

Claus O Wilke

List of Publications by Year in descending order

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Version: 2024-02-01

189
papers

21,340
citations

34016

52
h-index

13338

130
g-index

249
all docs

249
docs citations

249
times ranked

24693
citing authors

#	ARTICLE	IF	CITATIONS
1	Welcome to the Tidyverse. <i>Journal of Open Source Software</i> , 2019, 4, 1686.	2.0	9,245
2	Mistranslation-Induced Protein Misfolding as a Dominant Constraint on Coding-Sequence Evolution. <i>Cell</i> , 2008, 134, 341-352.	13.5	949
3	Why highly expressed proteins evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14338-14343.	3.3	738
4	Evolution of digital organisms at high mutation rates leads to survival of the flattest. <i>Nature</i> , 2001, 412, 331-333.	13.7	548
5	The evolutionary consequences of erroneous protein synthesis. <i>Nature Reviews Genetics</i> , 2009, 10, 715-724.	7.7	437
6	Residual Human Immunodeficiency Virus Type 1 Viremia in Some Patients on Antiretroviral Therapy Is Dominated by a Small Number of Invariant Clones Rarely Found in Circulating CD4 + T Cells. <i>Journal of Virology</i> , 2006, 80, 6441-6457.	1.5	377
7	A Single Determinant Dominates the Rate of Yeast Protein Evolution. <i>Molecular Biology and Evolution</i> , 2006, 23, 327-337.	3.5	373
8	Systematic humanization of yeast genes reveals conserved functions and genetic modularity. <i>Science</i> , 2015, 348, 921-925.	6.0	361
9	Maximum Allowed Solvent Accessibilities of Residues in Proteins. <i>PLoS ONE</i> , 2013, 8, e80635.	1.1	340
10	Thermodynamic prediction of protein neutrality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 606-611.	3.3	320
11	Avida: A Software Platform for Research in Computational Evolutionary Biology. <i>Artificial Life</i> , 2004, 10, 191-229.	1.0	280
12	A Universal Trend of Reduced mRNA Stability near the Translation-Initiation Site in Prokaryotes and Eukaryotes. <i>PLoS Computational Biology</i> , 2010, 6, e1000664.	1.5	266
13	Theory of Lethal Mutagenesis for Viruses. <i>Journal of Virology</i> , 2007, 81, 2930-2939.	1.5	250
14	Causes of evolutionary rate variation among protein sites. <i>Nature Reviews Genetics</i> , 2016, 17, 109-121.	7.7	247
15	Quasispecies theory in the context of population genetics. <i>BMC Evolutionary Biology</i> , 2005, 5, 44.	3.2	234
16	Translationally Optimal Codons Associate with Structurally Sensitive Sites in Proteins. <i>Molecular Biology and Evolution</i> , 2009, 26, 1571-1580.	3.5	183
17	Structural Determinants of the Rate of Protein Evolution in Yeast. <i>Molecular Biology and Evolution</i> , 2006, 23, 1751-1761.	3.5	162
18	The traveling-wave approach to asexual evolution: Muller's ratchet and speed of adaptation. <i>Theoretical Population Biology</i> , 2008, 73, 24-46.	0.5	149

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19	Thermodynamics of Neutral Protein Evolution. <i>Genetics</i> , 2007, 175, 255-266.	1.2	137
20	The Speed of Adaptation in Large Asexual Populations. <i>Genetics</i> , 2004, 167, 2045-2053.	1.2	125
21	Analysis of Human Immunodeficiency Virus Type 1 Viremia and Provirus in Resting CD4 ⁺ T Cells Reveals a Novel Source of Residual Viremia in Patients on Antiretroviral Therapy. <i>Journal of Virology</i> , 2009, 83, 8470-8481.	1.5	122
22	Discovery of Next-Generation Antimicrobials through Bacterial Self-Screening of Surface-Displayed Peptide Libraries. <i>Cell</i> , 2018, 172, 618-628.e13.	13.5	122
23	Decay dynamics of HIV-1 depend on the inhibited stages of the viral life cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4832-4837.	3.3	119
24	Evolution of mutational robustness. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2003, 522, 3-11.	0.4	116
25	The Relationship Between Relative Solvent Accessibility and Evolutionary Rate in Protein Evolution. <i>Genetics</i> , 2011, 188, 479-488.	1.2	116
26	BACPHLIP: predicting bacteriophage lifestyle from conserved protein domains. <i>PeerJ</i> , 2021, 9, e11396.	0.9	113
27	Adaptive Evolution on Neutral Networks. <i>Bulletin of Mathematical Biology</i> , 2001, 63, 715-730.	0.9	111
28	Adaptive Radiation from Resource Competition in Digital Organisms. <i>Science</i> , 2004, 305, 84-86.	6.0	110
29	The Relationship between dN/dS and Scaled Selection Coefficients. <i>Molecular Biology and Evolution</i> , 2015, 32, 1097-1108.	3.5	106
30	Dynamic fitness landscapes in molecular evolution. <i>Physics Reports</i> , 2001, 349, 395-446.	10.3	104
31	Biophysical Models of Protein Evolution: Understanding the Patterns of Evolutionary Sequence Divergence. <i>Annual Review of Biophysics</i> , 2017, 46, 85-103.	4.5	103
32	Interaction between directional epistasis and average mutational effects. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001, 268, 1469-1474.	1.2	100
33	Stability and the Evolvability of Function in a Model Protein. <i>Biophysical Journal</i> , 2004, 86, 2758-2764.	0.2	95
34	On the conservative nature of intragenic recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5380-5385.	3.3	95
35	Functional Sites Induce Long-Range Evolutionary Constraints in Enzymes. <i>PLoS Biology</i> , 2016, 14, e1002452.	2.6	94
36	Co-infection Weakens Selection Against Epistatic Mutations in RNA Viruses. <i>Genetics</i> , 2004, 168, 9-19.	1.2	88

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37	The biology of digital organisms. <i>Trends in Ecology and Evolution</i> , 2002, 17, 528-532.	4.2	86
38	Pyvolve: A Flexible Python Module for Simulating Sequences along Phylogenies. <i>PLoS ONE</i> , 2015, 10, e0139047.	1.1	83
39	Viral factors in influenza pandemic risk assessment. <i>ELife</i> , 2016, 5, .	2.8	82
40	Experiments on the role of deleterious mutations as stepping stones in adaptive evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3171-8.	3.3	76
41	Density-Dependent Selection in Vesicular Stomatitis Virus. <i>Journal of Virology</i> , 2004, 78, 5799-5804.	1.5	75
42	SELECTION FOR FITNESS VERSUS SELECTION FOR ROBUSTNESS IN RNA SECONDARY STRUCTURE FOLDING. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 2412-2420.	1.1	73
43	The look-ahead effect of phenotypic mutations. <i>Biology Direct</i> , 2008, 3, 18.	1.9	73
44	Single-Cell Virology: On-Chip Investigation of Viral Infection Dynamics. <i>Cell Reports</i> , 2017, 21, 1692-1704.	2.9	71
45	PeptideBuilder: A simple Python library to generate model peptides. <i>PeerJ</i> , 2013, 1, e80.	0.9	70
46	The Stochastic Edge in Adaptive Evolution. <i>Genetics</i> , 2008, 179, 603-620.	1.2	68
47	Limits on Replenishment of the Resting CD4+ T Cell Reservoir for HIV in Patients on HAART. <i>PLoS Pathogens</i> , 2007, 3, e122.	2.1	67
48	Limitations of alignment-free tools in total RNA-seq quantification. <i>BMC Genomics</i> , 2018, 19, 510.	1.2	64
49	Detecting Positive and Purifying Selection at Synonymous Sites in Yeast and Worm. <i>Molecular Biology and Evolution</i> , 2010, 27, 1912-1922.	3.5	62
50	Bringing Molecules Back into Molecular Evolution. <i>PLoS Computational Biology</i> , 2012, 8, e1002572.	1.5	62
51	Compensatory mutations cause excess of antagonistic epistasis in RNA secondary structure folding. <i>BMC Evolutionary Biology</i> , 2003, 3, 3.	3.2	61
52	EFFECTS OF POPULATION SIZE AND MUTATION RATE ON THE EVOLUTION OF MUTATIONAL ROBUSTNESS. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 666-674.	1.1	58
53	Phenotypic mixing and hiding may contribute to memory in viral quasispecies. <i>BMC Microbiology</i> , 2003, 3, 11.	1.3	57
54	T Cell Dynamics and the Response to HAART in a Cohort of HIV-1-Infected Elite Suppressors. <i>Clinical Infectious Diseases</i> , 2009, 49, 1763-1766.	2.9	57

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55	Large-scale analysis of post-translational modifications in <i>E. coli</i> under glucose-limiting conditions. <i>BMC Genomics</i> , 2017, 18, 301.	1.2	55
56	Slow Fitness Recovery in a Codon-Modified Viral Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 2997-3004.	3.5	54
57	Socioeconomic disparities in the presentation of acute bacterial sinusitis complications in children. <i>Laryngoscope</i> , 2014, 124, 1700-1706.	1.1	54
58	Contact Density Affects Protein Evolutionary Rate from Bacteria to Animals. <i>Journal of Molecular Evolution</i> , 2008, 66, 395-404.	0.8	53
59	Low-level HIV-1 replication and the dynamics of the resting CD4+T cell reservoir for HIV-1 in the setting of HAART. <i>BMC Infectious Diseases</i> , 2008, 8, 2.	1.3	51
60	Population Genetics of Translational Robustness. <i>Genetics</i> , 2006, 173, 473-481.	1.2	50
61	Risk factors for development of chronic rhinosinusitis in patients with allergic rhinitis. <i>International Forum of Allergy and Rhinology</i> , 2012, 2, 370-375.	1.5	49
62	Relationship between protein thermodynamic constraints and variation of evolutionary rates among sites. <i>Physical Biology</i> , 2015, 12, 025002.	0.8	49
63	Integrating Sequence Variation and Protein Structure to Identify Sites under Selection. <i>Molecular Biology and Evolution</i> , 2013, 30, 36-44.	3.5	47
64	Molecular clock in neutral protein evolution. , 2004, 5, 25.		46
65	The <i>E. coli</i> molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017, 7, 45303.	1.6	46
66	Sicegar: R package for sigmoidal and double-sigmoidal curve fitting. <i>PeerJ</i> , 2018, 6, e4251.	0.9	46
67	Viral evolution under the pressure of an adaptive immune system: Optimal mutation rates for viral escape. <i>Complexity</i> , 2002, 8, 28-33.	0.9	44
68	Predicting Evolutionary Site Variability from Structure in Viral Proteins: Buriedness, Packing, Flexibility, and Design. <i>Journal of Molecular Evolution</i> , 2014, 79, 130-142.	0.8	43
69	Signatures of protein biophysics in coding sequence evolution. <i>Current Opinion in Structural Biology</i> , 2010, 20, 385-389.	2.6	42
70	Sinonasal anatomic variants and asthma are associated with faster development of chronic rhinosinusitis in patients with allergic rhinitis. <i>International Forum of Allergy and Rhinology</i> , 2013, 3, 755-761.	1.5	42
71	Controlled Measurement and Comparative Analysis of Cellular Components in <i>E. coli</i> Reveals Broad Regulatory Changes in Response to Glucose Starvation. <i>PLoS Computational Biology</i> , 2015, 11, e1004400.	1.5	42
72	Geometric Constraints Dominate the Antigenic Evolution of Influenza H3N2 Hemagglutinin. <i>PLoS Pathogens</i> , 2015, 11, e1004940.	2.1	41

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73	Predicting the Tolerance of Proteins to Random Amino Acid Substitution. <i>Biophysical Journal</i> , 2005, 89, 3714-3720.	0.2	40
74	Lethal Mutagenesis of Bacteria. <i>Genetics</i> , 2008, 180, 1061-1070.	1.2	40
75	Translationally optimal codons associate with aggregation-prone sites in proteins. <i>Proteomics</i> , 2010, 10, 4163-4171.	1.3	40
76	Modeling coding-sequence evolution within the context of residue solvent accessibility. <i>BMC Evolutionary Biology</i> , 2012, 12, 179.	3.2	38
77	Metagenomic discovery of CRISPR-associated transposons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	38
78	Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. <i>PLoS Biology</i> , 2020, 18, e3000627.	2.6	37
79	Probability of Fixation of an Advantageous Mutant in a Viral Quasispecies. <i>Genetics</i> , 2003, 163, 467-474.	1.2	37
80	Selection for mutational robustness in finite populations. <i>Journal of Theoretical Biology</i> , 2006, 243, 181-190.	0.8	35
81	Breaking proteins with mutations: threads and thresholds in evolution. <i>Molecular Systems Biology</i> , 2007, 3, 76.	3.2	35
82	The Phenotype-Fitness Map in Experimental Evolution of Phages. <i>PLoS ONE</i> , 2011, 6, e27796.	1.1	35
83	Sequence amplification via cell passaging creates spurious signals of positive adaptation in influenza virus H3N2 hemagglutinin. <i>Virus Evolution</i> , 2016, 2, vew026.	2.2	35
84	Reduced mRNA Secondary-Structure Stability Near the Start Codon Indicates Functional Genes in Prokaryotes. <i>Genome Biology and Evolution</i> , 2012, 4, 80-88.	1.1	33
85	Avian Influenza Virus PB1 Gene in H3N2 Viruses Evolved in Humans To Reduce Interferon Inhibition by Skewing Codon Usage toward Interferon-Altered tRNA Pools. <i>MBio</i> , 2018, 9, .	1.8	33
86	REPLICATION AT PERIODICALLY CHANGING MULTIPLICITY OF INFECTION PROMOTES STABLE COEXISTENCE OF COMPETING VIRAL POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 900-905.	1.1	32
87	Predicting an epidemic trajectory is difficult. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28549-28551.	3.3	31
88	Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak. <i>Virus Evolution</i> , 2015, 1, vev006.	2.2	30
89	<i>Avida.</i> , 2009, , 3-35.		30
90	Constraints on the dominant mechanism for HIV viral dynamics in patients on raltegravir. <i>Antiviral Therapy</i> , 2009, 14, 263-271.	0.6	30

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91	Membrane Environment Imposes Unique Selection Pressures on Transmembrane Domains of G Protein-Coupled Receptors. <i>Journal of Molecular Evolution</i> , 2013, 76, 172-182.	0.8	29
92	Optimal adaptive performance and delocalization in NK fitness landscapes. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2002, 304, 495-506.	1.2	28
93	Cross-species comparison of site-specific evolutionary-rate variation in influenza haemagglutinin. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120334.	1.8	28
94	Methods of modelling viral disease dynamics across the within- and between-host scales: the impact of virus dose on host population immunity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1931-1941.	1.8	27
95	The Many Nuanced Evolutionary Consequences of Duplicated Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 304-314.	3.5	26
96	Constraints on the dominant mechanism for HIV viral dynamics in patients on raltegravir. <i>Antiviral Therapy</i> , 2009, 14, 263-71.	0.6	26
97	Specific and Nonspecific Host Adaptation during Arboviral Experimental Evolution. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 21, 71-81.	1.0	25
98	Incongruent fitness landscapes, not tradeoffs, dominate the adaptation of vesicular stomatitis virus to novel host types. <i>Journal of General Virology</i> , 2010, 91, 1484-1493.	1.3	24
99	Phenotypic differences in viral immune escape explained by linking within-host dynamics to host-population immunity. <i>Journal of Theoretical Biology</i> , 2010, 265, 501-510.	0.8	23
100	Short Communication: Dynamic Constraints on the Second Phase Compartment of HIV-Infected Cells. <i>AIDS Research and Human Retroviruses</i> , 2011, 27, 759-761.	0.5	23
101	Accelerated simulation of evolutionary trajectories in origin-fixation models. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160906.	1.5	22
102	Fitting outbreak models to data from many small norovirus outbreaks. <i>Epidemics</i> , 2014, 6, 18-29.	1.5	21
103	Extensively Parameterized Mutation-Selection Models Reliably Capture Site-Specific Selective Constraint. <i>Molecular Biology and Evolution</i> , 2016, 33, 2990-3002.	3.5	21
104	Reduced Protein Expression in a Virus Attenuated by Codon Deoptimization. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2957-2968.	0.8	21
105	Reduced stability of mRNA secondary structure near the translation-initiation site in dsDNA viruses. <i>BMC Evolutionary Biology</i> , 2011, 11, 59.	3.2	20
106	Contact Heterogeneity and Phylodynamics: How Contact Networks Shape Parasite Evolutionary Trees. <i>Interdisciplinary Perspectives on Infectious Diseases</i> , 2011, 2011, 1-9.	0.6	20
107	Comprehensive, structurally-informed alignment and phylogeny of vertebrate biogenic amine receptors. <i>PeerJ</i> , 2015, 3, e773.	0.9	20
108	Rapid Adaptive Amplification of Preexisting Variation in an RNA Virus. <i>Journal of Virology</i> , 2008, 82, 4354-4362.	1.5	19

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109	Simple model of evolution with variable system size. <i>Physical Review E</i> , 1997, 56, 7128-7131.	0.8	18
110	Genomic Evolution of Vesicular Stomatitis Virus Strains with Differences in Adaptability. <i>Journal of Virology</i> , 2010, 84, 4960-4968.	1.5	18
111	Does Mutational Robustness Inhibit Extinction by Lethal Mutagenesis in Viral Populations?. <i>PLoS Computational Biology</i> , 2010, 6, e1000811.	1.5	18
112	Amino-acid site variability among natural and designed proteins. <i>PeerJ</i> , 2013, 1, e211.	0.9	18
113	Predicting Growth Conditions from Internal Metabolic Fluxes in an In-Silico Model of <i>E. coli</i> . <i>PLoS ONE</i> , 2014, 9, e114608.	1.1	17
114	A Comparison of One-Rate and Two-Rate Inference Frameworks for Site-Specific dN/dS Estimation. <i>Genetics</i> , 2016, 204, 499-511.	1.2	17
115	Dissecting the roles of local packing density and longer-range effects in protein sequence evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 841-854.	1.5	17
116	Axion cyclotron emissivity of magnetized white dwarfs and neutron stars. <i>Physical Review D</i> , 1997, 56, 1313-1319.	1.6	16
117	Congruent Evolution of Fitness and Genetic Robustness in Vesicular Stomatitis Virus. <i>Journal of Virology</i> , 2013, 87, 4923-4928.	1.5	16
118	Within-Gene Shine-Dalgarno Sequences Are Not Selected for Function. <i>Molecular Biology and Evolution</i> , 2018, 35, 2487-2498.	3.5	16
119	More than efficacy revealed by single-cell analysis of antiviral therapeutics. <i>Science Advances</i> , 2019, 5, eaax4761.	4.7	16
120	A systematic analysis of the beta hairpin motif in the Protein Data Bank. <i>Protein Science</i> , 2021, 30, 613-623.	3.1	16
121	Aftershocks in coherent-noise models. <i>Physica D: Nonlinear Phenomena</i> , 1998, 120, 401-417.	1.3	15
122	Maternal Effects in Molecular Evolution. <i>Physical Review Letters</i> , 2002, 88, 078101.	2.9	15
123	Quasispecies in Time-Dependent Environments. , 2006, 299, 33-50.		15
124	RNaseIII and T4 Polynucleotide Kinase sequence biases and solutions during RNA-seq library construction. <i>Biology Direct</i> , 2013, 8, 16.	1.9	15
125	Computational and Functional Analysis of the Virus-Receptor Interface Reveals Host Range Trade-Offs in New World Arenaviruses. <i>Journal of Virology</i> , 2015, 89, 11643-11653.	1.5	15
126	Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein. <i>PLoS ONE</i> , 2017, 12, e0164905.	1.1	15

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127	Calculating site-specific evolutionary rates at the amino-acid or codon level yields similar rate estimates. PeerJ, 2017, 5, e3391.	0.9	15
128	Adaptive walks on time-dependent fitness landscapes. Physical Review E, 1999, 60, 2154-2159.	0.8	14
129	Measuring evolutionary rates of proteins in a structural context. F1000Research, 2017, 6, 1845.	0.8	14
130	Genealogical process on a correlated fitness landscape. The Journal of Experimental Zoology, 2002, 294, 274-284.	1.4	13
131	Temporal and spatial alterations in mutant swarm size of St. Louis encephalitis virus in mosquito hosts. Infection, Genetics and Evolution, 2011, 11, 460-468.	1.0	13
132	Beyond Thermodynamic Constraints: Evolutionary Sampling Generates Realistic Protein Sequence Variation. Genetics, 2018, 208, 1387-1395.	1.2	13
133	Phylogenetic Weighting Does Little to Improve the Accuracy of Evolutionary Coupling Analyses. Entropy, 2019, 21, 1000.	1.1	13
134	Transcript degradation and codon usage regulate gene expression in a lytic phage. Virus Evolution, 2019, 5, vez055.	2.2	13
135	Learning the local landscape of protein structures with convolutional neural networks. Journal of Biological Physics, 2021, 47, 435-454.	0.7	13
136	Digital Evolution in Time-Dependent Fitness Landscapes. Artificial Life, 2004, 10, 123-134.	1.0	12
137	Detecting Clusters of Mutations. PLoS ONE, 2008, 3, e3765.	1.1	12
138	Using the Mutation-Selection Framework to Characterize Selection on Protein Sequences. Genes, 2018, 9, 409.	1.0	12
139	Evolutionary couplings detect side-chain interactions. PeerJ, 2019, 7, e7280.	0.9	12
140	Lethal mutagenesis in a structured environment. Journal of Theoretical Biology, 2009, 261, 67-73.	0.8	11
141	Dynamic fitness landscapes: expansions for small mutation rates. Physica A: Statistical Mechanics and Its Applications, 2001, 290, 475-490.	1.2	10
142	Evolution of Resource Competition between Mutually Dependent Digital Organisms. Artificial Life, 2004, 10, 145-156.	1.0	10
143	Measuring evolutionary rates of proteins in a structural context. F1000Research, 2017, 6, 1845.	0.8	10
144	SELECTION FOR FITNESS VERSUS SELECTION FOR ROBUSTNESS IN RNA SECONDARY STRUCTURE FOLDING. Evolution; International Journal of Organic Evolution, 2001, 55, 2412.	1.1	9

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145	A Linear Relationship between Fitness and the Logarithm of the Critical Bottleneck Size in Vesicular Stomatitis Virus Populations. <i>Journal of Virology</i> , 2008, 82, 12589-12590.	1.5	9
146	Lethal Mutagenesis. , 2008, , 207-218.		9
147	Limited Utility of Residue Masking for Positive-Selection Inference. <i>Molecular Biology and Evolution</i> , 2014, 31, 2496-2500.	3.5	9
148	The utility of protein structure as a predictor of site-wise dN/dS varies widely among HIV-1 proteins. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150579.	1.5	9
149	Assessment of Raman Spectroscopy for Reducing Unnecessary Biopsies for Melanoma Screening. <i>Molecules</i> , 2020, 25, 2852.	1.7	9
150	At the mercy of viruses. <i>ELife</i> , 2016, 5, .	2.8	9
151	Analyzing machupo virus-receptor binding by molecular dynamics simulations. <i>PeerJ</i> , 2014, 2, e266.	0.9	9
152	Influenza passaging annotations: what they tell us and why we should listen. <i>Virus Evolution</i> , 2019, 5, vez016.	2.2	8
153	Experiments in Digital Evolution (Editors' Introduction to the Special Issue). <i>Artificial Life</i> , 2004, 10, 117-122.	1.0	7
154	Transcriptional Robustness Complements Nonsense-Mediated Decay in Humans. <i>PLoS Genetics</i> , 2011, 7, e1002296.	1.5	7
155	Intermediate divergence levels maximize the strength of structureâ€“sequence correlations in enzymes and viral proteins. <i>Protein Science</i> , 2016, 25, 1341-1353.	3.1	7
156	Principal-Oscillation-Pattern Analysis of Gene Expression. <i>PLoS ONE</i> , 2012, 7, e28805.	1.1	7
157	Kinetics of the viral cycle influence pharmacodynamics of antiretroviral therapy. <i>Biology Direct</i> , 2011, 6, 42.	1.9	6
158	Evolutionary paths of least resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12553-12554.	3.3	6
159	Predicting bacterial growth conditions from mRNA and protein abundances. <i>PLoS ONE</i> , 2018, 13, e0206634.	1.1	6
160	Pinetree: a step-wise gene expression simulator with codon-specific translation rates. <i>Bioinformatics</i> , 2019, 35, 4176-4178.	1.8	6
161	Moderate Amounts of Epistasis are Not Evolutionarily Stable in Small Populations. <i>Journal of Molecular Evolution</i> , 2020, 88, 435-444.	0.8	6
162	Modelling Stochastic Clonal Interference. <i>Natural Computing Series</i> , 2004, , 21-38.	2.2	6

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163	Robustness and Evolvability in Living Systems. <i>BioScience</i> , 2006, 56, 695.	2.2	5
164	A Comprehensive Coexpression Network Analysis in <i>Vibrio cholerae</i> . <i>MSystems</i> , 2020, 5, .	1.7	5
165	The evolution of logic circuits for the purpose of protein contact map prediction. <i>PeerJ</i> , 2017, 5, e3139.	0.9	5
166	Tradeoff between short-term and long-term adaptation in a changing environment. <i>Physical Review E</i> , 2005, 72, 041922.	0.8	4
167	INTERACTIONS BETWEEN EVOLUTIONARY PROCESSES AT HIGH MUTATION RATES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2303-2314.	1.1	4
168	A new twist in measuring mutation rates. <i>ELife</i> , 2017, 6, .	2.8	4
169	Combinatorial Approaches to Viral Attenuation. <i>MSystems</i> , 2018, 3, .	1.7	4
170	Site-Specific Amino Acid Distributions Follow a Universal Shape. <i>Journal of Molecular Evolution</i> , 2020, 88, 731-741.	0.8	4
171	REPLICATION AT PERIODICALLY CHANGING MULTIPLICITY OF INFECTION PROMOTES STABLE COEXISTENCE OF COMPETING VIRAL POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2004, 58, 900.	1.1	3
172	Eigen-Genomic System Dynamic-Pattern Analysis (ESDA): Modeling mRNA Degradation and Self-Regulation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 430-437.	1.9	3
173	The role of environmental factors on the evolution of phenotypic diversity in vesicular stomatitis virus populations. <i>Journal of General Virology</i> , 2013, 94, 860-868.	1.3	3
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