

Yuri I Wolf

List of Publications by Year in descending order

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Version: 2024-02-01

277
papers

68,797
citations

1981

104
h-index

867

250
g-index

337
all docs

337
docs citations

337
times ranked

67651
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, .	3.3	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, .	3.3	26
3	Epistasis at the SARS-CoV-2 Receptor-Binding Domain Interface and the Propitiously Boring Implications for Vaccine Escape. MBio, 2022, 13, e0013522.	1.8	35
4	Phylogenomic analysis of the diversity of graspetides and proteins involved in their biosynthesis. Biology Direct, 2022, 17, 7.	1.9	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.	2.1	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.	6.5	7
7	S51 Family Peptidases Provide Resistance to Peptidyl-Nucleotide Antibiotic McC. MBio, 2022, 13, e0080522.	1.8	0
8	Conservation and Evolution of the Sporulation Gene Set in Diverse Members of the <i>Firmicutes</i> . Journal of Bacteriology, 2022, 204, .	1.0	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, .	3.3	9
10	A Novel Flavi-like Virus in Alfalfa (<i>Medicago sativa</i> L.) Crops along the Snake River Valley. Viruses, 2022, 14, 1320.	1.5	7
11	COG database update: focus on microbial diversity, model organisms, and widespread pathogens. Nucleic Acids Research, 2021, 49, D274-D281.	6.5	441
12	Mutation-selection balance and compensatory mechanisms in tumour evolution. Nature Reviews Genetics, 2021, 22, 251-262.	7.7	38
13	Evolution of DNA packaging in gene transfer agents. Virus Evolution, 2021, 7, veab015.	2.2	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, .	3.3	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.	1.7	5
17	Expanded diversity of Asgard archaea and their relationships with eukaryotes. Nature, 2021, 593, 553-557.	13.7	161
18	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. F1000Research, 2021, 10, 315.	0.8	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, .	1.0	14
20	Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021, 10, 447.	0.8	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.	1.8	20
22	Evolution of human respiratory virus epidemics. <i>F1000Research</i> , 2021, 10, 447.	0.8	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, .	3.3	196
24	Evolution of Microbial Genomics: Conceptual Shifts over a Quarter Century. <i>Trends in Microbiology</i> , 2021, 29, 582-592.	3.5	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.	1.5	1
26	Substantial impact of post-vaccination contacts on cumulative infections during viral epidemics. <i>F1000Research</i> , 2021, 10, 315.	0.8	9
27	CRISPRclassify: Repeat-Based Classification of CRISPR Loci. <i>CRISPR Journal</i> , 2021, 4, 558-574.	1.4	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.	0.9	62
29	Ancient Gene Capture and Recent Gene Loss Shape the Evolution of Orthopoxvirus-Host Interaction Genes. <i>MBio</i> , 2021, 12, e0149521.	1.8	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.	1.4	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.	5.8	80
33	Evolutionary entanglement of mobile genetic elements and host defence systems: guns for hire. <i>Nature Reviews Genetics</i> , 2020, 21, 119-131.	7.7	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.	13.6	1,427
35	Deep phylogeny of cancer drivers and compensatory mutations. <i>Communications Biology</i> , 2020, 3, 551.	2.0	20
36	Seeker: alignment-free identification of bacteriophage genomes by deep learning. <i>Nucleic Acids Research</i> , 2020, 48, e121-e121.	6.5	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.	5.9	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, .	1.8	12
39	Prediction of the incubation period for COVID-19 and future virus disease outbreaks. <i>BMC Biology</i> , 2020, 18, 186.	1.7	16
40	Machine-learning approach expands the repertoire of anti-CRISPR protein families. <i>Nature Communications</i> , 2020, 11, 3784.	5.8	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.	6.5	66
42	Diverse enzymatic activities mediate antiviral immunity in prokaryotes. <i>Science</i> , 2020, 369, 1077-1084.	6.0	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.	0.9	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.	3.3	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.	1.7	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.	3.3	196
47	Unprecedented Diversity of Unique CRISPR-Cas-Related Systems and Cas1 Homologs in Asgard Archaea. <i>CRISPR Journal</i> , 2020, 3, 156-163.	1.4	17
48	Interplay between DNA damage repair and apoptosis shapes cancer evolution through aneuploidy and microsatellite instability. <i>Nature Communications</i> , 2020, 11, 1234.	5.8	23
49	Global Organization and Proposed Megataxonomy of the Virus World. <i>Microbiology and Molecular Biology Reviews</i> , 2020, 84, .	2.9	378
50	Mapping CRISPR spaceromes reveals vast host-specific viromes of prokaryotes. <i>Communications Biology</i> , 2020, 3, 321.	2.0	31
51	Game-Theoretical Modeling of Interviral Conflicts Mediated by Mini-CRISPR Arrays. <i>Frontiers in Microbiology</i> , 2020, 11, 381.	1.5	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, .	1.5	118
53	Histidine-Triad Hydrolases Provide Resistance to Peptide-Nucleotide Antibiotics. <i>MBio</i> , 2020, 11, .	1.8	5
54	CRISPR Arrays Away from <i>cas</i> Genes. <i>CRISPR Journal</i> , 2020, 3, 535-549.	1.4	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.	1.5	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.	3.3	14
57	Selection and Genome Plasticity as the Key Factors in the Evolution of Bacteria. <i>Physical Review X</i> , 2019, 9, .	2.8	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.	3.3	18
59	Classify viruses “the gain is worth the pain. <i>Nature</i> , 2019, 566, 318-320.	13.7	104
60	Translational coupling via termination-reinitiation in archaea and bacteria. <i>Nature Communications</i> , 2019, 10, 4006.	5.8	45
61	Systematic prediction of functionally linked genes in bacterial and archaeal genomes. <i>Nature Protocols</i> , 2019, 14, 3013-3031.	5.5	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.	3.3	18
63	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. <i>MBio</i> , 2019, 10, .	1.8	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.	3.3	18
65	Reply to Holmes and Duchêne, “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, .	1.8	18
66	Virus Genomes from Deep Sea Sediments Expand the Ocean Megavirome and Support Independent Origins of Viral Gigantism. <i>MBio</i> , 2019, 10, .	1.8	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.	3.3	46
68	Towards functional characterization of archaeal genomic dark matter. <i>Biochemical Society Transactions</i> , 2019, 47, 389-398.	1.6	35
69	Reply to “Evolutionary placement of Methanonatronarchaeia”™. <i>Nature Microbiology</i> , 2019, 4, 560-561.	5.9	7
70	Integrated mobile genetic elements in Thaumarchaeota. <i>Environmental Microbiology</i> , 2019, 21, 2056-2078.	1.8	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.	3.3	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.	5.8	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, .	1.5	13
74	Microbial genome analysis: the COG approach. <i>Briefings in Bioinformatics</i> , 2019, 20, 1063-1070.	3.2	186
75	Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life. <i>Methods in Molecular Biology</i> , 2019, 1910, 241-269.	0.4	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.	0.8	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.	0.8	27
78	Towards physical principles of biological evolution. <i>Physica Scripta</i> , 2018, 93, 043001.	1.2	26
79	Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2295-2310.	0.9	157
80	Taxonomy of the order Mononegavirales: update 2018. <i>Archives of Virology</i> , 2018, 163, 2283-2294.	0.9	153
81	Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	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.	3.3	23
83	Stable coevolutionary regimes for genetic parasites and their hosts: you must differ to coevolve. <i>Biology Direct</i> , 2018, 13, 27.	1.9	12
84	Origins and Evolution of the Global RNA Virome. <i>MBio</i> , 2018, 9, .	1.8	383
85	Classification and Nomenclature of CRISPR-Cas Systems: <i>Where from Here?</i> . <i>CRISPR Journal</i> , 2018, 1, 325-336.	1.4	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.	3.3	138
87	Estimation of universal and taxon-specific parameters of prokaryotic genome evolution. <i>PLoS ONE</i> , 2018, 13, e0195571.	1.1	5
88	<i>Escherichia coli</i> Itat is a type II toxin that inhibits translation by acetylating isoleucyl-tRNA ^{lle} . <i>Nucleic Acids Research</i> , 2018, 46, 7873-7885.	6.5	31
89	Proteomic Analysis of <i>Methanotrophonarchaeum thermophilum</i> AMET1, a Representative of a Putative New Class of Euryarchaeota, "Methanotrophonarchaeia". <i>Genes</i> , 2018, 9, 28.	1.0	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.	3.3	77

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91	Diversity and evolution of class 2 CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2017, 15, 169-182.	13.6	792
92	Early vertebrate origin and diversification of small transmembrane regulators of cellular ion transport. <i>Journal of Physiology</i> , 2017, 595, 4611-4630.	1.3	11
93	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, 17081.	5.9	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, .	1.8	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.	6.5	38
97	ARMAN™ archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, 60.	5.8	116
98	Evolutionary Genomics of Defense Systems in Archaea and Bacteria. <i>Annual Review of Microbiology</i> , 2017, 71, 233-261.	2.9	256
99	Two fundamentally different classes of microbial genes. <i>Nature Microbiology</i> , 2017, 2, 16208.	5.9	39
100	Extreme Deviations from Expected Evolutionary Rates in Archaeal Protein Families. <i>Genome Biology and Evolution</i> , 2017, 9, 2791-2811.	1.1	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.	1.1	3
102	Diverse functions of homologous actin isoforms are defined by their nucleotide, rather than their amino acid sequence. <i>ELife</i> , 2017, 6, .	2.8	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.	1.9	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.	3.3	125
107	Positive and strongly relaxed purifying selection drive the evolution of repeats in proteins. <i>Nature Communications</i> , 2016, 7, 13570.	5.8	35
108	Inevitability of Genetic Parasites. <i>Genome Biology and Evolution</i> , 2016, 8, 2856-2869.	1.1	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.	1.9	30
110	Evolvability of an Optimal Recombination Rate. <i>Genome Biology and Evolution</i> , 2016, 8, 70-77.	1.1	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.	1.1	216
112	Expanded microbial genome coverage and improved protein family annotation in the COG database. <i>Nucleic Acids Research</i> , 2015, 43, D261-D269.	6.5	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.	4.4	105
114	Functional Diversity of Haloacid Dehalogenase Superfamily Phosphatases from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 18678-18698.	1.6	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.	1.9	71
117	An updated evolutionary classification of CRISPR-Cas systems. <i>Nature Reviews Microbiology</i> , 2015, 13, 722-736.	13.6	2,081
118	Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems. <i>Molecular Cell</i> , 2015, 60, 385-397.	4.5	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.	3.3	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.	1.3	44
122	Genomes in turmoil: quantification of genome dynamics in prokaryote supergenomes. <i>BMC Biology</i> , 2014, 12, 66.	1.7	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.	3.3	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.	0.9	48
125	Pseudo-chaotic oscillations in CRISPR-virus coevolution predicted by bifurcation analysis. <i>Biology Direct</i> , 2014, 9, 13.	1.9	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.	1.1	154

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127	Small Proteins Can No Longer Be Ignored. <i>Annual Review of Biochemistry</i> , 2014, 83, 753-777.	5.0	346
128	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, 1268-1278.	1.1	21
129	Estimation of prokaryotic supergenome size and composition from gene frequency distributions. <i>BMC Genomics</i> , 2014, 15, S14.	1.2	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. <i>Biology Direct</i> , 2013, 8, 9.	1.9	102
131	Seeing the Tree of Life behind the phylogenetic forest. <i>BMC Biology</i> , 2013, 11, 46.	1.7	45
132	Quantifying the similarity of monotonic trajectories in rough and smooth fitness landscapes. <i>Molecular BioSystems</i> , 2013, 9, 1627.	2.9	5
133	An Insertion in the Catalytic Trigger Loop Gates the Secondary Channel of RNA Polymerase. <i>Journal of Molecular Biology</i> , 2013, 425, 82-93.	2.0	37
134	Differential Translation Tunes Uneven Production of Operon-Encoded Proteins. <i>Cell Reports</i> , 2013, 4, 938-944.	2.9	64
135	Reply to "Codon Usage Frequency of RNA Virus Genomes from High-Temperature Acidic-Environment Metagenomes" <i>Journal of Virology</i> , 2013, 87, 1920-1921.	1.5	5
136	The Vast, Conserved Mammalian lincRNome. <i>PLoS Computational Biology</i> , 2013, 9, e1002917.	1.5	62
137	The basic building blocks and evolution of CRISPR-Cas systems. <i>Biochemical Society Transactions</i> , 2013, 41, 1392-1400.	1.6	157
138	Evolutionary Dynamics of the Prokaryotic Adaptive Immunity System CRISPR-Cas in an Explicit Ecological Context. <i>Journal of Bacteriology</i> , 2013, 195, 3834-3844.	1.0	87
139	Gene Frequency Distributions Reject a Neutral Model of Genome Evolution. <i>Genome Biology and Evolution</i> , 2013, 5, 233-242.	1.1	61
140	Stability along with Extreme Variability in Core Genome Evolution. <i>Genome Biology and Evolution</i> , 2013, 5, 1393-1402.	1.1	38
141	Comparative genomics of defense systems in archaea and bacteria. <i>Nucleic Acids Research</i> , 2013, 41, 4360-4377.	6.5	365
142	Genome reduction as the dominant mode of evolution. <i>BioEssays</i> , 2013, 35, 829-837.	1.2	267
143	Universal Pacemaker of Genome Evolution. <i>PLoS Computational Biology</i> , 2012, 8, e1002785.	1.5	41
144	A Tight Link between Orthologs and Bidirectional Best Hits in Bacterial and Archaeal Genomes. <i>Genome Biology and Evolution</i> , 2012, 4, 1286-1294.	1.1	96

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145	Viral Diversity Threshold for Adaptive Immunity in Prokaryotes. MBio, 2012, 3, e00456-12.	1.8	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.	1.5	107
147	Evolution of microbes and viruses: a paradigm shift in evolutionary biology?. Frontiers in Cellular and Infection Microbiology, 2012, 2, 119.	1.8	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.	1.8	235
149	Nature and Intensity of Selection Pressure on CRISPR-Associated Genes. Journal of Bacteriology, 2012, 194, 1216-1225.	1.0	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.	1.9	142
151	Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life. Methods in Molecular Biology, 2012, 856, 53-79.	0.4	15
152	Phylogenomics of Prokaryotic Ribosomal Proteins. PLoS ONE, 2012, 7, e36972.	1.1	227
153	A comprehensive census of horizontal gene transfers from prokaryotes to unikonts. Genome Biology, 2011, 12, .	3.8	0
154	Phylogenomics of prokaryotic ribosomal proteins. Genome Biology, 2011, 12, .	13.9	0
155	Evolution and classification of the CRISPR-Cas systems. Nature Reviews Microbiology, 2011, 9, 467-477.	13.6	2,078
156	Computational methods for Gene Orthology inference. Briefings in Bioinformatics, 2011, 12, 379-391.	3.2	217
157	The Ecoresponsive Genome of <i>Daphnia pulex</i> . Science, 2011, 331, 555-561.	6.0	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.	0.8	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.	1.9	379
160	Arginyltransferase Is an ATP-Independent Self-Regulating Enzyme that Forms Distinct Functional Complexes In Vivo. Chemistry and Biology, 2011, 18, 121-130.	6.2	71
161	Defense Islands in Bacterial and Archaeal Genomes and Prediction of Novel Defense Systems. Journal of Bacteriology, 2011, 193, 6039-6056.	1.0	358
162	Predictability of Evolutionary Trajectories in Fitness Landscapes. PLoS Computational Biology, 2011, 7, e1002302.	1.5	67

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163	The Tree and Net Components of Prokaryote Evolution. <i>Genome Biology and Evolution</i> , 2010, 2, 745-756.	1.1	221
164	The common ancestry of life. <i>Biology Direct</i> , 2010, 5, 64.	1.9	18
165	Non-homologous isofunctional enzymes: A systematic analysis of alternative solutions in enzyme evolution. <i>Biology Direct</i> , 2010, 5, 31.	1.9	119
166	Constraints and plasticity in genome and molecular-phenome evolution. <i>Nature Reviews Genetics</i> , 2010, 11, 487-498.	7.7	152
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