

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	Generating dynamic gene expression patterns without the need for regulatory circuits. PLoS ONE, 2022, 17, e0268883.	1.1	0
2	BACPHLIP: predicting bacteriophage lifestyle from conserved protein domains. PeerJ, 2021, 9, e11396.	0.9	113
3	Modeling poliovirus replication dynamics from live time-lapse single-cell imaging data. Scientific Reports, 2021, 11, 9622.	1.6	3
4	A systematic analysis of the beta hairpin motif in the Protein Data Bank. Protein Science, 2021, 30, 613-623.	3.1	16
5	Opfi: A Python package for identifying gene clusters in large genomics and metagenomics data sets. Journal of Open Source Software, 2021, 6, 3678.	2.0	2
6	Learning the local landscape of protein structures with convolutional neural networks. Journal of Biological Physics, 2021, 47, 435-454.	0.7	13
7	Metagenomic discovery of CRISPR-associated transposons. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
8	Site-Specific Amino Acid Distributions Follow a Universal Shape. Journal of Molecular Evolution, 2020, 88, 731-741.	0.8	4
9	Predicting an epidemic trajectory is difficult. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 28549-28551.	3.3	31
10	TsrA Regulates Virulence and Intestinal Colonization in <i>Vibrio cholerae</i> . MSphere, 2020, 5, .	1.3	2
11	Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. PLoS Biology, 2020, 18, e3000627.	2.6	37
12	Assessment of Raman Spectroscopy for Reducing Unnecessary Biopsies for Melanoma Screening. Molecules, 2020, 25, 2852.	1.7	9
13	A Comprehensive Coexpression Network Analysis in <i>Vibrio cholerae</i> . MSystems, 2020, 5, .	1.7	5
14	Moderate Amounts of Epistasis are Not Evolutionarily Stable in Small Populations. Journal of Molecular Evolution, 2020, 88, 435-444.	0.8	6
15	Influenza passaging annotations: what they tell us and why we should listen. Virus Evolution, 2019, 5, vez016.	2.2	8
16	Pinetree: a step-wise gene expression simulator with codon-specific translation rates. Bioinformatics, 2019, 35, 4176-4178.	1.8	6
17	More than efficacy revealed by single-cell analysis of antiviral therapeutics. Science Advances, 2019, 5, eaax4761.	4.7	16
18	Phylogenetic Weighting Does Little to Improve the Accuracy of Evolutionary Coupling Analyses. Entropy, 2019, 21, 1000.	1.1	13

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19	Transcript degradation and codon usage regulate gene expression in a lytic phage. <i>Virus Evolution</i> , 2019, 5, vez055.	2.2	13
20	The Many Nuanced Evolutionary Consequences of Duplicated Genes. <i>Molecular Biology and Evolution</i> , 2019, 36, 304-314.	3.5	26
21	Welcome to the Tidyverse. <i>Journal of Open Source Software</i> , 2019, 4, 1686.	2.0	9,245
22	Evolutionary couplings detect side-chain interactions. <i>PeerJ</i> , 2019, 7, e7280.	0.9	12
23	Beyond Thermodynamic Constraints: Evolutionary Sampling Generates Realistic Protein Sequence Variation. <i>Genetics</i> , 2018, 208, 1387-1395.	1.2	13
24	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
25	Predicting bacterial growth conditions from mRNA and protein abundances. <i>PLoS ONE</i> , 2018, 13, e0206634.	1.1	6
26	Sicegar: R package for sigmoidal and double-sigmoidal curve fitting. <i>PeerJ</i> , 2018, 6, e4251.	0.9	46
27	Within-Gene Shine-Dalgarno Sequences Are Not Selected for Function. <i>Molecular Biology and Evolution</i> , 2018, 35, 2487-2498.	3.5	16
28	Combinatorial Approaches to Viral Attenuation. <i>MSystems</i> , 2018, 3, .	1.7	4
29	Limitations of alignment-free tools in total RNA-seq quantification. <i>BMC Genomics</i> , 2018, 19, 510.	1.2	64
30	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
31	Using the Mutation-Selection Framework to Characterize Selection on Protein Sequences. <i>Genes</i> , 2018, 9, 409.	1.0	12
32	Accelerated simulation of evolutionary trajectories in origin-fixation models. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20160906.	1.5	22
33	The E. coli molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017, 7, 45303.	1.6	46
34	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
35	Single-Cell Virology: On-Chip Investigation of Viral Infection Dynamics. <i>Cell Reports</i> , 2017, 21, 1692-1704.	2.9	71
36	Reduced Protein Expression in a Virus Attenuated by Codon Deoptimization. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2957-2968.	0.8	21

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37	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
38	A new twist in measuring mutation rates. <i>ELife</i> , 2017, 6, .	2.8	4
39	Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein. <i>PLoS ONE</i> , 2017, 12, e0164905.	1.1	15
40	Measuring evolutionary rates of proteins in a structural context. <i>F1000Research</i> , 2017, 6, 1845.	0.8	14
41	Measuring evolutionary rates of proteins in a structural context. <i>F1000Research</i> , 2017, 6, 1845.	0.8	10
42	The evolution of logic circuits for the purpose of protein contact map prediction. <i>PeerJ</i> , 2017, 5, e3139.	0.9	5
43	Calculating site-specific evolutionary rates at the amino-acid or codon level yields similar rate estimates. <i>PeerJ</i> , 2017, 5, e3391.	0.9	15
44	Functional Sites Induce Long-Range Evolutionary Constraints in Enzymes. <i>PLoS Biology</i> , 2016, 14, e1002452.	2.6	94
45	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
46	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
47	Extensively Parameterized Mutation-Selection Models Reliably Capture Site-Specific Selective Constraint. <i>Molecular Biology and Evolution</i> , 2016, 33, 2990-3002.	3.5	21
48	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
49	Intermediate divergence levels maximize the strength of structure-sequence correlations in enzymes and viral proteins. <i>Protein Science</i> , 2016, 25, 1341-1353.	3.1	7
50	Causes of evolutionary rate variation among protein sites. <i>Nature Reviews Genetics</i> , 2016, 17, 109-121.	7.7	247
51	At the mercy of viruses. <i>ELife</i> , 2016, 5, .	2.8	9
52	Viral factors in influenza pandemic risk assessment. <i>ELife</i> , 2016, 5, .	2.8	82
53	Reproducibility of SNV-calling in multiple sequencing runs from single tumors. <i>PeerJ</i> , 2016, 4, e1508.	0.9	3
54	Pyvolve: A Flexible Python Module for Simulating Sequences along Phylogenies. <i>PLoS ONE</i> , 2015, 10, e0139047.	1.1	83

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55	Systematic humanization of yeast genes reveals conserved functions and genetic modularity. <i>Science</i> , 2015, 348, 921-925.	6.0	361
56	Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak. <i>Virus Evolution</i> , 2015, 1, vev006.	2.2	30
57	The Relationship between dN/dS and Scaled Selection Coefficients. <i>Molecular Biology and Evolution</i> , 2015, 32, 1097-1108.	3.5	106
58	Geometric Constraints Dominate the Antigenic Evolution of Influenza H3N2 Hemagglutinin. <i>PLoS Pathogens</i> , 2015, 11, e1004940.	2.1	41
59	Relationship between protein thermodynamic constraints and variation of evolutionary rates among sites. <i>Physical Biology</i> , 2015, 12, 025002.	0.8	49
60	The utility of protein structure as a predictor of site-wise d N /d S varies widely among HIV-1 proteins. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150579.	1.5	9
61	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
62	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
63	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
64	Comprehensive, structurally-informed alignment and phylogeny of vertebrate biogenic amine receptors. <i>PeerJ</i> , 2015, 3, e773.	0.9	20
65	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
66	Long-Term Control of Viral Replication in a Group O, Human Immunodeficiency Virus Type 1-Infected Individual. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, 511-513.	0.5	2
67	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
68	Socioeconomic disparities in the presentation of acute bacterial sinusitis complications in children. <i>Laryngoscope</i> , 2014, 124, 1700-1706.	1.1	54
69	Limited Utility of Residue Masking for Positive-Selection Inference. <i>Molecular Biology and Evolution</i> , 2014, 31, 2496-2500.	3.5	9
70	Fitting outbreak models to data from many small norovirus outbreaks. <i>Epidemics</i> , 2014, 6, 18-29.	1.5	21
71	Analyzing machupo virus-receptor binding by molecular dynamics simulations. <i>PeerJ</i> , 2014, 2, e266.	0.9	9
72	RNaseIII and T4 Polynucleotide Kinase sequence biases and solutions during RNA-seq library construction. <i>Biology Direct</i> , 2013, 8, 16.	1.9	15

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73	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
74	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
75	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
76	Integrating Sequence Variation and Protein Structure to Identify Sites under Selection. <i>Molecular Biology and Evolution</i> , 2013, 30, 36-44.	3.5	47
77	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
78	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
79	Congruent Evolution of Fitness and Genetic Robustness in Vesicular Stomatitis Virus. <i>Journal of Virology</i> , 2013, 87, 4923-4928.	1.5	16
80	PeptideBuilder: A simple Python library to generate model peptides. <i>PeerJ</i> , 2013, 1, e80.	0.9	70
81	Maximum Allowed Solvent Accessibilities of Residues in Proteins. <i>PLoS ONE</i> , 2013, 8, e80635.	1.1	340
82	Amino-acid site variability among natural and designed proteins. <i>PeerJ</i> , 2013, 1, e211.	0.9	18
83	Bringing Molecules Back into Molecular Evolution. <i>PLoS Computational Biology</i> , 2012, 8, e1002572.	1.5	62
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	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
86	Modeling coding-sequence evolution within the context of residue solvent accessibility. <i>BMC Evolutionary Biology</i> , 2012, 12, 179.	3.2	38
87	Slow Fitness Recovery in a Codon-Modified Viral Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 2997-3004.	3.5	54
88	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
89	INTERACTIONS BETWEEN EVOLUTIONARY PROCESSES AT HIGH MUTATION RATES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2303-2314.	1.1	4
90	Principal-Oscillation-Pattern Analysis of Gene Expression. <i>PLoS ONE</i> , 2012, 7, e28805.	1.1	7

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91	The Phenotype-Fitness Map in Experimental Evolution of Phages. <i>PLoS ONE</i> , 2011, 6, e27796.	1.1	35
92	Kinetics of the viral cycle influence pharmacodynamics of antiretroviral therapy. <i>Biology Direct</i> , 2011, 6, 42.	1.9	6
93	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
94	Temporal and spatial alterations in mutant swarm size of St. Louis encephalitis virus in mosquito hosts. <i>Infection, Genetics and Evolution</i> , 2011, 11, 460-468.	1.0	13
95	The Relationship Between Relative Solvent Accessibility and Evolutionary Rate in Protein Evolution. <i>Genetics</i> , 2011, 188, 479-488.	1.2	116
96	Specific and Nonspecific Host Adaptation during Arboviral Experimental Evolution. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 21, 71-81.	1.0	25
97	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
98	Transcriptional Robustness Complements Nonsense-Mediated Decay in Humans. <i>PLoS Genetics</i> , 2011, 7, e1002296.	1.5	7
99	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
100	Signatures of protein biophysics in coding sequence evolution. <i>Current Opinion in Structural Biology</i> , 2010, 20, 385-389.	2.6	42
101	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
102	Translationally optimal codons associate with aggregation-prone sites in proteins. <i>Proteomics</i> , 2010, 10, 4163-4171.	1.3	40
103	Reply to Torre. <i>Clinical Infectious Diseases</i> , 2010, 50, 1425-1426.	2.9	2
104	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
105	Genomic Evolution of Vesicular Stomatitis Virus Strains with Differences in Adaptability. <i>Journal of Virology</i> , 2010, 84, 4960-4968.	1.5	18
106	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
107	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
108	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

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109	Does Mutational Robustness Inhibit Extinction by Lethal Mutagenesis in Viral Populations?. PLoS Computational Biology, 2010, 6, e1000811.	1.5	18
110	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. Journal of Virology, 2009, 83, 8470-8481.	1.5	122
111	T Cell Dynamics and the Response to HAART in a Cohort of HIV-1 Infected Elite Suppressors. Clinical Infectious Diseases, 2009, 49, 1763-1766.	2.9	57
112	Lethal mutagenesis in a structured environment. Journal of Theoretical Biology, 2009, 261, 67-73.	0.8	11
113	The evolutionary consequences of erroneous protein synthesis. Nature Reviews Genetics, 2009, 10, 715-724.	7.7	437
114	Translationally Optimal Codons Associate with Structurally Sensitive Sites in Proteins. Molecular Biology and Evolution, 2009, 26, 1571-1580.	3.5	183
115	Avida. , 2009, , 3-35.		30
116	Constraints on the dominant mechanism for HIV viral dynamics in patients on raltegravir. Antiviral Therapy, 2009, 14, 263-71.	0.6	26
117	Constraints on the dominant mechanism for HIV viral dynamics in patients on raltegravir. Antiviral Therapy, 2009, 14, 263-271.	0.6	30
118	Contact Density Affects Protein Evolutionary Rate from Bacteria to Animals. Journal of Molecular Evolution, 2008, 66, 395-404.	0.8	53
119	Low-level HIV-1 replication and the dynamics of the resting CD4 ⁺ T cell reservoir for HIV-1 in the setting of HAART. BMC Infectious Diseases, 2008, 8, 2.	1.3	51
120	The traveling-wave approach to asexual evolution: Muller's ratchet and speed of adaptation. Theoretical Population Biology, 2008, 73, 24-46.	0.5	149
121	The look-ahead effect of phenotypic mutations. Biology Direct, 2008, 3, 18.	1.9	73
122	Mistranslation-Induced Protein Misfolding as a Dominant Constraint on Coding-Sequence Evolution. Cell, 2008, 134, 341-352.	13.5	949
123	Rapid Adaptive Amplification of Preexisting Variation in an RNA Virus. Journal of Virology, 2008, 82, 4354-4362.	1.5	19
124	The Stochastic Edge in Adaptive Evolution. Genetics, 2008, 179, 603-620.	1.2	68
125	Decay dynamics of HIV-1 depend on the inhibited stages of the viral life cycle. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4832-4837.	3.3	119
126	A Linear Relationship between Fitness and the Logarithm of the Critical Bottleneck Size in Vesicular Stomatitis Virus Populations. Journal of Virology, 2008, 82, 12589-12590.	1.5	9

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127	Lethal Mutagenesis of Bacteria. <i>Genetics</i> , 2008, 180, 1061-1070.	1.2	40
128	Lethal Mutagenesis. , 2008, , 207-218.		9
129	Detecting Clusters of Mutations. <i>PLoS ONE</i> , 2008, 3, e3765.	1.1	12
130	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
131	Theory of Lethal Mutagenesis for Viruses. <i>Journal of Virology</i> , 2007, 81, 2930-2939.	1.5	250
132	Thermodynamics of Neutral Protein Evolution. <i>Genetics</i> , 2007, 175, 255-266.	1.2	137
133	Breaking proteins with mutations: threads and thresholds in evolution. <i>Molecular Systems Biology</i> , 2007, 3, 76.	3.2	35
134	Frequency-dependent selection in a periodic environment. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007, 381, 255-264.	1.2	1
135	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
136	Quasispecies in Time-Dependent Environments. , 2006, 299, 33-50.		15
137	Selection for mutational robustness in finite populations. <i>Journal of Theoretical Biology</i> , 2006, 243, 181-190.	0.8	35
138	Structural Determinants of the Rate of Protein Evolution in Yeast. <i>Molecular Biology and Evolution</i> , 2006, 23, 1751-1761.	3.5	162
139	Robustness and Evolvability in Living Systems. <i>BioScience</i> , 2006, 56, 695.	2.2	5
140	Population Genetics of Translational Robustness. <i>Genetics</i> , 2006, 173, 473-481.	1.2	50
141	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
142	A Single Determinant Dominates the Rate of Yeast Protein Evolution. <i>Molecular Biology and Evolution</i> , 2006, 23, 327-337.	3.5	373
143	Quasispecies theory in the context of population genetics. <i>BMC Evolutionary Biology</i> , 2005, 5, 44.	3.2	234
144	Molecular clocks: The heavy, the cold, and the slow. <i>Heredity</i> , 2005, 95, 115-115.	1.2	0

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145	On the conservative nature of intragenic recombination. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5380-5385.	3.3	95
146	Why highly expressed proteins evolve slowly. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14338-14343.	3.3	738
147	Thermodynamic prediction of protein neutrality. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 606-611.	3.3	320
148	Tradeoff between short-term and long-term adaptation in a changing environment. Physical Review E, 2005, 72, 041922.	0.8	4
149	Predicting the Tolerance of Proteins to Random Amino Acid Substitution. Biophysical Journal, 2005, 89, 3714-3720.	0.2	40
150	Avida: Evolution Experiments with Self-Replicating Computer Programs. , 2005, , 3-35.		3
151	Density-Dependent Selection in Vesicular Stomatitis Virus. Journal of Virology, 2004, 78, 5799-5804.	1.5	75
152	REPLICATION AT PERIODICALLY CHANGING MULTIPLICITY OF INFECTION PROMOTES STABLE COEXISTENCE OF COMPETING VIRAL POPULATIONS. Evolution; International Journal of Organic Evolution, 2004, 58, 900.	1.1	3
153	Co-infection Weakens Selection Against Epistatic Mutations in RNA Viruses. Genetics, 2004, 168, 9-19.	1.2	88
154	The Speed of Adaptation in Large Asexual Populations. Genetics, 2004, 167, 2045-2053.	1.2	125
155	Adaptive Radiation from Resource Competition in Digital Organisms. Science, 2004, 305, 84-86.	6.0	110
156	Avida: A Software Platform for Research in Computational Evolutionary Biology. Artificial Life, 2004, 10, 191-229.	1.0	280
157	Experiments in Digital Evolution (Editors' Introduction to the Special Issue). Artificial Life, 2004, 10, 117-122.	1.0	7
158	Evolution of Resource Competition between Mutually Dependent Digital Organisms. Artificial Life, 2004, 10, 145-156.	1.0	10
159	Digital Evolution in Time-Dependent Fitness Landscapes. Artificial Life, 2004, 10, 123-134.	1.0	12
160	REPLICATION AT PERIODICALLY CHANGING MULTIPLICITY OF INFECTION PROMOTES STABLE COEXISTENCE OF COMPETING VIRAL POPULATIONS. Evolution; International Journal of Organic Evolution, 2004, 58, 900-905.	1.1	32
161	Supplementary materials need the right format. Nature, 2004, 430, 291-291.	13.7	0
162	Molecular clock in neutral protein evolution. , 2004, 5, 25.		46

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163	Stability and the Evolvability of Function in a Model Protein. <i>Biophysical Journal</i> , 2004, 86, 2758-2764.	0.2	95
164	Modelling Stochastic Clonal Interference. <i>Natural Computing Series</i> , 2004, , 21-38.	2.2	6
165	Compensatory mutations cause excess of antagonistic epistasis in RNA secondary structure folding. <i>BMC Evolutionary Biology</i> , 2003, 3, 3.	3.2	61
166	Phenotypic mixing and hiding may contribute to memory in viral quasispecies. <i>BMC Microbiology</i> , 2003, 3, 11.	1.3	57
167	Evolution of mutational robustness. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2003, 522, 3-11.	0.4	116
168	Does the Red Queen Reign in the Kingdom of Digital Organisms?. <i>Lecture Notes in Computer Science</i> , 2003, , 405-414.	1.0	1
169	Probability of Fixation of an Advantageous Mutant in a Viral Quasispecies. <i>Genetics</i> , 2003, 163, 467-474.	1.2	37
170	Maternal Effects in Molecular Evolution. <i>Physical Review Letters</i> , 2002, 88, 078101.	2.9	15
171	The biology of digital organisms. <i>Trends in Ecology and Evolution</i> , 2002, 17, 528-532.	4.2	86
172	Genealogical process on a correlated fitness landscape. <i>The Journal of Experimental Zoology</i> , 2002, 294, 274-284.	1.4	13
173	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
174	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
175	Dynamic fitness landscapes in molecular evolution. <i>Physics Reports</i> , 2001, 349, 395-446.	10.3	104
176	Dynamic fitness landscapes: expansions for small mutation rates. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2001, 290, 475-490.	1.2	10
177	Adaptive Evolution on Neutral Networks. <i>Bulletin of Mathematical Biology</i> , 2001, 63, 715-730.	0.9	111
178	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
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