergroups. Nature Reviews Microbiology, 2008, 6, 925-939.	28.6	248
48	Genomic determinants of sporulation in <i>Bacilli</i> and <i>Clostridia</i>: towards the minimal set of sporulationâ€specific genes. Environmental Microbiology, 2012, 14, 2870-2890.	3.8	235
49	Search for a 'Tree of Life' in the thicket of the phylogenetic forest. Journal of Biology, 2009, 8, 59.	2.7	234
50	Prokaryotic homologs of Argonaute proteins are predicted to function as key components of a novel system of defense against mobile genetic elements. Biology Direct, 2009, 4, 29.	4.6	232
51	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. CRISPR Journal, 2018, 1, 325-336.	2.9	232
52	The universal distribution of evolutionary rates of genes and distinct characteristics of eukaryotic genes of different apparent ages. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7273-7280.	7.1	227
53	Phylogenomics of Prokaryotic Ribosomal Proteins. PLoS ONE, 2012, 7, e36972.	2.5	227
54	Is evolution Darwinian or/and Lamarckian?. Biology Direct, 2009, 4, 42.	4.6	224

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55	Coelomata and Not Ecdysozoa: Evidence From Genome-Wide Phylogenetic Analysis. Genome Research, 2003, 14, 29-36.	5.5	221
56	The Tree and Net Components of Prokaryote Evolution. Genome Biology and Evolution, 2010, 2, 745-756.	2.5	221
57	Prediction of the Archaeal Exosome and Its Connections with the Proteasome and the Translation and Transcription Machineries by a Comparative-Genomic Approach. Genome Research, 2001, 11, 240-252.	5.5	219
58	Computational methods for Gene Orthology inference. Briefings in Bioinformatics, 2011, 12, 379-391.	6.5	217
59	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, Methylacidiphilum infernorum, a representative of the bacterial phylum Verrucomicrobia. Biology Direct, 2008, 3, 26.	4.6	216
60	Archaeal Clusters of Orthologous Genes (arCOGs): An Update and Application for Analysis of Shared Features between Thermococcales, Methanococcales, and Methanobacteriales. Life, 2015, 5, 818-840.	2.4	216
61	A low-polynomial algorithm for assembling clusters of orthologous groups from intergenomic symmetric best matches. Bioinformatics, 2010, 26, 1481-1487.	4.1	213
62	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. Nature Microbiology, 2017, 2, 17081.	13.3	213
63	Deinococcus geothermalis: The Pool of Extreme Radiation Resistance Genes Shrinks. PLoS ONE, 2007, 2, e955.	2.5	212
64	No simple dependence between protein evolution rate and the number of protein-protein interactions: only the most prolific interactors tend to evolve slowly. BMC Evolutionary Biology, 2003, 3, 1.	3.2	200
65	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 15193-15199.	7.1	196
66	Ongoing global and regional adaptive evolution of SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	196
67	Photosystem I gene cassettes are present in marine virus genomes. Nature, 2009, 461, 258-262.	27.8	195
68	Conservation and Coevolution in the Scale-Free Human Gene Coexpression Network. Molecular Biology and Evolution, 2004, 21, 2058-2070.	8.9	192
69	The origins of phagocytosis and eukaryogenesis. Biology Direct, 2009, 4, 9.	4.6	190
70	Microbial genome analysis: the COG approach. Briefings in Bioinformatics, 2019, 20, 1063-1070.	6.5	186
71	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	2.1	184
72	Estimating the number of protein folds and families from complete genome data 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 299, 897-905.	4.2	182

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73	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. MBio, 2017, 8, .	4.1	181
74	Duplicated genes evolve slower than singletons despite the initial rate increase. BMC Evolutionary Biology, 2004, 4, 22.	3.2	176
75	Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. Biology Direct, 2006, 1, 34.	4.6	176
76	On the origin of the translation system and the genetic code in the RNA world by means of natural selection, exaptation, and subfunctionalization. Biology Direct, 2007, 2, 14.	4.6	173
77	Genomes in turmoil: quantification of genome dynamics in prokaryote supergenomes. BMC Biology, 2014, 12, 66.	3.8	170
78	Connected gene neighborhoods in prokaryotic genomes. Nucleic Acids Research, 2002, 30, 2212-2223.	14.5	167
79	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. Nucleic Acids Research, 2005, 33, 4626-4638.	14.5	165
80	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. Biology Direct, 2007, 2, 33.	4.6	164
81	Expanded diversity of Asgard archaea and their relationships with eukaryotes. Nature, 2021, 593, 553-557.	27.8	161
82	Three distinct modes of intron dynamics in the evolution of eukaryotes. Genome Research, 2007, 17, 1034-1044.	5.5	159
83	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. Nature Reviews Genetics, 2020, 21, 119-131.	16.3	159
84	Birth and death of protein domains: a simple model of evolution explains power law behavior. BMC Evolutionary Biology, 2002, 2, 18.	3.2	158
85	The basic building blocks and evolution of CRISPRâ€"Cas systems. Biochemical Society Transactions, 2013, 41, 1392-1400.	3.4	157
86	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	2.1	157
87	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. Nature Microbiology, 2020, 5, 1262-1270.	13.3	156
88	Origin of giant viruses from smaller DNA viruses not from a fourth domain of cellular life. Virology, 2014, 466-467, 38-52.	2.4	154
89	Distribution of Protein Folds in the Three Superkingdoms of Life. Genome Research, 1999, 9, 17-26.	5.5	154
90	The Deep Archaeal Roots of Eukaryotes. Molecular Biology and Evolution, 2008, 25, 1619-1630.	8.9	153

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91	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	2.1	153
92	Comparative genomics of Thermus thermophilus and Deinococcus radiodurans: divergent routes of adaptation to thermophily and radiation resistance. BMC Evolutionary Biology, 2005, 5, 57.	3.2	152
93	Constraints and plasticity in genome and molecular-phenome evolution. Nature Reviews Genetics, 2010, 11, 487-498.	16.3	152
94	Evolutionary primacy of sodium bioenergetics. Biology Direct, 2008, 3, 13.	4.6	144
95	Updated clusters of orthologous genes for Archaea: a complex ancestor of the Archaea and the byways of horizontal gene transfer. Biology Direct, 2012, 7, 46.	4.6	142
96	Systematic prediction of genes functionally linked to CRISPR-Cas systems by gene neighborhood analysis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5307-E5316.	7.1	138
97	Genome sequence of the deep-sea Â-proteobacterium Idiomarina loihiensis reveals amino acid fermentation as a source of carbon and energy. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 18036-18041.	7.1	135
98	Evolution of mosaic operons by horizontal gene transfer and gene displacement in situ. Genome Biology, 2003, 4, R55.	9.6	134
99	Global Analysis of Posttranslational Protein Arginylation. PLoS Biology, 2007, 5, e258.	5.6	132
100	Theory of prokaryotic genome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11399-11407.	7.1	125
101	Rickettsiae and Chlamydiae: evidence of horizontal gene transfer and gene exchange. Trends in Genetics, 1999, 15, 173-175.	6.7	124
102	Trends in Prokaryotic Evolution Revealed by Comparison of Closely Related Bacterial and Archaeal Genomes. Journal of Bacteriology, 2009, 191, 65-73.	2.2	121
103	Non-homologous isofunctional enzymes: A systematic analysis of alternative solutions in enzyme evolution. Biology Direct, 2010, 5, 31.	4.6	119
104	Evolution of microbes and viruses: a paradigm shift in evolutionary biology?. Frontiers in Cellular and Infection Microbiology, 2012, 2, 119.	3.9	119
105	<i>Cressdnaviricota</i> : a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. Journal of Virology, 2020, 94, .	3.4	118
106	â€˜ARMANâ€™ archaea depend on association with euryarchaeal host in culture and in situ. Nature Communications, 2017, 8, 60.	12.8	116
107	Viral Diversity Threshold for Adaptive Immunity in Prokaryotes. MBio, 2012, 3, e00456-12.	4.1	114
108	Purifying and directional selection in overlapping prokaryotic genes. Trends in Genetics, 2002, 18, 228-232.	6.7	110

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109	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. Genome Research, 2001, 11, 555-565.	5.5	110
110	Identification of Novel Positive-Strand RNA Viruses by Metagenomic Analysis of Archaea-Dominated Yellowstone Hot Springs. Journal of Virology, 2012, 86, 5562-5573.	3.4	107
111	No evidence of inhibition of horizontal gene transfer by CRISPRâ€"Cas on evolutionary timescales. ISME Journal, 2015, 9, 2021-2027.	9.8	105
112	Classify viruses â€" the gain is worth the pain. Nature, 2019, 566, 318-320.	27.8	104
113	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. Biology Direct, 2013, 8, 9.	4.6	102
114	Microevolutionary Genomics of Bacteria. Theoretical Population Biology, 2002, 61, 435-447.	1.1	100
115	Congruent evolution of different classes of non-coding DNA in prokaryotic genomes. Nucleic Acids Research, 2002, 30, 4264-4271.	14.5	99
116	Towards understanding the first genome sequence of a crenarchaeon by genome annotation using clusters of orthologous groups of proteins (COGs). Genome Biology, 2000, 1, research0009.1.	9.6	96
117	Evolution of the genetic code: partial optimization of a random code for robustness to translation error in a rugged fitness landscape. Biology Direct, 2007, 2, 24.	4.6	96
118	A Tight Link between Orthologs and Bidirectional Best Hits in Bacterial and Archaeal Genomes. Genome Biology and Evolution, 2012, 4, 1286-1294.	2.5	96
119	Genome-Wide Molecular Clock and Horizontal Gene Transfer in Bacterial Evolution. Journal of Bacteriology, 2004, 186, 6575-6585.	2.2	93
120	Scale-free networks in biology: new insights into the fundamentals of evolution?. BioEssays, 2002, 24, 105-109.	2.5	92
121	Evolutionary systems biology: links between gene evolution and function. Current Opinion in Biotechnology, 2006, 17, 481-487.	6.6	90
122	Nature and Intensity of Selection Pressure on CRISPR-Associated Genes. Journal of Bacteriology, 2012, 194, 1216-1225.	2.2	90
123	Evolutionary Dynamics of the Prokaryotic Adaptive Immunity System CRISPR-Cas in an Explicit Ecological Context. Journal of Bacteriology, 2013, 195, 3834-3844.	2.2	87
124	Inevitability of Genetic Parasites. Genome Biology and Evolution, 2016, 8, 2856-2869.	2.5	85
125	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. MBio, 2019, 10, .	4.1	85
126	Analysis of metagenome-assembled viral genomes from the human gut reveals diverse putative CrAss-like phages with unique genomic features. Nature Communications, 2021, 12, 1044.	12.8	80

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127	Evolution of gene fusions: horizontal transfer versus independent events. Genome Biology, 2002, 3, research0024.1.	9.6	78
128	Seeker: alignment-free identification of bacteriophage genomes by deep learning. Nucleic Acids Research, 2020, 48, e121-e121.	14.5	78
129	Physical foundations of biological complexity. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8678-E8687.	7.1	77
130	From Complete Genomes to Measures of Substitution Rate Variability Within and Between Proteins. Genome Research, 2000, 10, 991-1000.	5.5	76
131	Potential genomic determinants of hyperthermophily. Trends in Genetics, 2003, 19, 172-176.	6.7	74
132	Unifying measures of gene function and evolution. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 1507-1515.	2.6	74
133	Ancient Gene Capture and Recent Gene Loss Shape the Evolution of Orthopoxvirus-Host Interaction Genes. MBio, 2021, 12, e0149521.	4.1	74
134	Gene conversions in genes encoding outer-membrane proteins in H. pylori and C. pneumoniae. Trends in Genetics, 2001, 17, 7-10.	6.7	73
135	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium Anoxybacillus flavithermus WK1. Genome Biology, 2008, 9, R161.	9.6	71
136	Arginyltransferase Is an ATP-Independent Self-Regulating Enzyme that Forms Distinct Functional Complexes InÂVivo. Chemistry and Biology, 2011, 18, 121-130.	6.0	71
137	Babela massiliensis, a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. Biology Direct, 2015, 10, 13.	4.6	71
138	Gene gain and loss push prokaryotes beyond the homologous recombination barrier and accelerate genome sequence divergence. Nature Communications, 2019, 10, 5376.	12.8	71
139	Role of Hypermutability in the Evolution of the Genus<i>Oenococcus</i>. Journal of Bacteriology, 2008, 190, 564-570.	2.2	70
140	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2015, 290, 18678-18698.	3.4	70
141	Evolutionarily conserved genes preferentially accumulate introns. Genome Research, 2007, 17, 1045-1050.	5.5	68
142	Patterns of intron gain and conservation in eukaryotic genes. BMC Evolutionary Biology, 2007, 7, 192.	3.2	67
143	Predictability of Evolutionary Trajectories in Fitness Landscapes. PLoS Computational Biology, 2011, 7, e1002302.	3.2	67
144	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antivirus defense. Nucleic Acids Research, 2020, 48, 8828-8847.	14.5	66

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145	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. Cell Reports, 2013, 4, 938-944.	6.4	64
146	Drastic neofunctionalization associated with evolution of the timezyme AANAT 500 Mya. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 314-319.	7.1	64
147	Machine-learning approach expands the repertoire of anti-CRISPR protein families. Nature Communications, 2020, 11, 3784.	12.8	64
148	Ecdysozoan Clade Rejected by Genome-Wide Analysis of Rare Amino Acid Replacements. Molecular Biology and Evolution, 2007, 24, 1080-1090.	8.9	63
149	Universal distribution of protein evolution rates as a consequence of protein folding physics. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2983-2988.	7.1	63
150	Computational approaches for the analysis of gene neighbourhoods in prokaryotic genomes. Briefings in Bioinformatics, 2004, 5, 131-149.	6.5	62
151	The Vast, Conserved Mammalian lincRNome. PLoS Computational Biology, 2013, 9, e1002917.	3.2	62
152	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2021, 166, 3513-3566.	2.1	62
153	Gene Frequency Distributions Reject a Neutral Model of Genome Evolution. Genome Biology and Evolution, 2013, 5, 233-242.	2.5	61
154	Phylogenomics of Cas4 family nucleases. BMC Evolutionary Biology, 2017, 17, 232.	3.2	61
155	Inevitability of the emergence and persistence of genetic parasites caused by evolutionary instability of parasite-free states. Biology Direct, 2017, 12, 31.	4.6	59
156	The fundamental units, processes and patterns of evolution, and the Tree of Life conundrum. Biology Direct, 2009, 4, 33.	4.6	52
157	Simple stochastic birth and death models of genome evolution: was there enough time for us to evolve?. Bioinformatics, 2003, 19, 1889-1900.	4.1	51
158	ATGC: a database of orthologous genes from closely related prokaryotic genomes and a research platform for microevolution of prokaryotes. Nucleic Acids Research, 2009, 37, D448-D454.	14.5	49
159	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. Extremophiles, 2014, 18, 877-893.	2.3	48
160	Gene family evolution: an in-depth theoretical and simulation analysis of non-linear birth-death-innovation models. BMC Evolutionary Biology, 2004, 4, 32.	3.2	47
161	Evolution of the CRISPR-Cas adaptive immunity systems in prokaryotes: models and observations on virusâ€“host coevolution. Molecular BioSystems, 2015, 11, 20-27.	2.9	47
162	Reconstruction of the evolution of microbial defense systems. BMC Evolutionary Biology, 2017, 17, 94.	3.2	46

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163	Grammar of protein domain architectures. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3636-3645.	7.1	46
164	Seeing the Tree of Life behind the phylogenetic forest. BMC Biology, 2013, 11, 46.	3.8	45
165	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. RNA Biology, 2019, 16, 435-448.	3.1	45
166	Translational coupling via termination-reinitiation in archaea and bacteria. Nature Communications, 2019, 10, 4006.	12.8	45
167	Evolutionary Dynamics of N-Glycosylation Sites of Influenza Virus Hemagglutinin. PLOS Currents, 2009, 1, RRN1001.	1.4	45
168	Virus-host arms race at the joint origin of multicellularity and programmed cell death. Cell Cycle, 2014, 13, 3083-3088.	2.6	44
169	Diverse functions of homologous actin isoforms are defined by their nucleotide, rather than their amino acid sequence. ELife, 2017, 6, .	6.0	44
170	Evolutionary plasticity of protein families: Coupling between sequence and structure variation. Proteins: Structure, Function and Bioinformatics, 2005, 61, 535-544.	2.6	43
171	Analysis of Rare Amino Acid Replacements Supports the Coelomata Clade. Molecular Biology and Evolution, 2007, 24, 2594-2597.	8.9	41
172	Universal Pacemaker of Genome Evolution. PLoS Computational Biology, 2012, 8, e1002785.	3.2	41
173	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. Journal of Bacteriology, 2018, 200, .	2.2	41
174	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. MBio, 2019, 10, .	4.1	41
175	Two fundamentally different classes of microbial genes. Nature Microbiology, 2017, 2, 16208.	13.3	39
176	Stability along with Extreme Variability in Core Genome Evolution. Genome Biology and Evolution, 2013, 5, 1393-1402.	2.5	38
177	ATGC database and ATGC-COGs: an updated resource for micro- and macro-evolutionary studies of prokaryotic genomes and protein family annotation. Nucleic Acids Research, 2017, 45, D210-D218.	14.5	38
178	Integrated mobile genetic elements in Thaumarchaeota. Environmental Microbiology, 2019, 21, 2056-2078.	3.8	38
179	Mutationâ€"selection balance and compensatory mechanisms in tumour evolution. Nature Reviews Genetics, 2021, 22, 251-262.	16.3	38
180	An Insertion in the Catalytic Trigger Loop Gates the Secondary Channel of RNA Polymerase. Journal of Molecular Biology, 2013, 425, 82-93.	4.2	37

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181	Constant relative rate of protein evolution and detection of functional diversification among bacterial, archaeal and eukaryotic proteins. Genome Biology, 2001, 2, research0053.1.	9.6	36
182	Comparable contributions of structural-functional constraints and expression level to the rate of protein sequence evolution. Biology Direct, 2008, 3, 40.	4.6	36
183	Evolution of DNA packaging in gene transfer agents. Virus Evolution, 2021, 7, veab015.	4.9	36
184	Positive and strongly relaxed purifying selection drive the evolution of repeats in proteins. Nature Communications, 2016, 7, 13570.	12.8	35
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