Yuri I Wolf

List of Publications by Year in Descending Order

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

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	Toward a theory of evolution as multilevel learning.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	6
288	Thermodynamics of evolution and the origin of life.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119,	11.5	9
287	Epistasis at the SARS-CoV-2 Receptor-Binding Domain Interface and the Propitiously Boring Implications for Vaccine Escape.. *MBio*, **2022**, e0013522	7.8	3
286	Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis.. *Biology Direct*, **2022**, 17, 7	7.2	0
285	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	
284	S51 Family Peptidases Provide Resistance to Peptidyl-Nucleotide Antibiotic McC.. *MBio*, **2022**, e0080522	7.8	
283	Analysis of metagenome-assembled viral genomes from the human gut reveals diverse putative CrAss-like phages with unique genomic features. *Nature Communications*, **2021**, 12, 1044	17.4	20
282	Ongoing Global and Regional Adaptive Evolution of SARS-CoV-2 **2021**,		15
281	Expanded diversity of Asgard archaea and their relationships with eukaryotes. *Nature*, **2021**, 593, 553-557	50.4	41
280	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. *F1000Research*, **2021**, 10, 315	3.6	7
279	Non-essential ribosomal proteins in bacteria and archaea identified using COGs. *Journal of Bacteriology*, **2021**,	3.5	2
278	Evolution of human respiratory virus epidemics. *F1000Research*, **2021**, 10, 447	3.6	2
277	Allosteric Activation of SARS-CoV-2 RNA-Dependent RNA Polymerase by Remdesivir Triphosphate and Other Phosphorylated Nucleotides. *MBio*, **2021**, 12, e0142321	7.8	5
276	Evolution of human respiratory virus epidemics. *F1000Research*, **2021**, 10, 447	3.6	2
275	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. *Nucleic Acids Research*, **2021**, 49, D274-D281	20.1	84
274	Mutation-selection balance and compensatory mechanisms in tumour evolution. *Nature Reviews Genetics*, **2021**, 22, 251-262	30.1	16
273	Evolution of DNA packaging in gene transfer agents. *Virus Evolution*, **2021**, 7, veab015	3.7	11

272	Evolution in the weak-mutation limit: Stasis periods punctuated by fast transitions between saddle points on the fitness landscape. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	2
271	Defense Against Viruses and Other Genetic Parasites in Prokaryotes **2021**, 606-616		
270	Assessment of assumptions underlying models of prokaryotic pangenome evolution. *BMC Biology*, **2021**, 19, 27	7.3	1
269	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,	11.5	74
268	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. *Trends in Microbiology*, **2021**, 29, 582-592	12.4	12
267	Epistasis at the SARS-CoV-2 RBD Interface and the Propitiously Boring Implications for Vaccine Escape **2021**,		4
266	A Unique Gene Module in Archaea Centered on a Hypervariable Protein Containing Immunoglobulin Domains. *Frontiers in Microbiology*, **2021**, 12, 721392	5.7	0
265	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. *F1000Research*, **2021**, 10, 315	3.6	6
264	CRISPRclassify: Repeat-Based Classification of CRISPR Loci. *CRISPR Journal*, **2021**, 4, 558-574	2.5	1
263	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. *Archives of Virology*, **2021**, 166, 3513-3566	2.6	10
262	Ancient Gene Capture and Recent Gene Loss Shape the Evolution of Orthopoxvirus-Host Interaction Genes. *MBio*, **2021**, 12, e0149521	7.8	7
261	Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of. *CRISPR Journal*, **2021**, 4, 656-672	2.5	4
260	Conflict-driven evolution **2021**, 77-96		
259	Modified base-binding EVE and DCD domains: striking diversity of genomic contexts in prokaryotes and predicted involvement in a variety of cellular processes. *BMC Biology*, **2020**, 18, 159	7.3	1
258	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	11.5	120
257	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. *CRISPR Journal*, **2020**, 3, 156-163	2.5	8
256	Interplay between DNA damage repair and apoptosis shapes cancer evolution through aneuploidy and microsatellite instability. *Nature Communications*, **2020**, 11, 1234	17.4	11
255	Global Organization and Proposed Megataxonomy of the Virus World. *Microbiology and Molecular Biology Reviews*, **2020**, 84,	13.2	178

254	Mapping CRISPR spaceromes reveals vast host-specific viromes of prokaryotes. *Communications Biology*, **2020**, 3, 321	6.7	17
253	Game-Theoretical Modeling of Interviral Conflicts Mediated by Mini-CRISPR Arrays. *Frontiers in Microbiology*, **2020**, 11, 381	5.7	4
252	: a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. *Journal of Virology*, **2020**, 94,	6.6	47
251	Histidine-Triad Hydrolases Provide Resistance to Peptide-Nucleotide Antibiotics. *MBio*, **2020**, 11,	7.8	4
250	CRISPR Arrays Away from Genes. *CRISPR Journal*, **2020**, 3, 535-549	2.5	7
249	Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses **2020**,		10
248	Evolution of Human Respiratory Virus Epidemics **2020**,		7
247	Substantial Impact of Post Vaccination Contacts on Cumulative Infections during Viral Epidemics **2020**,		5
246	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. *Nature Reviews Microbiology*, **2020**, 18, 67-83	22.2	545
245	Deep phylogeny of cancer drivers and compensatory mutations. *Communications Biology*, **2020**, 3, 551	6.7	7
244	Seeker: alignment-free identification of bacteriophage genomes by deep learning. *Nucleic Acids Research*, **2020**, 48, e121	20.1	19
243	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. *Nature Microbiology*, **2020**, 5, 1262-1270	26.6	50
242	Selection for Reducing Energy Cost of Protein Production Drives the GC Content and Amino Acid Composition Bias in Gene Transfer Agents. *MBio*, **2020**, 11,	7.8	5
241	Prediction of the incubation period for COVID-19 and future virus disease outbreaks. *BMC Biology*, **2020**, 18, 186	7.3	10
240	Machine-learning approach expands the repertoire of anti-CRISPR protein families. *Nature Communications*, **2020**, 11, 3784	17.4	21
239	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antivirus defense. *Nucleic Acids Research*, **2020**, 48, 8828-8847	20.1	21
238	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. *Science*, **2020**, 369, 1077-1084	33.3	78
237	No waves of intelligent design. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 19639-19640	11.5	1

236	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. *Nature Reviews Genetics*, **2020**, 21, 119-131	30.1	77
235	Classify viruses - the gain is worth the pain. *Nature*, **2019**, 566, 318-320	50.4	78
234	Translational coupling via termination-reinitiation in archaea and bacteria. *Nature Communications*, **2019**, 10, 4006	17.4	21
233	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. *Nature Protocols*, **2019**, 14, 3013-3031	18.8	12
232	Multiplicative fitness, rapid haplotype discovery, and fitness decay explain evolution of human MHC. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 14098-14104	11.5	12
231	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. *MBio*, **2019**, 10,	7.8	23
230	In silico learning of tumor evolution through mutational time series. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 9501-9510	11.5	11
229	Reply to Holmes and Duchñe, "Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?": Deep Phylogenetic Analysis of RNA Viruses Is Highly Challenging but Not Meaningless. *MBio*, **2019**, 10,	7.8	9
228	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. *MBio*, **2019**, 10,	7.8	44
227	Grammar of protein domain architectures. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 3636-3645	11.5	23
226	Towards functional characterization of archaeal genomic dark matter. *Biochemical Society Transactions*, **2019**, 47, 389-398	5.1	16
225	Reply to 'Evolutionary placement of Methanonatronarchaeia'. *Nature Microbiology*, **2019**, 4, 560-561	26.6	2
224	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. *RNA Biology*, **2019**, 16, 435-448	4.8	20
223	Proteomic and genomic signatures of repeat instability in cancer and adjacent normal tissues. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 16987-16996	11.5	6
222	Selection and Genome Plasticity as the Key Factors in the Evolution of Bacteria. *Physical Review X*, **2019**, 9,	9.1	5
221	On the feasibility of saltational evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 21068-21075	11.5	7
220	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. *F1000Research*, **2019**, 8, 1000	3.6	7
219	A unique insert in the genomes of high-risk human papillomaviruses with a predicted dual role in conferring oncogenic risk. *F1000Research*, **2019**, 8, 1000	3.6	13

218	Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life. *Methods in Molecular Biology*, **2019**, 1910, 241-269	1.4	3
217	Integrated mobile genetic elements in Thaumarchaeota. *Environmental Microbiology*, **2019**, 21, 2056-2078	5.2	19
216	Reply to Hedrick and Klitz: High haplotype discovery rate in the HLA locus. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 23388-23389	11.5	1
215	Gene gain and loss push prokaryotes beyond the homologous recombination barrier and accelerate genome sequence divergence. *Nature Communications*, **2019**, 10, 5376	17.4	24
214	Antibody-Mediated Protective Mechanisms Induced by a Trivalent Parainfluenza Virus-Vectored Ebolavirus Vaccine. *Journal of Virology*, **2019**, 93,	6.6	6
213	Microbial genome analysis: the COG approach. *Briefings in Bioinformatics*, **2019**, 20, 1063-1070	13.4	80
212	Towards physical principles of biological evolution. *Physica Scripta*, **2018**, 93, 043001	2.6	15
211	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. *Archives of Virology*, **2018**, 163, 2295-2310	2.6	108
210	Taxonomy of the order Mononegavirales: update 2018. *Archives of Virology*, **2018**, 163, 2283-2294	2.6	111
209	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. *Journal of Bacteriology*, **2018**, 200,	3.5	29
208	Proteomic Analysis of Methanonatronarchaeum thermophilum AMET1, a Representative of a Putative New Class of Euryarchaeota, "Methanonatronarchaeia". *Genes*, **2018**, 9,	4.2	5
207	Physical foundations of biological complexity. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E8678-E8687	11.5	46
206	Criticality in tumor evolution and clinical outcome. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E11101-E11110	11.5	13
205	Stable coevolutionary regimes for genetic parasites and their hosts: you must differ to coevolve. *Biology Direct*, **2018**, 13, 27	7.2	6
204	Origins and Evolution of the Global RNA Virome. *MBio*, **2018**, 9,	7.8	219
203	Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?. *CRISPR Journal*, **2018**, 1, 325-336	2.5	140
202	Systematic prediction of genes functionally linked to CRISPR-Cas systems by gene neighborhood analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E5307-E5316	11.5	80
201	Estimation of universal and taxon-specific parameters of prokaryotic genome evolution. *PLoS ONE*, **2018**, 13, e0195571	3.7	5

200	Escherichia coli ItaT is a type II toxin that inhibits translation by acetylating isoleucyl-tRNAIle. *Nucleic Acids Research*, **2018**, 46, 7873-7885	20.1	21
199	Diversity and evolution of class 2 CRISPR-Cas systems. *Nature Reviews Microbiology*, **2017**, 15, 169-182	22.2	516
198	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. *Journal of Physiology*, **2017**, 595, 4611-4630	3.9	9
197	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. *Nature Microbiology*, **2017**, 2, 17081	26.6	126
196	Reconstruction of the evolution of microbial defense systems. *BMC Evolutionary Biology*, **2017**, 17, 94	3	27
195	Diverse functions of homologous actin isoforms are defined by their nucleotide, rather than their amino acid sequence. *ELife*, **2017**, 6,	8.9	23
194	Phylogenomics of Cas4 family nucleases. *BMC Evolutionary Biology*, **2017**, 17, 232	3	36
193	Inevitability of the emergence and persistence of genetic parasites caused by evolutionary instability of parasite-free states. *Biology Direct*, **2017**, 12, 31	7.2	35
192	High-quality genome sequence of the radioresistant bacterium KS 0460. *Standards in Genomic Sciences*, **2017**, 12, 46		7
191	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. *MBio*, **2017**, 8,	7.8	122
190	ATGC database and ATGC-COGs: an updated resource for micro- and macro-evolutionary studies of prokaryotic genomes and protein family annotation. *Nucleic Acids Research*, **2017**, 45, D210-D218	20.1	26
189	'ARMAN' archaea depend on association with euryarchaeal host in culture and in situ. *Nature Communications*, **2017**, 8, 60	17.4	56
188	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. *Annual Review of Microbiology*, **2017**, 71, 233-261	17.5	149
187	Extreme Deviations from Expected Evolutionary Rates in Archaeal Protein Families. *Genome Biology and Evolution*, **2017**, 9, 2791-2811	3.9	6
186	Net Evolutionary Loss of Residue Polarity in Drosophilid Protein Cores Indicates Ongoing Optimization of Amino Acid Composition. *Genome Biology and Evolution*, **2017**, 9, 2879-2892	3.9	3
185	Positive and strongly relaxed purifying selection drive the evolution of repeats in proteins. *Nature Communications*, **2016**, 7, 13570	17.4	17
184	Inevitability of Genetic Parasites. *Genome Biology and Evolution*, **2016**, 8, 2856-2869	3.9	53
183	Just how Lamarckian is CRISPR-Cas immunity: the continuum of evolvability mechanisms. *Biology Direct*, **2016**, 11, 9	7.2	24

182	Two fundamentally different classes of microbial genes. *Nature Microbiology*, **2016**, 2, 16208	26.6	26
181	Theory of prokaryotic genome evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 11399-11407	11.5	81
180	No evidence of inhibition of horizontal gene transfer by CRISPR-Cas on evolutionary timescales. *ISME Journal*, **2015**, 9, 2021-7	11.9	71
179	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from Saccharomyces cerevisiae: BIOCHEMICAL, STRUCTURAL, AND EVOLUTIONARY INSIGHTS. *Journal of Biological Chemistry*, **2015**, 290, 18678-98	5.4	52
178	Immunity, suicide or both? Ecological determinants for the combined evolution of anti-pathogen defense systems. *BMC Evolutionary Biology*, **2015**, 15, 43	3	24
177	Babela massiliensis, a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. *Biology Direct*, **2015**, 10, 13	7.2	31
176	An updated evolutionary classification of CRISPR-Cas systems. *Nature Reviews Microbiology*, **2015**, 13, 722-36	22.2	1434
175	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. *Molecular Cell*, **2015**, 60, 385-97	17.6	670
174	Mapping vaccinia virus DNA replication origins at nucleotide level by deep sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 10908-13	11.5	15
173	Evolution of the CRISPR-Cas adaptive immunity systems in prokaryotes: models and observations on virus-host coevolution. *Molecular BioSystems*, **2015**, 11, 20-7		34
172	Evolvability of an Optimal Recombination Rate. *Genome Biology and Evolution*, **2015**, 8, 70-7	3.9	12
171	Archaeal Clusters of Orthologous Genes (arCOGs): An Update and Application for Analysis of Shared Features between Thermococcales, Methanococcales, and Methanobacteriales. *Life*, **2015**, 5, 818-40	3	125
170	Expanded microbial genome coverage and improved protein family annotation in the COG database. *Nucleic Acids Research*, **2015**, 43, D261-9	20.1	818
169	Drastic neofunctionalization associated with evolution of the timezyme AANAT 500 Mya. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 314-9	11.5	46
168	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. *Extremophiles*, **2014**, 18, 877-93	3	43
167	Pseudo-chaotic oscillations in CRISPR-virus coevolution predicted by bifurcation analysis. *Biology Direct*, **2014**, 9, 13	7.2	6
166	Origin of giant viruses from smaller DNA viruses not from a fourth domain of cellular life. *Virology*, **2014**, 466-467, 38-52	3.6	109
165	Small proteins can no longer be ignored. *Annual Review of Biochemistry*, **2014**, 83, 753-77	29.1	217

164	Universal pacemaker of genome evolution in animals and fungi and variation of evolutionary rates in diverse organisms. *Genome Biology and Evolution*, **2014**, 6, 1268-78	3.9	19
163	Estimation of prokaryotic supergenome size and composition from gene frequency distributions. *BMC Genomics*, **2014**, 15 Suppl 6, S14	4.5	6
162	Virus-host arms race at the joint origin of multicellularity and programmed cell death. *Cell Cycle*, **2014**, 13, 3083-8	4.7	34
161	Genomes in turmoil: quantification of genome dynamics in prokaryote supergenomes. *BMC Biology*, **2014**, 12, 66	7.3	119
160	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. *Biology Direct*, **2013**, 8, 9	7.2	80
159	Seeing the Tree of Life behind the phylogenetic forest. *BMC Biology*, **2013**, 11, 46	7.3	38
158	Quantifying the similarity of monotonic trajectories in rough and smooth fitness landscapes. *Molecular BioSystems*, **2013**, 9, 1627-31		5
157	An insertion in the catalytic trigger loop gates the secondary channel of RNA polymerase. *Journal of Molecular Biology*, **2013**, 425, 82-93	6.5	32
156	Differential translation tunes uneven production of operon-encoded proteins. *Cell Reports*, **2013**, 4, 938-44	10.6	48
155	Reply to "codon usage frequency of RNA virus genomes from high-temperature acidic-environment metagenomes". *Journal of Virology*, **2013**, 87, 1920-1	6.6	4
154	The vast, conserved mammalian lincRNome. *PLoS Computational Biology*, **2013**, 9, e1002917	5	44
153	The basic building blocks and evolution of CRISPR-CAS systems. *Biochemical Society Transactions*, **2013**, 41, 1392-400	5.1	120
152	Evolutionary dynamics of the prokaryotic adaptive immunity system CRISPR-Cas in an explicit ecological context. *Journal of Bacteriology*, **2013**, 195, 3834-44	3.5	68
151	Gene frequency distributions reject a neutral model of genome evolution. *Genome Biology and Evolution*, **2013**, 5, 233-42	3.9	47
150	Stability along with extreme variability in core genome evolution. *Genome Biology and Evolution*, **2013**, 5, 1393-402	3.9	27
149	Comparative genomics of defense systems in archaea and bacteria. *Nucleic Acids Research*, **2013**, 41, 4360-77	20.1	255
148	Genome reduction as the dominant mode of evolution. *BioEssays*, **2013**, 35, 829-37	4.1	188
147	Genomic determinants of sporulation in Bacilli and Clostridia: towards the minimal set of sporulation-specific genes. *Environmental Microbiology*, **2012**, 14, 2870-90	5.2	168

146	Nature and intensity of selection pressure on CRISPR-associated genes. *Journal of Bacteriology*, **2012**, 194, 1216-25	3.5	69
145	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	7.2	120
144	Genome-wide comparative analysis of phylogenetic trees: the prokaryotic forest of life. *Methods in Molecular Biology*, **2012**, 856, 53-79	1.4	12
143	Phylogenomics of prokaryotic ribosomal proteins. *PLoS ONE*, **2012**, 7, e36972	3.7	180
142	Universal pacemaker of genome evolution. *PLoS Computational Biology*, **2012**, 8, e1002785	5	35
141	A tight link between orthologs and bidirectional best hits in bacterial and archaeal genomes. *Genome Biology and Evolution*, **2012**, 4, 1286-94	3.9	75
140	Viral diversity threshold for adaptive immunity in prokaryotes. *MBio*, **2012**, 3, e00456-12	7.8	83
139	Identification of novel positive-strand RNA viruses by metagenomic analysis of archaea-dominated Yellowstone hot springs. *Journal of Virology*, **2012**, 86, 5562-73	6.6	92
138	Evolution of microbes and viruses: a paradigm shift in evolutionary biology?. *Frontiers in Cellular and Infection Microbiology*, **2012**, 2, 119	5.9	94
137	Phylogenomics of prokaryotic ribosomal proteins **2011**, 12, P30		78
136	Evolution and classification of the CRISPR-Cas systems. *Nature Reviews Microbiology*, **2011**, 9, 467-77	22.2	1604
135	Computational methods for Gene Orthology inference. *Briefings in Bioinformatics*, **2011**, 12, 379-91	13.4	158
134	The ecoresponsive genome of Daphnia pulex. *Science*, **2011**, 331, 555-61	33.3	924
133	Comparison of phylogenetic trees and search for a central trend in the "forest of life". *Journal of Computational Biology*, **2011**, 18, 917-24	1.7	24
132	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. *Biology Direct*, **2011**, 6, 38	7.2	324
131	Arginyltransferase is an ATP-independent self-regulating enzyme that forms distinct functional complexes in vivo. *Chemistry and Biology*, **2011**, 18, 121-30		56
130	Defense islands in bacterial and archaeal genomes and prediction of novel defense systems. *Journal of Bacteriology*, **2011**, 193, 6039-56	3.5	209
129	Predictability of evolutionary trajectories in fitness landscapes. *PLoS Computational Biology*, **2011**, 7, e1002302	5	58

128	Constraints and plasticity in genome and molecular-phenome evolution. *Nature Reviews Genetics*, **2010**, 11, 487-98	30.1	117
127	EREM: Parameter Estimation and Ancestral Reconstruction by Expectation-Maximization Algorithm for a Probabilistic Model of Genomic Binary Characters Evolution. *Advances in Bioinformatics*, **2010**, 167408	5.5	6
126	Relative contributions of intrinsic structural-functional constraints and translation rate to the evolution of protein-coding genes. *Genome Biology and Evolution*, **2010**, 2, 190-9	3.9	22
125	A low-polynomial algorithm for assembling clusters of orthologous groups from intergenomic symmetric best matches. *Bioinformatics*, **2010**, 26, 1481-7	7.2	154
124	Universal distribution of protein evolution rates as a consequence of protein folding physics. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 2983-8	11.5	52
123	Constraints, Plasticity, and Universal Patterns in Genome and Phenome Evolution **2010**, 19-47		1
122	The tree and net components of prokaryote evolution. *Genome Biology and Evolution*, **2010**, 2, 745-56	3.9	182
121	The common ancestry of life. *Biology Direct*, **2010**, 5, 64	7.2	14
120	Non-homologous isofunctional enzymes: a systematic analysis of alternative solutions in enzyme evolution. *Biology Direct*, **2010**, 5, 31	7.2	97
119	Projection of seasonal influenza severity from sequence and serological data. *PLOS Currents*, **2010**, 2, RRN1200		8
118	The universal distribution of evolutionary rates of genes and distinct characteristics of eukaryotic genes of different apparent ages. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 7273-80	11.5	160
117	Trends in prokaryotic evolution revealed by comparison of closely related bacterial and archaeal genomes. *Journal of Bacteriology*, **2009**, 191, 65-73	3.5	107
116	ATGC: a database of orthologous genes from closely related prokaryotic genomes and a research platform for microevolution of prokaryotes. *Nucleic Acids Research*, **2009**, 37, D448-54	20.1	45
115	Search for a 'Tree of Life' in the thicket of the phylogenetic forest. *Journal of Biology*, **2009**, 8, 59		204
114	Photosystem I gene cassettes are present in marine virus genomes. *Nature*, **2009**, 461, 258-262	50.4	160
113	The complexity of the virus world. *Nature Reviews Microbiology*, **2009**, 7, 250-250	22.2	17
112	Eukaryotic large nucleo-cytoplasmic DNA viruses: clusters of orthologous genes and reconstruction of viral genome evolution. *Virology Journal*, **2009**, 6, 223	6.1	229
111	Comprehensive comparative-genomic analysis of type 2 toxin-antitoxin systems and related mobile stress response systems in prokaryotes. *Biology Direct*, **2009**, 4, 19	7.2	315

110	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	7.2	143
109	The fundamental units, processes and patterns of evolution, and the tree of life conundrum. *Biology Direct*, **2009**, 4, 33	7.2	43
108	Is evolution Darwinian or/and Lamarckian?. *Biology Direct*, **2009**, 4, 42	7.2	184
107	The origins of phagocytosis and eukaryogenesis. *Biology Direct*, **2009**, 4, 9	7.2	153
106	Evolutionary dynamics of N-glycosylation sites of influenza virus hemagglutinin. *PLOS Currents*, **2009**, 1, RRN1001		39
105	A maximum likelihood method for reconstruction of the evolution of eukaryotic gene structure. *Methods in Molecular Biology*, **2009**, 541, 357-71	1.4	5
104	The Big Bang of picorna-like virus evolution antedates the radiation of eukaryotic supergroups. *Nature Reviews Microbiology*, **2008**, 6, 925-39	22.2	204
103	Evolutionary primacy of sodium bioenergetics. *Biology Direct*, **2008**, 3, 13	7.2	109
102	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, Methylacidiphilum infernorum, a representative of the bacterial phylum Verrucomicrobia. *Biology Direct*, **2008**, 3, 26	7.2	168
101	Comparable contributions of structural-functional constraints and expression level to the rate of protein sequence evolution. *Biology Direct*, **2008**, 3, 40	7.2	31
100	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium Anoxybacillus flavithermus WK1. *Genome Biology*, **2008**, 9, R161	18.3	58
99	Genomics of bacteria and archaea: the emerging dynamic view of the prokaryotic world. *Nucleic Acids Research*, **2008**, 36, 6688-719	20.1	513
98	Role of hypermutability in the evolution of the genus Oenococcus. *Journal of Bacteriology*, **2008**, 190, 564-70	3.5	62
97	A korarchaeal genome reveals insights into the evolution of the Archaea. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 8102-7	11.5	214
96	The deep archaeal roots of eukaryotes. *Molecular Biology and Evolution*, **2008**, 25, 1619-30	8.3	143
95	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	7.2	125
94	Evolution of the genetic code: partial optimization of a random code for robustness to translation error in a rugged fitness landscape. *Biology Direct*, **2007**, 2, 24	7.2	74
93	Clusters of orthologous genes for 41 archaeal genomes and implications for evolutionary genomics of archaea. *Biology Direct*, **2007**, 2, 33	7.2	146

92	Long-term trends in evolution of indels in protein sequences. *BMC Evolutionary Biology*, **2007**, 7, 19	3	28
91	Patterns of intron gain and conservation in eukaryotic genes. *BMC Evolutionary Biology*, **2007**, 7, 192	3	62
90	Global analysis of posttranslational protein arginylation. *PLoS Biology*, **2007**, 5, e258	9.7	109
89	Duplicated gelsolin family genes in zebrafish: a novel scinderin-like gene (scinla) encodes the major corneal crystallin. *FASEB Journal*, **2007**, 21, 3318-28	0.9	21
88	Analysis of rare amino acid replacements supports the Coelomata clade. *Molecular Biology and Evolution*, **2007**, 24, 2594-7	8.3	28
87	Three distinct modes of intron dynamics in the evolution of eukaryotes. *Genome Research*, **2007**, 17, 1034-44	9.7	128
86	Evolutionarily conserved genes preferentially accumulate introns. *Genome Research*, **2007**, 17, 1045-50	9.7	59
85	Ecdysozoan clade rejected by genome-wide analysis of rare amino acid replacements. *Molecular Biology and Evolution*, **2007**, 24, 1080-90	8.3	47
84	Deinococcus geothermalis: the pool of extreme radiation resistance genes shrinks. *PLoS ONE*, **2007**, 2, e955	3.7	179
83	Coping with the quantitative genomics 'elephant': the correlation between the gene dispensability and evolution rate. *Trends in Genetics*, **2006**, 22, 354-7	8.5	20
82	Genome-wide analysis of substrate specificities of the Escherichia coli haloacid dehalogenase-like phosphatase family. *Journal of Biological Chemistry*, **2006**, 281, 36149-61	5.4	198
81	Unifying measures of gene function and evolution. *Proceedings of the Royal Society B: Biological Sciences*, **2006**, 273, 1507-15	4.4	65
80	Power Laws, Scale-Free Networks and Genome Biology **2006**,		22
79	Birth and Death Models of Genome Evolution **2006**, 65-85		2
78	The cyanobacterial genome core and the origin of photosynthesis. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 13126-31	11.5	236
77	Long intervals of stasis punctuated by bursts of positive selection in the seasonal evolution of influenza A virus. *Biology Direct*, **2006**, 1, 34	7.2	146
76	Comparative genomics of the lactic acid bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 15611-6	11.5	1053
75	Evolutionary systems biology: links between gene evolution and function. *Current Opinion in Biotechnology*, **2006**, 17, 481-7	11.4	79

74	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	7.2	803
73	Dollo parsimony and the reconstruction of genome evolution **2006**, 190-200		14
72	Correlations between Quantitative Measures of Genome Evolution, Expression and Function **2006**, 133-144		2
71	Ancestral paralogs and pseudoparalogs and their role in the emergence of the eukaryotic cell. *Nucleic Acids Research*, **2005**, 33, 4626-38	20.1	134
70	A universal trend of amino acid gain and loss in protein evolution. *Nature*, **2005**, 433, 633-8	50.4	212
69	Comparative genomics of Thermus thermophilus and Deinococcus radiodurans: divergent routes of adaptation to thermophily and radiation resistance. *BMC Evolutionary Biology*, **2005**, 5, 57	3	138
68	Evolutionary plasticity of protein families: coupling between sequence and structure variation. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61, 535-44	4.2	37
67	An Expectation-Maximization Algorithm for Analysis of Evolution of Exon-Intron Structure of Eukaryotic Genes. *Lecture Notes in Computer Science*, **2005**, 35-46	0.9	10
66	Conservation and coevolution in the scale-free human gene coexpression network. *Molecular Biology and Evolution*, **2004**, 21, 2058-70	8.3	155
65	Computational approaches for the analysis of gene neighbourhoods in prokaryotic genomes. *Briefings in Bioinformatics*, **2004**, 5, 131-49	13.4	55
64	Genome-wide molecular clock and horizontal gene transfer in bacterial evolution. *Journal of Bacteriology*, **2004**, 186, 6575-85	3.5	75
63	Genome sequence of the deep-sea gamma-proteobacterium Idiomarina loihiensis reveals amino acid fermentation as a source of carbon and energy. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 18036-41	11.5	110
62	Duplicated genes evolve slower than singletons despite the initial rate increase. *BMC Evolutionary Biology*, **2004**, 4, 22	3	150
61	Gene family evolution: an in-depth theoretical and simulation analysis of non-linear birth-death-innovation models. *BMC Evolutionary Biology*, **2004**, 4, 32	3	38
60	Coelomata and not Ecdysozoa: evidence from genome-wide phylogenetic analysis. *Genome Research*, **2004**, 14, 29-36	9.7	167
59	A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes. *Genome Biology*, **2004**, 5, R7	18.3	602
58	Simple stochastic birth and death models of genome evolution: was there enough time for us to evolve?. *Bioinformatics*, **2003**, 19, 1889-900	7.2	43
57	Remarkable interkingdom conservation of intron positions and massive, lineage-specific intron loss and gain in eukaryotic evolution. *Current Biology*, **2003**, 13, 1512-7	6.3	336

56	The COG database: an updated version includes eukaryotes. *BMC Bioinformatics*, **2003**, 4, 41	3.6	3212
55	No simple dependence between protein evolution rate and the number of protein-protein interactions: only the most prolific interactors tend to evolve slowly. *BMC Evolutionary Biology*, **2003**, 3, 1	3	158
54	Potential genomic determinants of hyperthermophily. *Trends in Genetics*, **2003**, 19, 172-6	8.5	66
53	Evolution of mosaic operons by horizontal gene transfer and gene displacement in situ. *Genome Biology*, **2003**, 4, R55	18.3	117
52	Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 10020-5	11.5	390
51	Gene loss, protein sequence divergence, gene dispensability, expression level, and interactivity are correlated in eukaryotic evolution. *Genome Research*, **2003**, 13, 2229-35	9.7	314
50	Birth and death of protein domains: a simple model of evolution explains power law behavior. *BMC Evolutionary Biology*, **2002**, 2, 18	3	134
49	Purifying and directional selection in overlapping prokaryotic genes. *Trends in Genetics*, **2002**, 18, 228-32	8.5	95
48	Genome trees and the tree of life. *Trends in Genetics*, **2002**, 18, 472-9	8.5	292
47	Scale-free networks in biology: new insights into the fundamentals of evolution?. *BioEssays*, **2002**, 24, 105-9	4.1	79
46	The structure of the protein universe and genome evolution. *Nature*, **2002**, 420, 218-23	50.4	456
45	Connected gene neighborhoods in prokaryotic genomes. *Nucleic Acids Research*, **2002**, 30, 2212-23	20.1	131
44	The role of lineage-specific gene family expansion in the evolution of eukaryotes. *Genome Research*, **2002**, 12, 1048-59	9.7	332
43	The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 4644-9	11.5	263
42	Essential genes are more evolutionarily conserved than are nonessential genes in bacteria. *Genome Research*, **2002**, 12, 962-8	9.7	330
41	Congruent evolution of different classes of non-coding DNA in prokaryotic genomes. *Nucleic Acids Research*, **2002**, 30, 4264-71	20.1	74
40	Horizontal Gene Transfer and its Role in the Evolution of Prokaryotes **2002**, 277-IX		4
39	Classification and evolution of P-loop GTPases and related ATPases. *Journal of Molecular Biology*, **2002**, 317, 41-72	6.5	882

38	Microevolutionary genomics of bacteria. *Theoretical Population Biology*, **2002**, 61, 435-47	1.2	79
37	Evolution of gene fusions: horizontal transfer versus independent events. *Genome Biology*, **2002**, 3, research0024	18.3	65
36	Selection in the evolution of gene duplications. *Genome Biology*, **2002**, 3, RESEARCH0008	18.3	491
35	Initial sequencing and analysis of the human genome. *Nature*, **2001**, 409, 860-921	50.4	17366
34	Gene conversions in genes encoding outer-membrane proteins in H. pylori and C. pneumoniae. *Trends in Genetics*, **2001**, 17, 7-10	8.5	69
33	Footprints of primordial introns on the eukaryotic genome: still no clear traces. *Trends in Genetics*, **2001**, 17, 499-501	8.5	18
32	Genome trees constructed using five different approaches suggest new major bacterial clades. *BMC Evolutionary Biology*, **2001**, 1, 8	3	231
31	Prediction of the archaeal exosome and its connections with the proteasome and the translation and transcription machineries by a comparative-genomic approach. *Genome Research*, **2001**, 11, 240-52	9.7	204
30	Constant relative rate of protein evolution and detection of functional diversification among bacterial, archaeal and eukaryotic proteins. *Genome Biology*, **2001**, 2, RESEARCH0053	18.3	29
29	Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum. *Journal of Bacteriology*, **2001**, 183, 4823-38	3.5	656
28	Genome Alignment, Evolution of Prokaryotic Genome Organization, and Prediction of Gene Function Using Genomic Context. *Genome Research*, **2001**, 11, 356-372	9.7	237
27	Genome of the extremely radiation-resistant bacterium Deinococcus radiodurans viewed from the perspective of comparative genomics. *Microbiology and Molecular Biology Reviews*, **2001**, 65, 44-79	13.2	512
26	Lineage-Specific Gene Expansions in Bacterial and Archaeal Genomes. *Genome Research*, **2001**, 11, 555-565	9.7	75
25	No footprints of primordial introns in a eukaryotic genome. *Trends in Genetics*, **2000**, 16, 333-4	8.5	25
24	Winnowing sequences from a database search. *Journal of Computational Biology*, **2000**, 7, 293-302	1.7	4
23	From complete genomes to measures of substitution rate variability within and between proteins. *Genome Research*, **2000**, 10, 991-1000	9.7	68
22	Estimating the number of protein folds and families from complete genome data. *Journal of Molecular Biology*, **2000**, 299, 897-905	6.5	164
21	Interkingdom gene fusions. *Genome Biology*, **2000**, 1, RESEARCH0013	18.3	17

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20	Towards understanding the first genome sequence of a crenarchaeon by genome annotation using clusters of orthologous groups of proteins (COGs). *Genome Biology*, **2000**, 1, RESEARCH0009	18.3	75
19	Rickettsiae and Chlamydiae: evidence of horizontal gene transfer and gene exchange. *Trends in Genetics*, **1999**, 15, 173-5	8.5	117
18	Short repeats and IS elements in the extremely radiation-resistant bacterium Deinococcus radiodurans and comparison to other bacterial species. *Research in Microbiology*, **1999**, 150, 711-24	4	20
17	Distribution of Protein Folds in the Three Superkingdoms of Life. *Genome Research*, **1999**, 9, 17-26	9.7	73
16	Evolution of Aminoacyl-tRNA Synthetases▯Analysis of Unique Domain Architectures and Phylogenetic Trees Reveals a Complex History of Horizontal Gene Transfer Events. *Genome Research*, **1999**, 9, 689-710	9.7	196
15	Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. *Trends in Genetics*, **1998**, 14, 442-4	8.5	294
14	A new superfamily of putative NTP-binding domains encoded by genomes of small DNA and RNA viruses. *FEBS Letters*, **1990**, 262, 145-8	3.8	276
13	Comparison of phylogenetic trees and search for a central trend in the ▯Forest of Life▯189-200		
12	A putative RNA-interference-based immune system in prokaryotes: the epitome of prokaryotic genomic diversity39-64		1
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7	Towards physical principles of biological evolution		2
6	Vast diversity of anti-CRISPR proteins predicted with a machine-learning approach		3
5	Seeker: Alignment-free identification of bacteriophage genomes by deep learning		7
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