

Yuri I Wolf

List of Publications by Year in descending order

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Version: 2024-02-01

277
papers

68,797
citations

1704

104
h-index

751

250
g-index

337
all docs

337
docs citations

337
times ranked

60581
citing authors

#	ARTICLE	IF	CITATIONS
1	Toward a theory of evolution as multilevel learning. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	32
2	Thermodynamics of evolution and the origin of life. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	26
3	Epistasis at the SARS-CoV-2 Receptor-Binding Domain Interface and the Propitiously Boring Implications for Vaccine Escape. MBio, 2022, 13, e0013522.	4.1	35
4	Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis. Biology Direct, 2022, 17, 7.	4.6	9
5	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.	4.7	8
6	The tRNA discriminator base defines the mutual orthogonality of two distinct pyrrolysyl-tRNA synthetase/tRNAPyl pairs in the same organism. Nucleic Acids Research, 2022, 50, 4601-4615.	14.5	7
7	S51 Family Peptidases Provide Resistance to Peptidyl-Nucleotide Antibiotic McC. MBio, 2022, 13, e0080522.	4.1	0
8	Conservation and Evolution of the Sporulation Gene Set in Diverse Members of the <i>Firmicutes</i> . Journal of Bacteriology, 2022, 204, .	2.2	20
9	Human pathogenic RNA viruses establish noncompeting lineages by occupying independent niches. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
10	A Novel Flavi-like Virus in Alfalfa (<i>Medicago sativa</i> L.) Crops along the Snake River Valley. Viruses, 2022, 14, 1320.	3.3	7
11	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. Nucleic Acids Research, 2021, 49, D274-D281.	14.5	441
12	Mutationâ€™selection balance and compensatory mechanisms in tumour evolution. Nature Reviews Genetics, 2021, 22, 251-262.	16.3	38
13	Evolution of DNA packaging in gene transfer agents. Virus Evolution, 2021, 7, veab015.	4.9	36
14	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, .	7.1	7
15	Defense Against Viruses and Other Genetic Parasites in Prokaryotes. , 2021, , 606-616.		1
16	Assessment of assumptions underlying models of prokaryotic pangenome evolution. BMC Biology, 2021, 19, 27.	3.8	5
17	Expanded diversity of Asgard archaea and their relationships with eukaryotes. Nature, 2021, 593, 553-557.	27.8	161
18	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. F1000Research, 2021, 10, 315.	1.6	7

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19	Nonessential Ribosomal Proteins in Bacteria and Archaea Identified Using Clusters of Orthologous Genes. <i>Journal of Bacteriology</i> , 2021, 203, .	2.2	14
20	Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021, 10, 447.	1.6	5
21	Allosteric Activation of SARS-CoV-2 RNA-Dependent RNA Polymerase by Remdesivir Triphosphate and Other Phosphorylated Nucleotides. <i>MBio</i> , 2021, 12, e0142321.	4.1	20
22	Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021, 10, 447.	1.6	9
23	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, .	7.1	196
24	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021, 29, 582-592.	7.7	33
25	A Unique Gene Module in Thermococcales Archaea Centered on a Hypervariable Protein Containing Immunoglobulin Domains. <i>Frontiers in Microbiology</i> , 2021, 12, 721392.	3.5	1
26	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. <i>F1000Research</i> , 2021, 10, 315.	1.6	9
27	CRISPRclassify: Repeat-Based Classification of CRISPR Loci. <i>CRISPR Journal</i> , 2021, 4, 558-574.	2.9	12
28	2021 Taxonomic update of phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2021, 166, 3513-3566.	2.1	62
29	Ancient Gene Capture and Recent Gene Loss Shape the Evolution of Orthopoxvirus-Host Interaction Genes. <i>MBio</i> , 2021, 12, e0149521.	4.1	74
30	Evolution of Type IV CRISPR-Cas Systems: Insights from CRISPR Loci in Integrative Conjugative Elements of <i>Acidithiobacillia</i> . <i>CRISPR Journal</i> , 2021, 4, 656-672.	2.9	21
31	Conflict-driven evolution. , 2021, , 77-96.		1
32	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.	12.8	80
33	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. <i>Nature Reviews Genetics</i> , 2020, 21, 119-131.	16.3	159
34	Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants. <i>Nature Reviews Microbiology</i> , 2020, 18, 67-83.	28.6	1,427
35	Deep phylogeny of cancer drivers and compensatory mutations. <i>Communications Biology</i> , 2020, 3, 551.	4.4	20
36	Seeker: alignment-free identification of bacteriophage genomes by deep learning. <i>Nucleic Acids Research</i> , 2020, 48, e121-e121.	14.5	78

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37	Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. <i>Nature Microbiology</i> , 2020, 5, 1262-1270.	13.3	156
38	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, .	4.1	12
39	Prediction of the incubation period for COVID-19 and future virus disease outbreaks. <i>BMC Biology</i> , 2020, 18, 186.	3.8	16
40	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020, 11, 3784.	12.8	64
41	Evolutionary and functional classification of the CARF domain superfamily, key sensors in prokaryotic antiviral defense. <i>Nucleic Acids Research</i> , 2020, 48, 8828-8847.	14.5	66
42	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020, 369, 1077-1084.	12.6	302
43	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	2.1	184
44	No waves of intelligent design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19639-19640.	7.1	1
45	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.	3.8	4
46	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.	7.1	196
47	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , 2020, 3, 156-163.	2.9	17
48	Interplay between DNA damage repair and apoptosis shapes cancer evolution through aneuploidy and microsatellite instability. <i>Nature Communications</i> , 2020, 11, 1234.	12.8	23
49	Global Organization and Proposed Megataxonomy of the Virus World. <i>Microbiology and Molecular Biology Reviews</i> , 2020, 84, .	6.6	378
50	Mapping CRISPR spaceromes reveals vast host-specific viromes of prokaryotes. <i>Communications Biology</i> , 2020, 3, 321.	4.4	31
51	Game-Theoretical Modeling of Interviral Conflicts Mediated by Mini-CRISPR Arrays. <i>Frontiers in Microbiology</i> , 2020, 11, 381.	3.5	6
52	<i>Cressdnaviricota</i> : a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. <i>Journal of Virology</i> , 2020, 94, .	3.4	118
53	Histidine-Triad Hydrolases Provide Resistance to Peptide-Nucleotide Antibiotics. <i>MBio</i> , 2020, 11, .	4.1	5
54	CRISPR Arrays Away from <i>cas</i> Genes. <i>CRISPR Journal</i> , 2020, 3, 535-549.	2.9	18

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55	Comparative genomics and evolution of trans-activating RNAs in Class 2 CRISPR-Cas systems. <i>RNA Biology</i> , 2019, 16, 435-448.	3.1	45
56	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.	7.1	14
57	Selection and Genome Plasticity as the Key Factors in the Evolution of Bacteria. <i>Physical Review X</i> , 2019, 9, .	8.9	9
58	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.	7.1	18
59	Classify viruses â€” the gain is worth the pain. <i>Nature</i> , 2019, 566, 318-320.	27.8	104
60	Translational coupling via termination-reinitiation in archaea and bacteria. <i>Nature Communications</i> , 2019, 10, 4006.	12.8	45
61	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019, 14, 3013-3031.	12.0	21
62	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.	7.1	18
63	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019, 10, .	4.1	41
64	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.	7.1	18
65	Reply to Holmes and DuchÃªne, â€œCan Sequence Phylogenies Safely Infer the Origin of the Global Virome?â€ Deep Phylogenetic Analysis of RNA Viruses Is Highly Challenging but Not Meaningless. <i>MBio</i> , 2019, 10, .	4.1	18
66	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. <i>MBio</i> , 2019, 10, .	4.1	85
67	Grammar of protein domain architectures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3636-3645.	7.1	46
68	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019, 47, 389-398.	3.4	35
69	Reply to â€”Evolutionary placement of Methanonatronarchaeiaâ€™. <i>Nature Microbiology</i> , 2019, 4, 560-561.	13.3	7
70	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019, 21, 2056-2078.	3.8	38
71	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.	7.1	1
72	Gene gain and loss push prokaryotes beyond the homologous recombination barrier and accelerate genome sequence divergence. <i>Nature Communications</i> , 2019, 10, 5376.	12.8	71

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73	Antibody-Mediated Protective Mechanisms Induced by a Trivalent Parainfluenza Virus-Vectored Ebola Virus Vaccine. <i>Journal of Virology</i> , 2019, 93, .	3.4	13
74	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019, 20, 1063-1070.	6.5	186
75	Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life. <i>Methods in Molecular Biology</i> , 2019, 1910, 241-269.	0.9	5
76	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.	1.6	10
77	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.	1.6	27
78	Towards physical principles of biological evolution. <i>Physica Scripta</i> , 2018, 93, 043001.	2.5	26
79	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2295-2310.	2.1	157
80	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	2.1	153
81	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	41
82	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.	7.1	23
83	Stable coevolutionary regimes for genetic parasites and their hosts: you must differ to coevolve. <i>Biology Direct</i> , 2018, 13, 27.	4.6	12
84	Origins and Evolution of the Global RNA Virome. <i>MBio</i> , 2018, 9, .	4.1	383
85	Classification and Nomenclature of CRISPR-Cas Systems: <i>Where from Here?</i> . <i>CRISPR Journal</i> , 2018, 1, 325-336.	2.9	232
86	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.	7.1	138
87	Estimation of universal and taxon-specific parameters of prokaryotic genome evolution. <i>PLoS ONE</i> , 2018, 13, e0195571.	2.5	5
88	<i>Escherichia coli</i> Itat is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA ^{Leu} . <i>Nucleic Acids Research</i> , 2018, 46, 7873-7885.	14.5	31
89	Proteomic Analysis of <i>Methanotropharchaeum thermophilum</i> AMET1, a Representative of a Putative New Class of Euryarchaeota, "Methanotropharchaeia". <i>Genes</i> , 2018, 9, 28.	2.4	8
90	Physical foundations of biological complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8678-E8687.	7.1	77

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91	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017, 15, 169-182.	28.6	792
92	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. <i>Journal of Physiology</i> , 2017, 595, 4611-4630.	2.9	11
93	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, 17081.	13.3	213
94	Reconstruction of the evolution of microbial defense systems. <i>BMC Evolutionary Biology</i> , 2017, 17, 94.	3.2	46
95	The CRISPR Spacer Space Is Dominated by Sequences from Species-Specific Mobilomes. <i>MBio</i> , 2017, 8, .	4.1	181
96	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.	14.5	38
97	ARMAN™ archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, 60.	12.8	116
98	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 233-261.	7.3	256
99	Two fundamentally different classes of microbial genes. <i>Nature Microbiology</i> , 2017, 2, 16208.	13.3	39
100	Extreme Deviations from Expected Evolutionary Rates in Archaeal Protein Families. <i>Genome Biology and Evolution</i> , 2017, 9, 2791-2811.	2.5	11
101	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.	2.5	3
102	Diverse functions of homologous actin isoforms are defined by their nucleotide, rather than their amino acid sequence. <i>ELife</i> , 2017, 6, .	6.0	44
103	Phylogenomics of Cas4 family nucleases. <i>BMC Evolutionary Biology</i> , 2017, 17, 232.	3.2	61
104	Inevitability of the emergence and persistence of genetic parasites caused by evolutionary instability of parasite-free states. <i>Biology Direct</i> , 2017, 12, 31.	4.6	59
105	High-quality genome sequence of the radioresistant bacterium <i>Deinococcus ficus</i> KS 0460. <i>Standards in Genomic Sciences</i> , 2017, 12, 46.	1.5	10
106	Theory of prokaryotic genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11399-11407.	7.1	125
107	Positive and strongly relaxed purifying selection drive the evolution of repeats in proteins. <i>Nature Communications</i> , 2016, 7, 13570.	12.8	35
108	Inevitability of Genetic Parasites. <i>Genome Biology and Evolution</i> , 2016, 8, 2856-2869.	2.5	85

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109	Just how Lamarckian is CRISPR-Cas immunity: the continuum of evolvability mechanisms. <i>Biology Direct</i> , 2016, 11, 9.	4.6	30
110	Evolvability of an Optimal Recombination Rate. <i>Genome Biology and Evolution</i> , 2016, 8, 70-77.	2.5	13
111	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, 818-840.	2.4	216
112	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015, 43, D261-D269.	14.5	1,345
113	No evidence of inhibition of horizontal gene transfer by CRISPR-Cas on evolutionary timescales. <i>ISME Journal</i> , 2015, 9, 2021-2027.	9.8	105
114	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	3.4	70
115	Immunity, suicide or both? Ecological determinants for the combined evolution of anti-pathogen defense systems. <i>BMC Evolutionary Biology</i> , 2015, 15, 43.	3.2	29
116	<i>Babela massiliensis</i> , a representative of a widespread bacterial phylum with unusual adaptations to parasitism in amoebae. <i>Biology Direct</i> , 2015, 10, 13.	4.6	71
117	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	28.6	2,081
118	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015, 60, 385-397.	9.7	971
119	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, 10908-10913.	7.1	23
120	Evolution of the CRISPR-Cas adaptive immunity systems in prokaryotes: models and observations on virus-host coevolution. <i>Molecular BioSystems</i> , 2015, 11, 20-27.	2.9	47
121	Virus-host arms race at the joint origin of multicellularity and programmed cell death. <i>Cell Cycle</i> , 2014, 13, 3083-3088.	2.6	44
122	Genomes in turmoil: quantification of genome dynamics in prokaryote supergenomes. <i>BMC Biology</i> , 2014, 12, 66.	3.8	170
123	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, 314-319.	7.1	64
124	Dark matter in archaeal genomes: a rich source of novel mobile elements, defense systems and secretory complexes. <i>Extremophiles</i> , 2014, 18, 877-893.	2.3	48
125	Pseudo-chaotic oscillations in CRISPR-virus coevolution predicted by bifurcation analysis. <i>Biology Direct</i> , 2014, 9, 13.	4.6	8
126	Origin of giant viruses from smaller DNA viruses not from a fourth domain of cellular life. <i>Virology</i> , 2014, 466-467, 38-52.	2.4	154

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127	Small Proteins Can No Longer Be Ignored. Annual Review of Biochemistry, 2014, 83, 753-777.	11.1	346
128	Universal Pacemaker of Genome Evolution in Animals and Fungi and Variation of Evolutionary Rates in Diverse Organisms. Genome Biology and Evolution, 2014, 6, 1268-1278.	2.5	21
129	Estimation of prokaryotic supergenome size and composition from gene frequency distributions. BMC Genomics, 2014, 15, S14.	2.8	7
130	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. Biology Direct, 2013, 8, 9.	4.6	102
131	Seeing the Tree of Life behind the phylogenetic forest. BMC Biology, 2013, 11, 46.	3.8	45
132	Quantifying the similarity of monotonic trajectories in rough and smooth fitness landscapes. Molecular BioSystems, 2013, 9, 1627.	2.9	5
133	An Insertion in the Catalytic Trigger Loop Gates the Secondary Channel of RNA Polymerase. Journal of Molecular Biology, 2013, 425, 82-93.	4.2	37
134	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. Cell Reports, 2013, 4, 938-944.	6.4	64
135	Reply to "Codon Usage Frequency of RNA Virus Genomes from High-Temperature Acidic-Environment Metagenomes" Journal of Virology, 2013, 87, 1920-1921.	3.4	5
136	The Vast, Conserved Mammalian lincRNome. PLoS Computational Biology, 2013, 9, e1002917.	3.2	62
137	The basic building blocks and evolution of CRISPR-Cas systems. Biochemical Society Transactions, 2013, 41, 1392-1400.	3.4	157
138	Evolutionary Dynamics of the Prokaryotic Adaptive Immunity System CRISPR-Cas in an Explicit Ecological Context. Journal of Bacteriology, 2013, 195, 3834-3844.	2.2	87
139	Gene Frequency Distributions Reject a Neutral Model of Genome Evolution. Genome Biology and Evolution, 2013, 5, 233-242.	2.5	61
140	Stability along with Extreme Variability in Core Genome Evolution. Genome Biology and Evolution, 2013, 5, 1393-1402.	2.5	38
141	Comparative genomics of defense systems in archaea and bacteria. Nucleic Acids Research, 2013, 41, 4360-4377.	14.5	365
142	Genome reduction as the dominant mode of evolution. BioEssays, 2013, 35, 829-837.	2.5	267
143	Universal Pacemaker of Genome Evolution. PLoS Computational Biology, 2012, 8, e1002785.	3.2	41
144	A Tight Link between Orthologs and Bidirectional Best Hits in Bacterial and Archaeal Genomes. Genome Biology and Evolution, 2012, 4, 1286-1294.	2.5	96

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145	Viral Diversity Threshold for Adaptive Immunity in Prokaryotes. MBio, 2012, 3, e00456-12.	4.1	114
146	Identification of Novel Positive-Strand RNA Viruses by Metagenomic Analysis of Archaea-Dominated Yellowstone Hot Springs. Journal of Virology, 2012, 86, 5562-5573.	3.4	107
147	Evolution of microbes and viruses: a paradigm shift in evolutionary biology?. Frontiers in Cellular and Infection Microbiology, 2012, 2, 119.	3.9	119
148	Genomic determinants of sporulation in <i>Bacilli</i> and <i>Clostridia</i> : towards the minimal set of sporulation-specific genes. Environmental Microbiology, 2012, 14, 2870-2890.	3.8	235
149	Nature and Intensity of Selection Pressure on CRISPR-Associated Genes. Journal of Bacteriology, 2012, 194, 1216-1225.	2.2	90
150	Updated clusters of orthologous genes for Archaea: a complex ancestor of the Archaea and the byways of horizontal gene transfer. Biology Direct, 2012, 7, 46.	4.6	142
151	Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life. Methods in Molecular Biology, 2012, 856, 53-79.	0.9	15
152	Phylogenomics of Prokaryotic Ribosomal Proteins. PLoS ONE, 2012, 7, e36972.	2.5	227
153	A comprehensive census of horizontal gene transfers from prokaryotes to unikonts. Genome Biology, 2011, 12, .	8.8	0
154	Phylogenomics of prokaryotic ribosomal proteins. Genome Biology, 2011, 12, .	9.6	0
155	Evolution and classification of the CRISPR-Cas systems. Nature Reviews Microbiology, 2011, 9, 467-477.	28.6	2,078
156	Computational methods for Gene Orthology inference. Briefings in Bioinformatics, 2011, 12, 379-391.	6.5	217
157	The Ecoresponsive Genome of <i>Daphnia pulex</i> . Science, 2011, 331, 555-561.	12.6	1,086
158	Comparison of Phylogenetic Trees and Search for a Central Trend in the "Forest of Life". Journal of Computational Biology, 2011, 18, 917-924.	1.6	27
159	Unification of Cas protein families and a simple scenario for the origin and evolution of CRISPR-Cas systems. Biology Direct, 2011, 6, 38.	4.6	379
160	Arginyltransferase Is an ATP-Independent Self-Regulating Enzyme that Forms Distinct Functional Complexes In Vivo. Chemistry and Biology, 2011, 18, 121-130.	6.0	71
161	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. Journal of Bacteriology, 2011, 193, 6039-6056.	2.2	358
162	Predictability of Evolutionary Trajectories in Fitness Landscapes. PLoS Computational Biology, 2011, 7, e1002302.	3.2	67

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163	The Tree and Net Components of Prokaryote Evolution. <i>Genome Biology and Evolution</i> , 2010, 2, 745-756.	2.5	221
164	The common ancestry of life. <i>Biology Direct</i> , 2010, 5, 64.	4.6	18
165	Non-homologous isofunctional enzymes: A systematic analysis of alternative solutions in enzyme evolution. <i>Biology Direct</i> , 2010, 5, 31.	4.6	119
166	Constraints and plasticity in genome and molecular-phenome evolution. <i>Nature Reviews Genetics</i> , 2010, 11, 487-498.	16.3	152
167	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, 2010, 1-4.	5.7	8
168	Relative Contributions of Intrinsic Structural and Functional Constraints and Translation Rate to the Evolution of Protein-Coding Genes. <i>Genome Biology and Evolution</i> , 2010, 2, 190-199.	2.5	23
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