Eugene V Koonin

List of Publications by Year
in descending order

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576 papers	103,839 citations	191 150 h-index	289 293 g-index
695 all docs	695 docs citations	695 times ranked	66322 citing authors

#	ARTICLE	IF	CITATIONS
1	The COG database: an updated version includes eukaryotes. BMC Bioinformatics, 2003, 4, 41.	1.2	3,913
2	The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Research, 2000, 28, 33-36.	6.5	3,734
3	Cpf1 Is a Single RNA-Guided Endonuclease of a Class 2 CRISPR-Cas System. Cell, 2015, 163, 759-771.	13.5	3,558
4	A Genomic Perspective on Protein Families. Science, 1997, 278, 631-637.	6.0	3,352
5	Nucleic acid detection with CRISPR-Cas13a/C2c2. Science, 2017, 356, 438-442.	6.0	2,275
6	In vivo genome editing using Staphylococcus aureus Cas9. Nature, 2015, 520, 186-191.	13.7	2,237
7	Small CRISPR RNAs Guide Antiviral Defense in Prokaryotes. Science, 2008, 321, 960-964.	6.0	2,138
8	An updated evolutionary classification of CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2015, 13, 722-736.	13.6	2,081
9	Evolution and classification of the CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2011, 9, 467-477.	13.6	2,078
10	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science, 2016, 353, aaf5573.	6.0	1,647
11	Evolutionary classification of CRISPRâ€“Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	13.6	1,427
12	Bacterial Rhodopsin: Evidence for a New Type of Phototrophy in the Sea. Science, 2000, 289, 1902-1906.	6.0	1,357
13	Expanded microbial genome coverage and improved protein family annotation in the COG database. Nucleic Acids Research, 2015, 43, D261-D269.	6.5	1,345
14	Orthologs, Paralogs, and Evolutionary Genomics. Annual Review of Genetics, 2005, 39, 309-338.	3.2	1,084
15	Diversity, classification and evolution of CRISPR-Cas systems. Current Opinion in Microbiology, 2017, 37, 67-78.	2.3	1,076
16	Horizontal Gene Transfer in Prokaryotes: Quantification and Classification. Annual Review of Microbiology, 2001, 55, 709-742.	2.9	1,024
17	Evolution and Taxonomy of Positive-Strand RNA Viruses: Implications of Comparative Analysis of Amino Acid Sequences. Critical Reviews in Biochemistry and Molecular Biology, 1993, 28, 375-430.	2.3	999
18	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. Molecular Cell, 2015, 60, 385-397.	4.5	971

#	ARTICLE	IF	CITATIONS
19	A putative RNA-interference-based immune system in prokaryotes: computational analysis of the predicted enzymatic machinery, functional analogies with eukaryotic RNAi, and hypothetical mechanisms of action. Biology Direct, 2006, 1, 7.	1.9	961
20	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. Genome Biology, 2004, 5, R7.	13.9	814
21	Diversity and evolution of class 2 CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2017, 15, 169-182.	13.6	792
22	Evolutionary history and higher order classification of AAA+ ATPases. Journal of Structural Biology, 2004, 146, 11-31.	1.3	711
23	A superfamily of conserved domains in DNA damageâ€•responsive cell cycle checkpoint proteins. FASEB Journal, 1997, 11, 68-76.	0.2	684
24	Genomics of bacteria and archaea: the emerging dynamic view of the prokaryotic world. Nucleic Acids Research, 2008, 36, 6688-6719.	6.5	642
25	Selection in the evolution of gene duplications. Genome Biology, 2002, 3, research0008.1.	13.9	625
26	Novel domains of the prokaryotic two-component signal transduction systems. FEMS Microbiology Letters, 2001, 203, 11-21.	0.7	597
27	Virus taxonomy in the age of metagenomics. Nature Reviews Microbiology, 2017, 15, 161-168.	13.6	590
28	Comparative genomics, minimal gene-sets and the last universal common ancestor. Nature Reviews Microbiology, 2003, 1, 127-136.	13.6	582
29	Conserved sequence motifs in the initiator proteins for rolling circle DNA replication encoded by diverse replicons from eubacteria, eucaryotes and archaebacteria. Nucleic Acids Research, 1992, 20, 3279-3285.	6.5	567
30	The ancient Virus World and evolution of cells. Biology Direct, 2006, 1, 29.	1.9	559
31	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. Cell, 2016, 165, 949-962.	13.5	552
32	Evolutionary genomics of nucleo-cytoplasmic large DNA viruses. Virus Research, 2006, 117, 156-184.	1.1	541
33	The structure of the protein universe and genome evolution. Nature, 2002, 420, 218-223.	13.7	536
34	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. Science, 2016, 353, aad5147.	6.0	523
35	Functional and evolutionary implications of gene orthology. Nature Reviews Genetics, 2013, 14, 360-366.	7.7	516
36	Origin of a substantial fraction of human regulatory sequences from transposable elements. Trends in Genetics, 2003, 19, 68-72.	2.9	511

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37	The virophage as a unique parasite of the giant mimivirus. Nature, 2008, 455, 100-104.	13.7	505
38	Common Origin of Four Diverse Families of Large Eukaryotic DNA Viruses. Journal of Virology, 2001, 75, 11720-11734.	1.5	495
39	Viral proteins containing the purine NTP-binding sequence pattern. Nucleic Acids Research, 1989, 17, 8413-8438.	6.5	450
40	RNA-guided DNA insertion with CRISPR-associated transposases. Science, 2019, 365, 48-53.	6.0	448
41	Cas13b Is a Type VI-B CRISPR-Associated RNA-Guided RNase Differentially Regulated by Accessory Proteins Csx27 and Csx28. Molecular Cell, 2017, 65, 618-630.e7.	4.5	445
42	Origins and evolution of eukaryotic RNA interference. Trends in Ecology and Evolution, 2008, 23, 578-587.	4.2	442
43	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. Nucleic Acids Research, 2021, 49, D274-D281.	6.5	441
44	Introns and the origin of nucleusâ€"cytosol compartmentalization. Nature, 2006, 440, 41-45.	13.7	438
45	The DNA-repair protein AlkB, EGL-9, and leprecan define new families of 2-oxoglutarate- and iron-dependent dioxygenases. Genome Biology, 2001, 2, research0007.1.	13.9	437
46	Minimum Information about an Uncultivated Virus Genome (MIUViG). Nature Biotechnology, 2019, 37, 29-37.	9.4	414
47	Origins and evolution of viruses of eukaryotes: The ultimate modularity. Virology, 2015, 479-480, 2-25.	1.1	413
48	STAND, a Class of P-Loop NTPases Including Animal and Plant Regulators of Programmed Cell Death: Multiple, Complex Domain Architectures, Unusual Phyletic Patterns, and Evolution by Horizontal Gene Transfer. Journal of Molecular Biology, 2004, 343, 1-28.	2.0	407
49	Classification and evolution of type II CRISPR-Cas systems. Nucleic Acids Research, 2014, 42, 6091-6105.	6.5	401
50	The evolutionary journey of Argonaute proteins. Nature Structural and Molecular Biology, 2014, 21, 743-753.	3.6	400
51	Comprehensive comparative-genomic analysis of Type 2 toxin-antitoxin systems and related mobile stress response systems in prokaryotes. Biology Direct, 2009, 4, 19.	1.9	390
52	Giant Marseillevirus highlights the role of amoebae as a melting pot in emergence of chimeric microorganisms. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21848-21853.	3.3	385
53	Origins and Evolution of the Global RNA Virome. MBio, 2018, 9, .	1.8	383
54	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. Biology Direct, 2011, 6, 38.	1.9	379

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55	Global Organization and Proposed Megataxonomy of the Virus World. Microbiology and Molecular Biology Reviews, 2020, 84, .	2.9	378
56	Gene Loss, Protein Sequence Divergence, Gene Dispensability, Expression Level, and Interactivity Are Correlated in Eukaryotic Evolution. Genome Research, 2003, 13, 2229-2235.	2.4	367
57	Comparative genomics of defense systems in archaea and bacteria. Nucleic Acids Research, 2013, 41, 4360-4377.	6.5	365
58	â€¦Functional motifsâ€¦. Nature Genetics, 1996, 13, 266-268.	9.4	362
59	Orthology, paralogy and proposed classification for paralog subtypes. Trends in Genetics, 2002, 18, 619-620.	2.9	360
60	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. Journal of Bacteriology, 2011, 193, 6039-6056.	1.0	358
61	Cas13d Is a Compact RNA-Targeting Type VI CRISPR Effector Positively Modulated by a WYL-Domain-Containing Accessory Protein. Molecular Cell, 2018, 70, 327-339.e5.	4.5	356
62	'Conserved hypothetical' proteins: prioritization of targets for experimental study. Nucleic Acids Research, 2004, 32, 5452-5463.	6.5	346
63	Functionally diverse type V CRISPR-Cas systems. Science, 2019, 363, 88-91.	6.0	342
64	Origin of first cells at terrestrial, anoxic geothermal fields. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E821-30.	3.3	341
65	Toprim--a conserved catalytic domain in type IA and II topoisomerases, DnaG-type primases, OLD family nucleases and RecR proteins. Nucleic Acids Research, 1998, 26, 4205-4213.	6.5	338
66	Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. Trends in Genetics, 1998, 14, 442-444.	2.9	337
67	A new superfamily of putative NTP-binding domains encoded by genomes of small DNA and RNA viruses. FEBS Letters, 1990, 262, 145-148.	1.3	336
68	Genome trees and the tree of life. Trends in Genetics, 2002, 18, 472-479.	2.9	336
69	Putative papain-related thiol proteases of positive-strand RNA viruses Identification of rubi- and aphthovirus proteases and delineation of a novel conserved domain associated with proteases of rubi-, Î±- and coronaviruses. FEBS Letters, 1991, 288, 201-205.	1.3	333
70	Prokaryotic Virus Orthologous Groups (pVOGs): a resource for comparative genomics and protein family annotation. Nucleic Acids Research, 2017, 45, D491-D498.	6.5	333
71	A DNA repair system specific for thermophilic Archaea and bacteria predicted by genomic context analysis. Nucleic Acids Research, 2002, 30, 482-496.	6.5	331
72	On the origin of genomes and cells within inorganic compartments. Trends in Genetics, 2005, 21, 647-654.	2.9	331

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73	Eukaryotic large nucleo-cytoplasmic DNA viruses: Clusters of orthologous genes and reconstruction of viral genome evolution. Virology Journal, 2009, 6, 223.	1.4	321
74	Who's your neighbor? New computational approaches for functional genomics. Nature Biotechnology, 2000, 18, 609-613.	9.4	319
75	Algorithms for computing parsimonious evolutionary scenarios for genome evolution, the last universal common ancestor and dominance of horizontal gene transfer in the evolution of prokaryotes. BMC Evolutionary Biology, 2003, 3, 2.	3.2	316
76	Phylogeny of Cas9 determines functional exchangeability of dual-RNA and Cas9 among orthologous type II CRISPR-Cas systems. Nucleic Acids Research, 2014, 42, 2577-2590.	6.5	315
77	Construction and analysis of bacterial artificial chromosome libraries from a marine microbial assemblage. Environmental Microbiology, 2000, 2, 516-529.	1.8	313
78	Did DNA replication evolve twice independently?. Nucleic Acids Research, 1999, 27, 3389-3401.	6.5	312
79	Eukaryotic DNA Polymerases: Proposal for a Revised Nomenclature. Journal of Biological Chemistry, 2001, 276, 43487-43490.	1.6	307
80	Annotation and Classification of CRISPR-Cas Systems. Methods in Molecular Biology, 2015, 1311, 47-75.	0.4	304
81	Comparison of archaeal and bacterial genomes: computer analysis of protein sequences predicts novel functions and suggests a chimeric origin for the archaea. Molecular Microbiology, 1997, 25, 619-637.	1.2	302
82	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. Science, 2020, 369, 1077-1084.	6.0	302
83	HOWMANYGENESCANMAKE ACELL: The Minimal-Gene-Set Concept. Annual Review of Genomics and Human Genetics, 2000, 1, 99-116.	2.5	297
84	Origin and evolution of spliceosomal introns. Biology Direct, 2012, 7, 11.	1.9	292
85	Origin and evolution of the genetic code: The universal enigma. IUBMB Life, 2009, 61, 99-111.	1.5	288
86	Comparative genomics of the FtsK-HerA superfamily of pumping ATPases: implications for the origins of chromosome segregation, cell division and viral capsid packaging. Nucleic Acids Research, 2004, 32, 5260-5279.	6.5	284
87	The origin and early evolution of eukaryotes in the light of phylogenomics. Genome Biology, 2010, 11, 209.	13.9	282
88	New dimensions of the virus world discovered through metagenomics. Trends in Microbiology, 2010, 18, 11-19.	3.5	282
89	The cyanobacterial genome core and the origin of photosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13126-13131.	3.3	277
90	The Impact of Comparative Genomics on Our Understanding of Evolution. Cell, 2000, 101, 573-576.	13.5	273

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91	Genome Alignment, Evolution of Prokaryotic Genome Organization, and Prediction of Gene Function Using Genomic Context. Genome Research, 2001, 11, 356-372.	2.4	270
92	Genome reduction as the dominant mode of evolution. BioEssays, 2013, 35, 829-837.	1.2	267
93	Origins and evolution of CRISPR-Cas systems. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180087.	1.8	258
94	â€œMegaviralesâ€, a proposed new order for eukaryotic nucleocytoplasmic large DNA viruses. Archives of Virology, 2013, 158, 2517-2521.	0.9	256
95	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. Annual Review of Microbiology, 2017, 71, 233-261.	2.9	256
96	Engineering of CRISPR-Cas12b for human genome editing. Nature Communications, 2019, 10, 212.	5.8	249
97	A diverse superfamily of enzymes with ATPâ€dependent carboxylateâ€"amine/thiol ligase activity. Protein Science, 1997, 6, 2639-2643.	3.1	248
98	The Big Bang of picorna-like virus evolution antedates the radiation of eukaryotic supergroups. Nature Reviews Microbiology, 2008, 6, 925-939.	13.6	248
99	The origin of introns and their role in eukaryogenesis: a compromise solution to the introns-early versus introns-late debate?. Biology Direct, 2006, 1, 22.	1.9	247
100	Origin and evolution of the archaeo-eukaryotic primase superfamily and related palm-domain proteins: structural insights and new members. Nucleic Acids Research, 2005, 33, 3875-3896.	6.5	246
101	Discovery of an expansive bacteriophage family that includes the most abundant viruses from the human gut. Nature Microbiology, 2018, 3, 38-46.	5.9	245
102	Evolutionary Genomics of Lactic Acid Bacteria. Journal of Bacteriology, 2007, 189, 1199-1208.	1.0	242
103	A dual function of the CRISPRâ€"Cas system in bacterial antivirus immunity and DNA repair. Molecular Microbiology, 2011, 79, 484-502.	1.2	241
104	Abundance of type I toxinâ€"antitoxin systems in bacteria: searches for new candidates and discovery of novel families. Nucleic Acids Research, 2010, 38, 3743-3759.	6.5	237
105	Search for a 'Tree of Life' in the thicket of the phylogenetic forest. Journal of Biology, 2009, 8, 59.	2.7	234
106	Giant viruses with an expanded complement of translation system components. Science, 2017, 356, 82-85.	6.0	234
107	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.	1.9	232
108	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. CRISPR Journal, 2018, 1, 325-336.	1.4	232

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109	Phylogenomics of Prokaryotic Ribosomal Proteins. PLoS ONE, 2012, 7, e36972.	1.1	227
110	Is evolution Darwinian or/and Lamarckian?. Biology Direct, 2009, 4, 42.	1.9	224
111	The Tree and Net Components of Prokaryote Evolution. Genome Biology and Evolution, 2010, 2, 745-756.	1.1	221
112	Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. Biology Direct, 2013, 8, 15.	1.9	221
113	Analogous Enzymes: Independent Inventions in Enzyme Evolution. Genome Research, 1998, 8, 779-790.	2.4	220
114	Adaptations of the helix-grip fold for ligand binding and catalysis in the START domain superfamily. Proteins: Structure, Function and Bioinformatics, 2001, 43, 134-144.	1.5	218
115	Evolutionary connection between the catalytic subunits of DNA-dependent RNA polymerases and eukaryotic RNA-dependent RNA polymerases and the origin of RNA polymerases. BMC Structural Biology, 2003, 3, 1.	2.3	218
116	Computational methods for Gene Orthology inference. Briefings in Bioinformatics, 2011, 12, 379-391.	3.2	217
117	A conserved NTP-motif in putative helicases. Nature, 1988, 333, 22-22.	13.7	216
118	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.	1.1	216
119	Phylogeny of capsid proteins of rod-shaped and filamentous RNA plant viruses: Two families with distinct patterns of sequence and probably structure conservation. Virology, 1991, 184, 79-86.	1.1	214
120	Mammalian retrovirus-like protein PEG10 packages its own mRNA and can be pseudotyped for mRNA delivery. Science, 2021, 373, 882-889.	6.0	214
121	A low-polynomial algorithm for assembling clusters of orthologous groups from intergenomic symmetric best matches. Bioinformatics, 2010, 26, 1481-1487.	1.8	213
122	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. Nature Microbiology, 2017, 2, 17081.	5.9	213
123	Evolution of diverse cell division and vesicle formation systems in Archaea. Nature Reviews Microbiology, 2010, 8, 731-741.	13.6	212
124	Multiple origins of viral capsid proteins from cellular ancestors. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2401-E2410.	3.3	211
125	Recruitment of CRISPR-Cas systems by Tn7-like transposons. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7358-E7366.	3.3	210
126	CRISPRâ€“Cas in mobile genetic elements: counter-defence and beyond. Nature Reviews Microbiology, 2019, 17, 513-525.	13.6	205

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127	Virus World as an Evolutionary Network of Viruses and Capsidless Selfish Elements. Microbiology and Molecular Biology Reviews, 2014, 78, 278-303.	2.9	200
128	Evolutionary genomics of archaeal viruses: Unique viral genomes in the third domain of life. Virus Research, 2006, 117, 52-67.	1.1	198
129	A virocentric perspective on the evolution of life. Current Opinion in Virology, 2013, 3, 546-557.	2.6	198
130	Origin and Evolution of Eukaryotic Large Nucleo-Cytoplasmic DNA Viruses. Intervirology, 2010, 53, 284-292.	1.2	196
131	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.	3.3	196
132	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, .	3.3	196
133	Photosystem I gene cassettes are present in marine virus genomes. Nature, 2009, 461, 258-262.	13.7	195
134	Provirophages and transpovirons as the diverse mobilome of giant viruses. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18078-18083.	3.3	194
135	Darwinian evolution in the light of genomics. Nucleic Acids Research, 2008, 37, 1011-1034.	6.5	191
136	The origins of phagocytosis and eukaryogenesis. Biology Direct, 2009, 4, 9.	1.9	190
137	Metagenomics reshapes the concepts of RNA virus evolution by revealing extensive horizontal virus transfer. Virus Research, 2018, 244, 36-52.	1.1	190
138	A distinct abundant group of microbial rhodopsins discovered using functional metagenomics. Nature, 2018, 558, 595-599.	13.7	190
139	The rhomboids: a nearly ubiquitous family of intramembrane serine proteases that probably evolved by multiple ancient horizontal gene transfers. Genome Biology, 2003, 4, R19.	13.9	189
140	Differences in DNA methylation between human neuronal and glial cells are concentrated in enhancers and non-CpG sites. Nucleic Acids Research, 2014, 42, 109-127.	6.5	187
141	Evolution of genome architecture. International Journal of Biochemistry and Cell Biology, 2009, 41, 298-306.	1.2	186
142	Microbial genome analysis: the COG approach. Briefings in Bioinformatics, 2019, 20, 1063-1070.	3.2	186
143	Role of CED-4 in the activation of CED-3. Nature, 1997, 388, 728-729.	13.7	185
144	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. Archives of Virology, 2020, 165, 3023-3072.	0.9	184

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145	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. MBio, 2017, 8, .	1.8	181
146	A Novel Family of Sequence-specific Endoribonucleases Associated with the Clustered Regularly Interspaced Short Palindromic Repeats. Journal of Biological Chemistry, 2008, 283, 20361-20371.	1.6	177
147	Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. Biology Direct, 2006, 1, 34.	1.9	176
148	Viruses of archaea: Structural, functional, environmental and evolutionary genomics. Virus Research, 2018, 244, 181-193.	1.1	175
149	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.	1.9	173
150	Computer-assisted dissection of rolling circle DNA replication. BioSystems, 1993, 30, 241-268.	0.9	172
151	Polintons: a hotbed of eukaryotic virus, transposon and plasmid evolution. Nature Reviews Microbiology, 2015, 13, 105-115.	13.6	172
152	Novel Predicted RNA-Binding Domains Associated with the Translation Machinery. Journal of Molecular Evolution, 1999, 48, 291-302.	0.8	170
153	Genomes in turmoil: quantification of genome dynamics in prokaryote supergenomes. BMC Biology, 2014, 12, 66.	1.7	170
154	The enigmatic archaeal virosphere. Nature Reviews Microbiology, 2017, 15, 724-739.	13.6	169
155	Connected gene neighborhoods in prokaryotic genomes. Nucleic Acids Research, 2002, 30, 2212-2223.	6.5	167
156	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. Nucleic Acids Research, 2005, 33, 4626-4638.	6.5	165
157	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. Biology Direct, 2007, 2, 33.	1.9	164
158	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. Frontiers in Genetics, 2014, 5, 102.	1.1	164
159	A superfamily of archaeal, bacterial, and eukaryotic proteins homologous to animal transglutaminases. Protein Science, 1999, 8, 1714-1719.	3.1	161
160	Expanded diversity of Asgard archaea and their relationships with eukaryotes. Nature, 2021, 593, 553-557.	13.7	161
161	A Detailed History of Intron-rich Eukaryotic Ancestors Inferred from a Global Survey of 100 Complete Genomes. PLoS Computational Biology, 2011, 7, e1002150.	1.5	160
162	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. Nature Reviews Genetics, 2020, 21, 119-131.	7.7	159

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163	Birth and death of protein domains: a simple model of evolution explains power law behavior. BMC Evolutionary Biology, 2002, 2, 18.	3.2	158
164	CRISPR-Cas. RNA Biology, 2013, 10, 679-686.	1.5	158
165	The basic building blocks and evolution of CRISPRâ€"Cas systems. Biochemical Society Transactions, 2013, 41, 1392-1400.	1.6	157
166	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. Archives of Virology, 2018, 163, 2295-2310.	0.9	157
167	Casposons: a new superfamily of self-synthesizing DNA transposons at the origin of prokaryotic CRISPR-Cas immunity. BMC Biology, 2014, 12, 36.	1.7	156
168	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. Nature Microbiology, 2020, 5, 1262-1270.	5.9	156
169	Hidden evolutionary complexity of Nucleo-Cytoplasmic Large DNA viruses of eukaryotes. Virology Journal, 2012, 9, 161.	1.4	155
170	Programmable RNA targeting with the single-protein CRISPR effector Cas7-11. Nature, 2021, 597, 720-725.	13.7	155
171	Origin of giant viruses from smaller DNA viruses not from a fourth domain of cellular life. Virology, 2014, 466-467, 38-52.	1.1	154
172	Distribution of Protein Folds in the Three Superkingdoms of Life. Genome Research, 1999, 9, 17-26.	2.4	154
173	Beyond complete genomes: from sequence to structure and function. Current Opinion in Structural Biology, 1998, 8, 355-363.	2.6	153
174	The Deep Archaeal Roots of Eukaryotes. Molecular Biology and Evolution, 2008, 25, 1619-1630.	3.5	153
175	Evolution of protein domain promiscuity in eukaryotes. Genome Research, 2008, 18, 449-461.	2.4	153
176	Taxonomy of the order Mononegavirales: update 2018. Archives of Virology, 2018, 163, 2283-2294.	0.9	153
177	Functional Long Non-coding RNAs Evolve from Junk Transcripts. Cell, 2020, 183, 1151-1161.	13.5	153
178	Constraints and plasticity in genome and molecular-phenome evolution. Nature Reviews Genetics, 2010, 11, 487-498.	7.7	152
179	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. Science, 2021, 374, 57-65.	6.0	152
180	From complete genome sequence to â€˜completeâ€™ understanding?. Trends in Biotechnology, 2010, 28, 398-406.	4.9	151

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181	The Double-Stranded DNA Virosphere as a Modular Hierarchical Network of Gene Sharing. MBio, 2016, 7, .	1.8	151
182	Origin of viruses: primordial replicators recruiting capsids from hosts. Nature Reviews Microbiology, 2019, 17, 449-458.	13.6	151
183	A novel family of predicted phosphoesterases includes Drosophila prune protein and bacterial recJ exonuclease. Trends in Biochemical Sciences, 1998, 23, 17-19.	3.7	149
184	A superfamily of metalloenzymes unifies phosphopentomutase and cofactorâ€independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. Protein Science, 1998, 7, 1829-1835.	3.1	148
185	Evolutionary primacy of sodium bioenergetics. Biology Direct, 2008, 3, 13.	1.9	144
186	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.	1.9	142
187	Evolution of adaptive immunity from transposable elements combined with innate immune systems. Nature Reviews Genetics, 2015, 16, 184-192.	7.7	141
188	Eukaryotic translation elongation factor 1Î³ contains a glutathione transferase domainâ€"Study of a diverse, ancient protein super family using motif search and structural modeling. Protein Science, 1994, 3, 2045-2055.	3.1	140
189	Co-evolution of primordial membranes and membrane proteins. Trends in Biochemical Sciences, 2009, 34, 206-215.	3.7	140
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