

Yuri I Wolf

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2513350/yuri-i-wolf-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

289
papers

52,053
citations

94
h-index

227
g-index

337
ext. papers

61,919
ext. citations

10
avg, IF

7.42
L-index

#	Paper	IF	Citations
289	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
288	The COG database: an updated version includes eukaryotes. <i>BMC Bioinformatics</i> , 2003 , 4, 41	3.6	3212
287	Evolution and classification of the CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2011 , 9, 467-77	22.2	1604
286	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015 , 13, 722-36	22.2	1434
285	Comparative genomics of the lactic acid bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 15611-6	11.5	1053
284	The ecoresponsive genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011 , 331, 555-61	33.3	924
283	Classification and evolution of P-loop GTPases and related ATPases. <i>Journal of Molecular Biology</i> , 2002 , 317, 41-72	6.5	882
282	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
281	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
280	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015 , 60, 385-97	17.6	670
279	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
278	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. <i>Genome Biology</i> , 2004 , 5, R7	18.3	602
277	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
276	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017 , 15, 169-182	22.2	516
275	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
274	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
273	Selection in the evolution of gene duplications. <i>Genome Biology</i> , 2002 , 3, RESEARCH0008	18.3	491

272	The structure of the protein universe and genome evolution. <i>Nature</i> , 2002 , 420, 218-23	50.4	456
271	Genome sequence of the cyanobacterium <i>Prochlorococcus marinus</i> SS120, a nearly minimal oxyphototrophic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 10020-5	11.5	390
270	Remarkable interkingdom conservation of intron positions and massive, lineage-specific intron loss and gain in eukaryotic evolution. <i>Current Biology</i> , 2003 , 13, 1512-7	6.3	336
269	The role of lineage-specific gene family expansion in the evolution of eukaryotes. <i>Genome Research</i> , 2002 , 12, 1048-59	9.7	332
268	Essential genes are more evolutionarily conserved than are nonessential genes in bacteria. <i>Genome Research</i> , 2002 , 12, 962-8	9.7	330
267	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
266	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
265	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
264	Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. <i>Trends in Genetics</i> , 1998 , 14, 442-4	8.5	294
263	Genome trees and the tree of life. <i>Trends in Genetics</i> , 2002 , 18, 472-9	8.5	292
262	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
261	The complete genome of hyperthermophile <i>Methanopyrus kandleri</i> AV19 and monophyly of archaeal methanogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 4644-9	11.5	263
260	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , 2013 , 41, 4360-77	20.1	255
259	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
258	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
257	Genome trees constructed using five different approaches suggest new major bacterial clades. <i>BMC Evolutionary Biology</i> , 2001 , 1, 8	3	231
256	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
255	Origins and Evolution of the Global RNA Virome. <i>MBio</i> , 2018 , 9,	7.8	219

254	Small proteins can no longer be ignored. <i>Annual Review of Biochemistry</i> , 2014 , 83, 753-77	29.1	217
253	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
252	A universal trend of amino acid gain and loss in protein evolution. <i>Nature</i> , 2005 , 433, 633-8	50.4	212
251	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
250	Search for a 'Tree of Life' in the thicket of the phylogenetic forest. <i>Journal of Biology</i> , 2009 , 8, 59		204
249	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
248	Prediction of the archaeal exosome and its connections with the proteasome and the translation and transcription machineries by a comparative-genomic approach. <i>Genome Research</i> , 2001 , 11, 240-52	9.7	204
247	Genome-wide analysis of substrate specificities of the Escherichia coli haloacid dehalogenase-like phosphatase family. <i>Journal of Biological Chemistry</i> , 2006 , 281, 36149-61	5.4	198
246	Evolution of Aminoacyl-tRNA Synthetases Analysis of Unique Domain Architectures and Phylogenetic Trees Reveals a Complex History of Horizontal Gene Transfer Events. <i>Genome Research</i> , 1999 , 9, 689-710	9.7	196
245	Genome reduction as the dominant mode of evolution. <i>BioEssays</i> , 2013 , 35, 829-37	4.1	188
244	Is evolution Darwinian or/and Lamarckian?. <i>Biology Direct</i> , 2009 , 4, 42	7.2	184
243	The tree and net components of prokaryote evolution. <i>Genome Biology and Evolution</i> , 2010 , 2, 745-56	3.9	182
242	Phylogenomics of prokaryotic ribosomal proteins. <i>PLoS ONE</i> , 2012 , 7, e36972	3.7	180
241	Deinococcus geothermalis: the pool of extreme radiation resistance genes shrinks. <i>PLoS ONE</i> , 2007 , 2, e955	3.7	179
240	Global Organization and Proposed Megataxonomy of the Virus World. <i>Microbiology and Molecular Biology Reviews</i> , 2020 , 84,	13.2	178
239	Genomic determinants of sporulation in Bacilli and Clostridia: towards the minimal set of sporulation-specific genes. <i>Environmental Microbiology</i> , 2012 , 14, 2870-90	5.2	168
238	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, Methylacidiphilum infernorum, a representative of the bacterial phylum Verrucomicrobia. <i>Biology Direct</i> , 2008 , 3, 26	7.2	168
237	Coelomata and not Ecdysozoa: evidence from genome-wide phylogenetic analysis. <i>Genome Research</i> , 2004 , 14, 29-36	9.7	167

236	Estimating the number of protein folds and families from complete genome data. <i>Journal of Molecular Biology</i> , 2000 , 299, 897-905	6.5	164
235	The universal distribution of evolutionary rates of genes and distinct characteristics of eukaryotic genes of different apparent ages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 7273-80	11.5	160
234	Photosystem I gene cassettes are present in marine virus genomes. <i>Nature</i> , 2009 , 461, 258-262	50.4	160
233	Computational methods for Gene Orthology inference. <i>Briefings in Bioinformatics</i> , 2011 , 12, 379-91	13.4	158
232	No simple dependence between protein evolution rate and the number of protein-protein interactions: only the most prolific interactors tend to evolve slowly. <i>BMC Evolutionary Biology</i> , 2003 , 3, 1	3	158
231	Conservation and coevolution in the scale-free human gene coexpression network. <i>Molecular Biology and Evolution</i> , 2004 , 21, 2058-70	8.3	155
230	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
229	The origins of phagocytosis and eukaryogenesis. <i>Biology Direct</i> , 2009 , 4, 9	7.2	153
228	Duplicated genes evolve slower than singletons despite the initial rate increase. <i>BMC Evolutionary Biology</i> , 2004 , 4, 22	3	150
227	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017 , 71, 233-261	17.5	149
226	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
225	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
224	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
223	The deep archaeal roots of eukaryotes. <i>Molecular Biology and Evolution</i> , 2008 , 25, 1619-30	8.3	143
222	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. <i>CRISPR Journal</i> , 2018 , 1, 325-336	2.5	140
221	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
220	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
219	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

218	Connected gene neighborhoods in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002 , 30, 2212-23	20.1	131
217	Three distinct modes of intron dynamics in the evolution of eukaryotes. <i>Genome Research</i> , 2007 , 17, 1034-44	7.4	128
216	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
215	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
214	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
213	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , 2017 , 8,	7.8	122
212	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
211	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
210	The basic building blocks and evolution of CRISPR-CAS systems. <i>Biochemical Society Transactions</i> , 2013 , 41, 1392-400	5.1	120
209	Genomes in turmoil: quantification of genome dynamics in prokaryote supergenomes. <i>BMC Biology</i> , 2014 , 12, 66	7.3	119
208	Constraints and plasticity in genome and molecular-phenome evolution. <i>Nature Reviews Genetics</i> , 2010 , 11, 487-98	30.1	117
207	Evolution of mosaic operons by horizontal gene transfer and gene displacement in situ. <i>Genome Biology</i> , 2003 , 4, R55	18.3	117
206	Rickettsiae and Chlamydiae: evidence of horizontal gene transfer and gene exchange. <i>Trends in Genetics</i> , 1999 , 15, 173-5	8.5	117
205	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2283-2294	2.6	111
204	Genome sequence of the deep-sea gamma-proteobacterium <i>Idiomarina loihiensis</i> reveals amino acid fermentation as a source of carbon and energy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 18036-41	11.5	110
203	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
202	Evolutionary primacy of sodium bioenergetics. <i>Biology Direct</i> , 2008 , 3, 13	7.2	109
201	Global analysis of posttranslational protein arginylation. <i>PLoS Biology</i> , 2007 , 5, e258	9.7	109

200	Taxonomy of the family Arenaviridae and the order Bunyvirales: update 2018. <i>Archives of Virology</i> , 2018 , 163, 2295-2310	2.6	108
199	Trends in prokaryotic evolution revealed by comparison of closely related bacterial and archaeal genomes. <i>Journal of Bacteriology</i> , 2009 , 191, 65-73	3.5	107
198	Non-homologous isofunctional enzymes: a systematic analysis of alternative solutions in enzyme evolution. <i>Biology Direct</i> , 2010 , 5, 31	7.2	97
197	Purifying and directional selection in overlapping prokaryotic genes. <i>Trends in Genetics</i> , 2002 , 18, 228-328.5		95
196	Evolution of microbes and viruses: a paradigm shift in evolutionary biology?. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 119	5.9	94
195	Identification of novel positive-strand RNA viruses by metagenomic analysis of archaea-dominated Yellowstone hot springs. <i>Journal of Virology</i> , 2012 , 86, 5562-73	6.6	92
194	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. <i>Nucleic Acids Research</i> , 2021 , 49, D274-D281	20.1	84
193	Viral diversity threshold for adaptive immunity in prokaryotes. <i>MBio</i> , 2012 , 3, e00456-12	7.8	83
192	Theory of prokaryotic genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 11399-11407	11.5	81
191	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
190	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1063-1070	13.4	80
189	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
188	Evolutionary systems biology: links between gene evolution and function. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 481-7	11.4	79
187	Scale-free networks in biology: new insights into the fundamentals of evolution?. <i>BioEssays</i> , 2002 , 24, 105-9	4.1	79
186	Microevolutionary genomics of bacteria. <i>Theoretical Population Biology</i> , 2002 , 61, 435-47	1.2	79
185	Classify viruses - the gain is worth the pain. <i>Nature</i> , 2019 , 566, 318-320	50.4	78
184	Phylogenomics of prokaryotic ribosomal proteins 2011 , 12, P30		78
183	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020 , 369, 1077-1084	33.3	78

182	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
181	A tight link between orthologs and bidirectional best hits in bacterial and archaeal genomes. <i>Genome Biology and Evolution</i> , 2012 , 4, 1286-94	3.9	75
180	Genome-wide molecular clock and horizontal gene transfer in bacterial evolution. <i>Journal of Bacteriology</i> , 2004 , 186, 6575-85	3.5	75
179	Towards understanding the first genome sequence of a crenarchaeon by genome annotation using clusters of orthologous groups of proteins (COGs). <i>Genome Biology</i> , 2000 , 1, RESEARCH0009	18.3	75
178	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. <i>Genome Research</i> , 2001 , 11, 555-565	7.5	75
177	Evolution of the genetic code: partial optimization of a random code for robustness to translation error in a rugged fitness landscape. <i>Biology Direct</i> , 2007 , 2, 24	7.2	74
176	Congruent evolution of different classes of non-coding DNA in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2002 , 30, 4264-71	20.1	74
175	Ongoing global and regional adaptive evolution of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	74
174	Distribution of Protein Folds in the Three Superkingdoms of Life. <i>Genome Research</i> , 1999 , 9, 17-26	9.7	73
173	No evidence of inhibition of horizontal gene transfer by CRISPR-Cas on evolutionary timescales. <i>ISME Journal</i> , 2015 , 9, 2021-7	11.9	71
172	Nature and intensity of selection pressure on CRISPR-associated genes. <i>Journal of Bacteriology</i> , 2012 , 194, 1216-25	3.5	69
171	Gene conversions in genes encoding outer-membrane proteins in <i>H. pylori</i> and <i>C. pneumoniae</i> . <i>Trends in Genetics</i> , 2001 , 17, 7-10	8.5	69
170	Evolutionary dynamics of the prokaryotic adaptive immunity system CRISPR-Cas in an explicit ecological context. <i>Journal of Bacteriology</i> , 2013 , 195, 3834-44	3.5	68
169	From complete genomes to measures of substitution rate variability within and between proteins. <i>Genome Research</i> , 2000 , 10, 991-1000	9.7	68
168	Potential genomic determinants of hyperthermophily. <i>Trends in Genetics</i> , 2003 , 19, 172-6	8.5	66
167	Unifying measures of gene function and evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006 , 273, 1507-15	4.4	65
166	Evolution of gene fusions: horizontal transfer versus independent events. <i>Genome Biology</i> , 2002 , 3, research0004	3.5	64
165	Role of hypermutability in the evolution of the genus <i>Oenococcus</i> . <i>Journal of Bacteriology</i> , 2008 , 190, 564-70	3.5	62

164	Patterns of intron gain and conservation in eukaryotic genes. <i>BMC Evolutionary Biology</i> , 2007 , 7, 192	3	62
163	Evolutionarily conserved genes preferentially accumulate introns. <i>Genome Research</i> , 2007 , 17, 1045-50	9.7	59
162	Predictability of evolutionary trajectories in fitness landscapes. <i>PLoS Computational Biology</i> , 2011 , 7, e1002302	5	58
161	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
160	'ARMAN' archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017 , 8, 60	17.4	56
159	Arginyltransferase is an ATP-independent self-regulating enzyme that forms distinct functional complexes in vivo. <i>Chemistry and Biology</i> , 2011 , 18, 121-30		56
158	Computational approaches for the analysis of gene neighbourhoods in prokaryotic genomes. <i>Briefings in Bioinformatics</i> , 2004 , 5, 131-49	13.4	55
157	Inevitability of Genetic Parasites. <i>Genome Biology and Evolution</i> , 2016 , 8, 2856-2869	3.9	53
156	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
155	Universal distribution of protein evolution rates as a consequence of protein folding physics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 2983-8	11.5	52
154	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. <i>Nature Microbiology</i> , 2020 , 5, 1262-1270	26.6	50
153	Differential translation tunes uneven production of operon-encoded proteins. <i>Cell Reports</i> , 2013 , 4, 938-44	14.6	48
152	: a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. <i>Journal of Virology</i> , 2020 , 94,	6.6	47
151	Gene frequency distributions reject a neutral model of genome evolution. <i>Genome Biology and Evolution</i> , 2013 , 5, 233-42	3.9	47
150	Ecdysozoan clade rejected by genome-wide analysis of rare amino acid replacements. <i>Molecular Biology and Evolution</i> , 2007 , 24, 1080-90	8.3	47
149	Physical foundations of biological complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E8678-E8687	11.5	46
148	Drastic neofunctionalization associated with evolution of the timezyme AANAT 500 Mya. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 314-9	11.5	46
147	ATGC: a database of orthologous genes from closely related prokaryotic genomes and a research platform for microevolution of prokaryotes. <i>Nucleic Acids Research</i> , 2009 , 37, D448-54	20.1	45

146	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. <i>MBio</i> , 2019 , 10,	7.8	44
145	The vast, conserved mammalian lincRNome. <i>PLoS Computational Biology</i> , 2013 , 9, e1002917	5	44
144	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
143	The fundamental units, processes and patterns of evolution, and the tree of life conundrum. <i>Biology Direct</i> , 2009 , 4, 33	7.2	43
142	Simple stochastic birth and death models of genome evolution: was there enough time for us to evolve?. <i>Bioinformatics</i> , 2003 , 19, 1889-900	7.2	43
141	Expanded diversity of Asgard archaea and their relationships with eukaryotes. <i>Nature</i> , 2021 , 593, 553-557	7.4	41
140	Evolutionary dynamics of N-glycosylation sites of influenza virus hemagglutinin. <i>PLOS Currents</i> , 2009 , 1, RRN1001		39
139	Seeing the Tree of Life behind the phylogenetic forest. <i>BMC Biology</i> , 2013 , 11, 46	7.3	38
138	Gene family evolution: an in-depth theoretical and simulation analysis of non-linear birth-death-innovation models. <i>BMC Evolutionary Biology</i> , 2004 , 4, 32	3	38
137	Evolutionary plasticity of protein families: coupling between sequence and structure variation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 535-44	4.2	37
136	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , 2017 , 17, 232	3	36
135	Inevitability of the emergence and persistence of genetic parasites caused by evolutionary instability of parasite-free states. <i>Biology Direct</i> , 2017 , 12, 31	7.2	35
134	Universal pacemaker of genome evolution. <i>PLoS Computational Biology</i> , 2012 , 8, e1002785	5	35
133	Evolution of the CRISPR-Cas adaptive immunity systems in prokaryotes: models and observations on virus-host coevolution. <i>Molecular BioSystems</i> , 2015 , 11, 20-7		34
132	Virus-host arms race at the joint origin of multicellularity and programmed cell death. <i>Cell Cycle</i> , 2014 , 13, 3083-8	4.7	34
131	An insertion in the catalytic trigger loop gates the secondary channel of RNA polymerase. <i>Journal of Molecular Biology</i> , 2013 , 425, 82-93	6.5	32
130	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
129	Comparable contributions of structural-functional constraints and expression level to the rate of protein sequence evolution. <i>Biology Direct</i> , 2008 , 3, 40	7.2	31

128	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	29
127	Constant relative rate of protein evolution and detection of functional diversification among bacterial, archaeal and eukaryotic proteins. <i>Genome Biology</i> , 2001 , 2, RESEARCH0053	18.3	29
126	Long-term trends in evolution of indels in protein sequences. <i>BMC Evolutionary Biology</i> , 2007 , 7, 19	3	28
125	Analysis of rare amino acid replacements supports the Coelomata clade. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2594-7	8.3	28
124	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , 2017 , 17, 94	3	27
123	Stability along with extreme variability in core genome evolution. <i>Genome Biology and Evolution</i> , 2013 , 5, 1393-402	3.9	27
122	ATGC database and ATGC-COGs: an updated resource for micro- and macro-evolutionary studies of prokaryotic genomes and protein family annotation. <i>Nucleic Acids Research</i> , 2017 , 45, D210-D218	20.1	26
121	Two fundamentally different classes of microbial genes. <i>Nature Microbiology</i> , 2016 , 2, 16208	26.6	26
120	No footprints of primordial introns in a eukaryotic genome. <i>Trends in Genetics</i> , 2000 , 16, 333-4	8.5	25
119	Immunity, suicide or both? Ecological determinants for the combined evolution of anti-pathogen defense systems. <i>BMC Evolutionary Biology</i> , 2015 , 15, 43	3	24
118	Just how Lamarckian is CRISPR-Cas immunity: the continuum of evolvability mechanisms. <i>Biology Direct</i> , 2016 , 11, 9	7.2	24
117	Comparison of phylogenetic trees and search for a central trend in the "forest of life". <i>Journal of Computational Biology</i> , 2011 , 18, 917-24	1.7	24
116	Gene gain and loss push prokaryotes beyond the homologous recombination barrier and accelerate genome sequence divergence. <i>Nature Communications</i> , 2019 , 10, 5376	17.4	24
115	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
114	Grammar of protein domain architectures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 3636-3645	11.5	23
113	Diverse functions of homologous actin isoforms are defined by their nucleotide, rather than their amino acid sequence. <i>ELife</i> , 2017 , 6,	8.9	23
112	Relative contributions of intrinsic structural-functional constraints and translation rate to the evolution of protein-coding genes. <i>Genome Biology and Evolution</i> , 2010 , 2, 190-9	3.9	22
111	Power Laws, Scale-Free Networks and Genome Biology 2006 ,		22

110	Translational coupling via termination-reinitiation in archaea and bacteria. <i>Nature Communications</i> , 2019 , 10, 4006	17.4	21
109	Duplicated gelsolin family genes in zebrafish: a novel scinderin-like gene (scinla) encodes the major corneal crystallin. <i>FASEB Journal</i> , 2007 , 21, 3318-28	0.9	21
108	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020 , 11, 3784	17.4	21
107	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
106	Escherichia coli IttA 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
105	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
104	Coping with the quantitative genomics 'elephant': the correlation between the gene dispensability and evolution rate. <i>Trends in Genetics</i> , 2006 , 22, 354-7	8.5	20
103	Short repeats and IS elements in the extremely radiation-resistant bacterium <i>Deinococcus radiodurans</i> and comparison to other bacterial species. <i>Research in Microbiology</i> , 1999 , 150, 711-24	4	20
102	Analysis of metagenome-assembled viral genomes from the human gut reveals diverse putative CrAss-like phages with unique genomic features. <i>Nature Communications</i> , 2021 , 12, 1044	17.4	20
101	Universal pacemaker of genome evolution in animals and fungi and variation of evolutionary rates in diverse organisms. <i>Genome Biology and Evolution</i> , 2014 , 6, 1268-78	3.9	19
100	Seeker: alignment-free identification of bacteriophage genomes by deep learning. <i>Nucleic Acids Research</i> , 2020 , 48, e121	20.1	19
99	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019 , 21, 2056-2073	3.2	19
98	Footprints of primordial introns on the eukaryotic genome: still no clear traces. <i>Trends in Genetics</i> , 2001 , 17, 499-501	8.5	18
97	Mapping CRISPR spaceromes reveals vast host-specific viromes of prokaryotes. <i>Communications Biology</i> , 2020 , 3, 321	6.7	17
96	Positive and strongly relaxed purifying selection drive the evolution of repeats in proteins. <i>Nature Communications</i> , 2016 , 7, 13570	17.4	17
95	The complexity of the virus world. <i>Nature Reviews Microbiology</i> , 2009 , 7, 250-250	22.2	17
94	Interkingdom gene fusions. <i>Genome Biology</i> , 2000 , 1, RESEARCH0013	18.3	17
93	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019 , 47, 389-398	5.1	16

92	Mutation-selection balance and compensatory mechanisms in tumour evolution. <i>Nature Reviews Genetics</i> , 2021 , 22, 251-262	30.1	16
91	Mapping vaccinia virus DNA replication origins at nucleotide level by deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 10908-13	11.5	15
90	Towards physical principles of biological evolution. <i>Physica Scripta</i> , 2018 , 93, 043001	2.6	15
89	Ongoing Global and Regional Adaptive Evolution of SARS-CoV-2 2021 ,		15
88	The common ancestry of life. <i>Biology Direct</i> , 2010 , 5, 64	7.2	14
87	Dollo parsimony and the reconstruction of genome evolution 2006 , 190-200		14
86	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. <i>F1000Research</i> , 2019 , 8, 1000	3.6	13
85	Criticality in tumor evolution and clinical outcome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11101-E11110	11.5	13
84	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019 , 14, 3013-3031	18.8	12
83	Multiplicative fitness, rapid haplotype discovery, and fitness decay explain evolution of human MHC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 14098-14104	11.5	12
82	Evolvability of an Optimal Recombination Rate. <i>Genome Biology and Evolution</i> , 2015 , 8, 70-7	3.9	12
81	Genome-wide comparative analysis of phylogenetic trees: the prokaryotic forest of life. <i>Methods in Molecular Biology</i> , 2012 , 856, 53-79	1.4	12
80	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021 , 29, 582-592	12.4	12
79	In silico learning of tumor evolution through mutational time series. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 9501-9510	11.5	11
78	Interplay between DNA damage repair and apoptosis shapes cancer evolution through aneuploidy and microsatellite instability. <i>Nature Communications</i> , 2020 , 11, 1234	17.4	11
77	Evolution of DNA packaging in gene transfer agents. <i>Virus Evolution</i> , 2021 , 7, veab015	3.7	11
76	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses 2020 ,		10
75	Prediction of the incubation period for COVID-19 and future virus disease outbreaks. <i>BMC Biology</i> , 2020 , 18, 186	7.3	10

74	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021 , 166, 3513-3566	2.6	10
73	An Expectation-Maximization Algorithm for Analysis of Evolution of Exon-Intron Structure of Eukaryotic Genes. <i>Lecture Notes in Computer Science</i> , 2005 , 35-46	0.9	10
72	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
71	Reply to Holmes and Duch�ne, "Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?": Deep Phylogenetic Analysis of RNA Viruses Is Highly Challenging but Not Meaningless. <i>MBio</i> , 2019 , 10,	7.8	9
70	Thermodynamics of evolution and the origin of life.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	9
69	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
68	Projection of seasonal influenza severity from sequence and serological data. <i>PLOS Currents</i> , 2010 , 2, RRN1200		8
67	High-quality genome sequence of the radioresistant bacterium KS 0460. <i>Standards in Genomic Sciences</i> , 2017 , 12, 46		7
66	On the feasibility of saltational evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 21068-21075	11.5	7
65	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. <i>F1000Research</i> , 2019 , 8, 1000	3.6	7
64	CRISPR Arrays Away from Genes. <i>CRISPR Journal</i> , 2020 , 3, 535-549	2.5	7
63	Seeker: Alignment-free identification of bacteriophage genomes by deep learning		7
62	Evolution of Human Respiratory Virus Epidemics 2020 ,		7
61	Deep phylogeny of cancer drivers and compensatory mutations. <i>Communications Biology</i> , 2020 , 3, 551	6.7	7
60	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. <i>F1000Research</i> , 2021 , 10, 315	3.6	7
59	Ancient Gene Capture and Recent Gene Loss Shape the Evolution of Orthopoxvirus-Host Interaction Genes. <i>MBio</i> , 2021 , 12, e0149521	7.8	7
58	Proteomic and genomic signatures of repeat instability in cancer and adjacent normal tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 16987-16996	11.5	6
57	Pseudo-chaotic oscillations in CRISPR-virus coevolution predicted by bifurcation analysis. <i>Biology Direct</i> , 2014 , 9, 13	7.2	6

56	Estimation of prokaryotic supergenome size and composition from gene frequency distributions. <i>BMC Genomics</i> , 2014 , 15 Suppl 6, S14	4.5	6
55	Extreme Deviations from Expected Evolutionary Rates in Archaeal Protein Families. <i>Genome Biology and Evolution</i> , 2017 , 9, 2791-2811	3.9	6
54	EREM: Parameter Estimation and Ancestral Reconstruction by Expectation-Maximization Algorithm for a Probabilistic Model of Genomic Binary Characters Evolution. <i>Advances in Bioinformatics</i> , 2010 , 1674-708	5.5	6
53	Toward a theory of evolution as multilevel learning.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	6
52	Antibody-Mediated Protective Mechanisms Induced by a Trivalent Parainfluenza Virus-Vectored Ebola Virus Vaccine. <i>Journal of Virology</i> , 2019 , 93,	6.6	6
51	Stable coevolutionary regimes for genetic parasites and their hosts: you must differ to coevolve. <i>Biology Direct</i> , 2018 , 13, 27	7.2	6
50	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. <i>F1000Research</i> , 2021 , 10, 315	3.6	6
49	Proteomic Analysis of Methanonatronarchaeum thermophilum AMET1, a Representative of a Putative New Class of Euryarchaeota, "Methanonatronarchaeia". <i>Genes</i> , 2018 , 9,	4.2	5
48	Selection and Genome Plasticity as the Key Factors in the Evolution of Bacteria. <i>Physical Review X</i> , 2019 , 9,	9.1	5
47	Quantifying the similarity of monotonic trajectories in rough and smooth fitness landscapes. <i>Molecular BioSystems</i> , 2013 , 9, 1627-31		5
46	A maximum likelihood method for reconstruction of the evolution of eukaryotic gene structure. <i>Methods in Molecular Biology</i> , 2009 , 541, 357-71	1.4	5
45	Substantial Impact of Post Vaccination Contacts on Cumulative Infections during Viral Epidemics 2020 ,		5
44	Selection for Reducing Energy Cost of Protein Production Drives the GC Content and Amino Acid Composition Bias in Gene Transfer Agents. <i>MBio</i> , 2020 , 11,	7.8	5
43	Allosteric Activation of SARS-CoV-2 RNA-Dependent RNA Polymerase by Remdesivir Triphosphate and Other Phosphorylated Nucleotides. <i>MBio</i> , 2021 , 12, e0142321	7.8	5
42	Estimation of universal and taxon-specific parameters of prokaryotic genome evolution. <i>PLoS ONE</i> , 2018 , 13, e0195571	3.7	5
41	Game-Theoretical Modeling of Interviral Conflicts Mediated by Mini-CRISPR Arrays. <i>Frontiers in Microbiology</i> , 2020 , 11, 381	5.7	4
40	Histidine-Triad Hydrolases Provide Resistance to Peptide-Nucleotide Antibiotics. <i>MBio</i> , 2020 , 11,	7.8	4
39	Reply to "codon usage frequency of RNA virus genomes from high-temperature acidic-environment metagenomes". <i>Journal of Virology</i> , 2013 , 87, 1920-1	6.6	4

38	Horizontal Gene Transfer and its Role in the Evolution of Prokaryotes 2002 , 277-IX		4
37	Winnowing sequences from a database search. <i>Journal of Computational Biology</i> , 2000 , 7, 293-302	1.7	4
36	The CRISPR spacer space is dominated by sequences from the species-specific mobilome		4
35	Epistasis at the SARS-CoV-2 RBD Interface and the Propitiously Boring Implications for Vaccine Escape 2021 ,		4
34	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
33	Net Evolutionary Loss of Residue Polarity in Drosophilid Protein Cores Indicates Ongoing Optimization of Amino Acid Composition. <i>Genome Biology and Evolution</i> , 2017 , 9, 2879-2892	3.9	3
32	Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life. <i>Methods in Molecular Biology</i> , 2019 , 1910, 241-269	1.4	3
31	Vast diversity of anti-CRISPR proteins predicted with a machine-learning approach		3
30	Unique genomic features of crAss-like phages, the dominant component of the human gut virome		3
29	Epistasis at the SARS-CoV-2 Receptor-Binding Domain Interface and the Propitiously Boring Implications for Vaccine Escape.. <i>MBio</i> , 2022 , e0013522	7.8	3
28	Reply to 'Evolutionary placement of Methanonatronarchaeia'. <i>Nature Microbiology</i> , 2019 , 4, 560-561	26.6	2
27	Birth and Death Models of Genome Evolution 2006 , 65-85		2
26	Towards physical principles of biological evolution		2
25	Virus genomes from deep sea sediments expand the ocean megavirome and support independent origins of viral gigantism		2
24	Non-essential ribosomal proteins in bacteria and archaea identified using COGs. <i>Journal of Bacteriology</i> , 2021 ,	3.5	2
23	Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021 , 10, 447	3.6	2
22	Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021 , 10, 447	3.6	2
21	Evolution in the weak-mutation limit: Stasis periods punctuated by fast transitions between saddle points on the fitness landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2

20	Correlations between Quantitative Measures of Genome Evolution, Expression and Function 2006 , 133-144	2
19	Modified base-binding EVE and DCD domains: striking diversity of genomic contexts in prokaryotes and predicted involvement in a variety of cellular processes. <i>BMC Biology</i> , 2020 , 18, 159	7.3 1
18	Constraints, Plasticity, and Universal Patterns in Genome and Phenome Evolution 2010 , 19-47	1
17	A putative RNA-interference-based immune system in prokaryotes: the epitome of prokaryotic genomic diversity ³⁹⁻⁶⁴	1
16	Phylogenetic evidence of headful packaging strategy in gene transfer agents	1
15	Towards comprehensive characterization of CRISPR-linked genes	1
14	Genome plasticity, a key factor of evolution in prokaryotes	1
13	Expanding diversity of Asgard archaea and the elusive ancestry of eukaryotes	1
12	Inevitability of the emergence and persistence of genetic parasites caused by thermodynamic instability of parasite-free states	1
11	No waves of intelligent design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 19639-19640	11.5 1
10	Reply to Hedrick and Klitz: High haplotype discovery rate in the HLA locus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23388-23389	11.5 1
9	Assessment of assumptions underlying models of prokaryotic pangenome evolution. <i>BMC Biology</i> , 2021 , 19, 27	7.3 1
8	CRISPRclassify: Repeat-Based Classification of CRISPR Loci. <i>CRISPR Journal</i> , 2021 , 4, 558-574	2.5 1
7	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
6	Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis.. <i>Biology Direct</i> , 2022 , 17, 7	7.2 0
5	Comparison of phylogenetic trees and search for a central trend in the Forest of Life ¹⁸⁹⁻²⁰⁰	
4	Defense Against Viruses and Other Genetic Parasites in Prokaryotes 2021 , 606-616	
3	Conflict-driven evolution 2021 , 77-96	

- 2 A novel group of negative-sense RNA viruses associated with epizootics in managed and free-ranging freshwater turtles in Florida, USA.. *PLoS Pathogens*, **2022**, 18, e1010258 7.6
- 1 S51 Family Peptidases Provide Resistance to Peptidyl-Nucleotide Antibiotic McC.. *MBio*, **2022**, e00805227.8