

Eugene V Koonin

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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.

582 papers	74,841 citations	137 h-index	262 g-index
693 ext. papers	91,806 ext. citations	11.5 avg, IF	8.55 L-index

#	Paper	IF	Citations
582	The COG database: an updated version includes eukaryotes. <i>BMC Bioinformatics</i> , 2003 , 4, 41	3.6	3212
581	A genomic perspective on protein families. <i>Science</i> , 1997 , 278, 631-7	33.3	2787
580	The COG database: a tool for genome-scale analysis of protein functions and evolution. <i>Nucleic Acids Research</i> , 2000 , 28, 33-6	20.1	2692
579	Cpf1 is a single RNA-guided endonuclease of a class 2 CRISPR-Cas system. <i>Cell</i> , 2015 , 163, 759-71	56.2	2414
578	In vivo genome editing using <i>Staphylococcus aureus</i> Cas9. <i>Nature</i> , 2015 , 520, 186-91	50.4	1700
577	Small CRISPR RNAs guide antiviral defense in prokaryotes. <i>Science</i> , 2008 , 321, 960-4	33.3	1698
576	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2011 , 9, 467-77	22.2	1604
575	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015 , 13, 722-36	22.2	1434
574	Nucleic acid detection with CRISPR-Cas13a/C2c2. <i>Science</i> , 2017 , 356, 438-442	33.3	1240
573	Bacterial rhodopsin: evidence for a new type of phototrophy in the sea. <i>Science</i> , 2000 , 289, 1902-6	33.3	1143
572	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. <i>Science</i> , 2016 , 353, aaf5573	33.3	1037
571	Horizontal gene transfer in prokaryotes: quantification and classification. <i>Annual Review of Microbiology</i> , 2001 , 55, 709-42	17.5	859
570	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
569	Orthologs, paralogs, and evolutionary genomics. <i>Annual Review of Genetics</i> , 2005 , 39, 309-38	14.5	814
568	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
567	Evolution and taxonomy of positive-strand RNA viruses: implications of comparative analysis of amino acid sequences. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1993 , 28, 375-430	8.7	801
566	Diversity, classification and evolution of CRISPR-Cas systems. <i>Current Opinion in Microbiology</i> , 2017 , 37, 67-78	7.9	720

565	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015 , 60, 385-97	17.6	670
564	Evolutionary history and higher order classification of AAA+ ATPases. <i>Journal of Structural Biology</i> , 2004 , 146, 11-31	3.4	622
563	A superfamily of conserved domains in DNA damage- responsive cell cycle checkpoint proteins. <i>FASEB Journal</i> , 1997 , 11, 68-76	0.9	609
562	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. <i>Genome Biology</i> , 2004 , 5, R7	18.3	602
561	Novel domains of the prokaryotic two-component signal transduction systems. <i>FEMS Microbiology Letters</i> , 2001 , 203, 11-21	2.9	550
560	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
559	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017 , 15, 169-182	22.2	516
558	Genomics of bacteria and archaea: the emerging dynamic view of the prokaryotic world. <i>Nucleic Acids Research</i> , 2008 , 36, 6688-719	20.1	513
557	Conserved sequence motifs in the initiator proteins for rolling circle DNA replication encoded by diverse replicons from eubacteria, eucaryotes and archaebacteria. <i>Nucleic Acids Research</i> , 1992 , 20, 3279-85	20.1	502
556	Selection in the evolution of gene duplications. <i>Genome Biology</i> , 2002 , 3, RESEARCH0008	18.3	491
555	Comparative genomics, minimal gene-sets and the last universal common ancestor. <i>Nature Reviews Microbiology</i> , 2003 , 1, 127-36	22.2	468
554	Origin of a substantial fraction of human regulatory sequences from transposable elements. <i>Trends in Genetics</i> , 2003 , 19, 68-72	8.5	459
553	The structure of the protein universe and genome evolution. <i>Nature</i> , 2002 , 420, 218-23	50.4	456
552	Evolutionary genomics of nucleo-cytoplasmic large DNA viruses. <i>Virus Research</i> , 2006 , 117, 156-84	6.4	455
551	The ancient Virus World and evolution of cells. <i>Biology Direct</i> , 2006 , 1, 29	7.2	441
550	Common origin of four diverse families of large eukaryotic DNA viruses. <i>Journal of Virology</i> , 2001 , 75, 11720-34	6.6	419
549	The virophage as a unique parasite of the giant mimivirus. <i>Nature</i> , 2008 , 455, 100-4	50.4	389
548	Introns and the origin of nucleus-cytosol compartmentalization. <i>Nature</i> , 2006 , 440, 41-5	50.4	385

547	Viral proteins containing the purine NTP-binding sequence pattern. <i>Nucleic Acids Research</i> , 1989 , 17, 8413-40	20.1	378
546	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. <i>Science</i> , 2016 , 353, aad5147	33.3	378
545	Consensus statement: Virus taxonomy in the age of metagenomics. <i>Nature Reviews Microbiology</i> , 2017 , 15, 161-168	22.2	375
544	Crystal Structure of Cpf1 in Complex with Guide RNA and Target DNA. <i>Cell</i> , 2016 , 165, 949-62	56.2	362
543	BRCA1 protein products ... Functional motifs. <i>Nature Genetics</i> , 1996 , 13, 266-8	36.3	343
542	The DNA-repair protein AlkB, EGL-9, and leprecan define new families of 2-oxoglutarate- and iron-dependent dioxygenases. <i>Genome Biology</i> , 2001 , 2, RESEARCH0007	18.3	337
541	Functional and evolutionary implications of gene orthology. <i>Nature Reviews Genetics</i> , 2013 , 14, 360-6	30.1	327
540	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. <i>Journal of Molecular Biology</i> , 2004 , 343, 1-28	6.5	327
539	Origins and evolution of eukaryotic RNA interference. <i>Trends in Ecology and Evolution</i> , 2008 , 23, 578-87	10.9	326
538	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
537	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
536	Gene loss, protein sequence divergence, gene dispensability, expression level, and interactivity are correlated in eukaryotic evolution. <i>Genome Research</i> , 2003 , 13, 2229-35	9.7	314
535	Origins and evolution of viruses of eukaryotes: The ultimate modularity. <i>Virology</i> , 2015 , 479-480, 2-25	3.6	309
534	Orthology, paralogy and proposed classification for paralog subtypes. <i>Trends in Genetics</i> , 2002 , 18, 619-20	20.5	299
533	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
532	Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. <i>Trends in Genetics</i> , 1998 , 14, 442-4	8.5	294
531	Genome trees and the tree of life. <i>Trends in Genetics</i> , 2002 , 18, 472-9	8.5	292
530	Toprim--a conserved catalytic domain in type IA and II topoisomerases, DnaG-type primases, OLD family nucleases and RecR proteins. <i>Nucleic Acids Research</i> , 1998 , 26, 4205-13	20.1	290

529	Classification and evolution of type II CRISPR-Cas systems. <i>Nucleic Acids Research</i> , 2014 , 42, 6091-105	20.1	288
528	On the origin of genomes and cells within inorganic compartments. <i>Trends in Genetics</i> , 2005 , 21, 647-54	8.5	284
527	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-, alpha- and coronaviruses. <i>FEBS Letters</i> , 1991 , 288, 201-5	3.8	281
526	Did DNA replication evolve twice independently?. <i>Nucleic Acids Research</i> , 1999 , 27, 3389-401	20.1	280
525	'Conserved hypothetical' proteins: prioritization of targets for experimental study. <i>Nucleic Acids Research</i> , 2004 , 32, 5452-63	20.1	279
524	Construction and analysis of bacterial artificial chromosome libraries from a marine microbial assemblage. <i>Environmental Microbiology</i> , 2000 , 2, 516-29	5.2	277
523	A new superfamily of putative NTP-binding domains encoded by genomes of small DNA and RNA viruses. <i>FEBS Letters</i> , 1990 , 262, 145-8	3.8	276
522	Who's your neighbor? New computational approaches for functional genomics. <i>Nature Biotechnology</i> , 2000 , 18, 609-13	44.5	275
521	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
520	Comparison of archaeal and bacterial genomes: computer analysis of protein sequences predicts novel functions and suggests a chimeric origin for the archaea. <i>Molecular Microbiology</i> , 1997 , 25, 619-37	4.1	271
519	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. <i>BMC Evolutionary Biology</i> , 2003 , 3, 2	3	271
518	Giant Marseillevirus highlights the role of amoebae as a melting pot in emergence of chimeric microorganisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 21848-53	11.5	270
517	Eukaryotic DNA polymerases: proposal for a revised nomenclature. <i>Journal of Biological Chemistry</i> , 2001 , 276, 43487-90	5.4	264
516	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , 2013 , 41, 4360-77	20.1	255
515	Origin of first cells at terrestrial, anoxic geothermal fields. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E821-30	11.5	254
514	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
513	The origin and early evolution of eukaryotes in the light of phylogenomics. <i>Genome Biology</i> , 2010 , 11, 209	18.3	244
512	How many genes can make a cell: the minimal-gene-set concept. <i>Annual Review of Genomics and Human Genetics</i> , 2000 , 1, 99-116	9.7	241

511	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 743-53.6	17.6	240
510	Genome Alignment, Evolution of Prokaryotic Genome Organization, and Prediction of Gene Function Using Genomic Context. <i>Genome Research</i> , 2001 , 11, 356-372	9.7	237
509	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
508	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
507	RNA-guided DNA insertion with CRISPR-associated transposases. <i>Science</i> , 2019 , 365, 48-53	33.3	232
506	Eukaryotic large nucleo-cytoplasmic DNA viruses: clusters of orthologous genes and reconstruction of viral genome evolution. <i>Virology Journal</i> , 2009 , 6, 223	6.1	229
505	The impact of comparative genomics on our understanding of evolution. <i>Cell</i> , 2000 , 101, 573-6	56.2	227
504	Origins and Evolution of the Global RNA Virome. <i>MBio</i> , 2018 , 9,	7.8	219
503	New dimensions of the virus world discovered through metagenomics. <i>Trends in Microbiology</i> , 2010 , 18, 11-9	12.4	217
502	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
501	Origin and evolution of the genetic code: the universal enigma. <i>IUBMB Life</i> , 2009 , 61, 99-111	4.7	215
500	A diverse superfamily of enzymes with ATP-dependent carboxylate-amine/thiol ligase activity. <i>Protein Science</i> , 1997 , 6, 2639-43	6.3	213
499	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
498	Evolutionary genomics of lactic acid bacteria. <i>Journal of Bacteriology</i> , 2007 , 189, 1199-208	3.5	209
497	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
496	Search for a 'Tree of Life' in the thicket of the phylogenetic forest. <i>Journal of Biology</i> , 2009 , 8, 59		204
495	The Big Bang of picorna-like virus evolution antedates the radiation of eukaryotic supergroups. <i>Nature Reviews Microbiology</i> , 2008 , 6, 925-39	22.2	204
494	Analogous enzymes: independent inventions in enzyme evolution. <i>Genome Research</i> , 1998 , 8, 779-90	9.7	204

493	Origin and evolution of the archaeo-eukaryotic primase superfamily and related palm-domain proteins: structural insights and new members. <i>Nucleic Acids Research</i> , 2005 , 33, 3875-96	20.1	201
492	Origin and evolution of spliceosomal introns. <i>Biology Direct</i> , 2012 , 7, 11	7.2	199
491	A dual function of the CRISPR-Cas system in bacterial antiviral immunity and DNA repair. <i>Molecular Microbiology</i> , 2011 , 79, 484-502	4.1	199
490	The origin of introns and their role in eukaryogenesis: a compromise solution to the introns-early versus introns-late debate?. <i>Biology Direct</i> , 2006 , 1, 22	7.2	198
489	Phylogeny of capsid proteins of rod-shaped and filamentous RNA plant viruses: two families with distinct patterns of sequence and probably structure conservation. <i>Virology</i> , 1991 , 184, 79-86	3.6	196
488	Adaptations of the helix-grip fold for ligand binding and catalysis in the START domain superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 43, 134-44	4.2	194
487	"Megavirales", a proposed new order for eukaryotic nucleocytoplasmic large DNA viruses. <i>Archives of Virology</i> , 2013 , 158, 2517-21	2.6	193
486	Prokaryotic Virus Orthologous Groups (pVOGs): a resource for comparative genomics and protein family annotation. <i>Nucleic Acids Research</i> , 2017 , 45, D491-D498	20.1	189
485	Genome reduction as the dominant mode of evolution. <i>BioEssays</i> , 2013 , 35, 829-37	4.1	188
484	Is evolution Darwinian or/and Lamarckian?. <i>Biology Direct</i> , 2009 , 4, 42	7.2	184
483	The tree and net components of prokaryote evolution. <i>Genome Biology and Evolution</i> , 2010 , 2, 745-56	3.9	182
482	Phylogenomics of prokaryotic ribosomal proteins. <i>PLoS ONE</i> , 2012 , 7, e36972	3.7	180
481	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019 , 37, 29-37	44.5	180
480	Global Organization and Proposed Megataxonomy of the Virus World. <i>Microbiology and Molecular Biology Reviews</i> , 2020 , 84,	13.2	178
479	The rhomboids: a nearly ubiquitous family of intramembrane serine proteases that probably evolved by multiple ancient horizontal gene transfers. <i>Genome Biology</i> , 2003 , 4, R19	18.3	178
478	Evolutionary connection between the catalytic subunits of DNA-dependent RNA polymerases and eukaryotic RNA-dependent RNA polymerases and the origin of RNA polymerases. <i>BMC Structural Biology</i> , 2003 , 3, 1	2.7	175
477	Role of CED-4 in the activation of CED-3. <i>Nature</i> , 1997 , 388, 728-9	50.4	174
476	Evolutionary genomics of archaeal viruses: unique viral genomes in the third domain of life. <i>Virus Research</i> , 2006 , 117, 52-67	6.4	173

475	Functionally diverse type V CRISPR-Cas systems. <i>Science</i> , 2019 , 363, 88-91	33.3	169
474	Annotation and Classification of CRISPR-Cas Systems. <i>Methods in Molecular Biology</i> , 2015 , 1311, 47-75	1.4	168
473	Evolution of diverse cell division and vesicle formation systems in Archaea. <i>Nature Reviews Microbiology</i> , 2010 , 8, 731-41	22.2	165
472	Darwinian evolution in the light of genomics. <i>Nucleic Acids Research</i> , 2009 , 37, 1011-34	20.1	164
471	Virus world as an evolutionary network of viruses and capsidless selfish elements. <i>Microbiology and Molecular Biology Reviews</i> , 2014 , 78, 278-303	13.2	160
470	Photosystem I gene cassettes are present in marine virus genomes. <i>Nature</i> , 2009 , 461, 258-262	50.4	160
469	Computational methods for Gene Orthology inference. <i>Briefings in Bioinformatics</i> , 2011 , 12, 379-91	13.4	158
468	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
467	Origin and evolution of eukaryotic large nucleo-cytoplasmic DNA viruses. <i>Intervirology</i> , 2010 , 53, 284-92	2.5	156
466	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
465	A conserved NTP-motif in putative helicases. <i>Nature</i> , 1988 , 333, 22	50.4	155
464	A low-polynomial algorithm for assembling clusters of orthologous groups from intergenomic symmetric best matches. <i>Bioinformatics</i> , 2010 , 26, 1481-7	7.2	154
463	The origins of phagocytosis and eukaryogenesis. <i>Biology Direct</i> , 2009 , 4, 9	7.2	153
462	A virocentric perspective on the evolution of life. <i>Current Opinion in Virology</i> , 2013 , 3, 546-57	7.5	151
461	Engineering of CRISPR-Cas12b for human genome editing. <i>Nature Communications</i> , 2019 , 10, 212	17.4	149
460	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017 , 71, 233-261	17.5	149
459	Novel predicted RNA-binding domains associated with the translation machinery. <i>Journal of Molecular Evolution</i> , 1999 , 48, 291-302	3.1	149
458	Computer-assisted dissection of rolling circle DNA replication. <i>BioSystems</i> , 1993 , 30, 241-68	1.9	149

457	Giant viruses with an expanded complement of translation system components. <i>Science</i> , 2017 , 356, 82-85	3.3	148
456	Provirophages and transpovirons as the diverse mobilome of giant viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 18078-83	11.5	148
455	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
454	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
453	Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. <i>Biology Direct</i> , 2006 , 1, 34	7.2	146
452	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
451	The deep archaeal roots of eukaryotes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1619-30	8.3	143
450	A superfamily of archaeal, bacterial, and eukaryotic proteins homologous to animal transglutaminases. <i>Protein Science</i> , 1999 , 8, 1714-9	6.3	142
449	Multiple origins of viral capsid proteins from cellular ancestors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E2401-E2410	11.5	140
448	Beyond complete genomes: from sequence to structure and function. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 355-63	8.1	140
447	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. <i>CRISPR Journal</i> , 2018 , 1, 325-336	2.5	140
446	Evolution of protein domain promiscuity in eukaryotes. <i>Genome Research</i> , 2008 , 18, 449-61	9.7	139
445	Evolution of genome architecture. <i>International Journal of Biochemistry and Cell Biology</i> , 2009 , 41, 298-306	9.6	135
444	A novel family of predicted phosphoesterases includes Drosophila prune protein and bacterial RecJ exonuclease. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 17-9	10.3	134
443	A superfamily of metalloenzymes unifies phosphopentomutase and cofactor-independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. <i>Protein Science</i> , 1998 , 7, 1829-35	6.3	134
442	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
441	Birth and death of protein domains: a simple model of evolution explains power law behavior. <i>BMC Evolutionary Biology</i> , 2002 , 2, 18	3	134
440	Differences in DNA methylation between human neuronal and glial cells are concentrated in enhancers and non-CpG sites. <i>Nucleic Acids Research</i> , 2014 , 42, 109-27	20.1	131

439	Connected gene neighborhoods in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002 , 30, 2212-23	20.1	131
438	CRISPR-Cas: evolution of an RNA-based adaptive immunity system in prokaryotes. <i>RNA Biology</i> , 2013 , 10, 679-86	4.8	127
437	Eukaryotic translation elongation factor 1 gamma contains a glutathione transferase domain--study of a diverse, ancient protein superfamily using motif search and structural modeling. <i>Protein Science</i> , 1994 , 3, 2045-54	6.3	127
436	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
435	Origins and evolution of CRISPR-Cas systems. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019 , 374, 20180087	5.8	126
434	From complete genome sequence to 'complete' understanding?. <i>Trends in Biotechnology</i> , 2010 , 28, 398-406	4.6	126
433	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
432	On the origin of the translation system and the genetic code in the RNA world by means of natural selection, exaptation, and subfunctionalization. <i>Biology Direct</i> , 2007 , 2, 14	7.2	125
431	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
430	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , 2017 , 8,	7.8	122
429	Prokaryotic genomes: the emerging paradigm of genome-based microbiology. <i>Current Opinion in Genetics and Development</i> , 1997 , 7, 757-63	4.9	122
428	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 15193-15199	11.5	120
427	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
426	The basic building blocks and evolution of CRISPR-CAS systems. <i>Biochemical Society Transactions</i> , 2013 , 41, 1392-400	5.1	120
425	Genomes in turmoil: quantification of genome dynamics in prokaryote supergenomes. <i>BMC Biology</i> , 2014 , 12, 66	7.3	119
424	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014 , 5, 102	4.5	118
423	A detailed history of intron-rich eukaryotic ancestors inferred from a global survey of 100 complete genomes. <i>PLoS Computational Biology</i> , 2011 , 7, e1002150	5	118
422	Constraints and plasticity in genome and molecular-phenome evolution. <i>Nature Reviews Genetics</i> , 2010 , 11, 487-98	30.1	117

4 ²¹	Polintons: a hotbed of eukaryotic virus, transposon and plasmid evolution. <i>Nature Reviews Microbiology</i> , 2015 , 13, 105-15	22.2	116
4 ²⁰	Hidden evolutionary complexity of Nucleo-Cytoplasmic Large DNA viruses of eukaryotes. <i>Virology Journal</i> , 2012 , 9, 161	6.1	116
4 ¹⁹	The Double-Stranded DNA Virosphere as a Modular Hierarchical Network of Gene Sharing. <i>MBio</i> , 2016 , 7,	7.8	115
4 ¹⁸	Divergence and convergence in enzyme evolution. <i>Journal of Biological Chemistry</i> , 2012 , 287, 21-28	5.4	115
4 ¹⁷	Co-evolution of primordial membranes and membrane proteins. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 206-15	10.3	114
4 ¹⁶	Metagenomics reshapes the concepts of RNA virus evolution by revealing extensive horizontal virus transfer. <i>Virus Research</i> , 2018 , 244, 36-52	6.4	113
4 ¹⁵	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2283-2294	2.6	111
4 ¹⁴	Evolution of adaptive immunity from transposable elements combined with innate immune systems. <i>Nature Reviews Genetics</i> , 2015 , 16, 184-92	30.1	110
4 ¹³	Origin of giant viruses from smaller DNA viruses not from a fourth domain of cellular life. <i>Virology</i> , 2014 , 466-467, 38-52	3.6	109
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