

Claus O Wilke

List of Publications by Year in Descending Order

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

193
papers

12,261
citations

48
h-index

108
g-index

249
ext. papers

17,208
ext. citations

6.6
avg, IF

6.71
L-index

#	Paper	IF	Citations
193	Generating dynamic gene expression patterns without the need for regulatory circuits. <i>PLoS ONE</i> , 2022 , 17, e0268883	3.7	
192	Learning the local landscape of protein structures with convolutional neural networks. <i>Journal of Biological Physics</i> , 2021 , 47, 435-454	1.6	1
191	BACPHLIP: predicting bacteriophage lifestyle from conserved protein domains. <i>PeerJ</i> , 2021 , 9, e11396	3.1	20
190	Modeling poliovirus replication dynamics from live time-lapse single-cell imaging data. <i>Scientific Reports</i> , 2021 , 11, 9622	4.9	0
189	A systematic analysis of the beta hairpin motif in the Protein Data Bank. <i>Protein Science</i> , 2021 , 30, 613-623	3.3	5
188	TsrA Regulates Virulence and Intestinal Colonization in. <i>MSphere</i> , 2020 , 5,	5	1
187	Humanization of yeast genes with multiple human orthologs reveals functional divergence between paralogs. <i>PLoS Biology</i> , 2020 , 18, e3000627	9.7	10
186	Assessment of Raman Spectroscopy for Reducing Unnecessary Biopsies for Melanoma Screening. <i>Molecules</i> , 2020 , 25,	4.8	6
185	A Comprehensive Coexpression Network Analysis in <i>Vibrio cholerae</i> . <i>MSystems</i> , 2020 , 5,	7.6	1
184	Moderate Amounts of Epistasis are Not Evolutionarily Stable in Small Populations. <i>Journal of Molecular Evolution</i> , 2020 , 88, 435-444	3.1	2
183	Site-Specific Amino Acid Distributions Follow a Universal Shape. <i>Journal of Molecular Evolution</i> , 2020 , 88, 731-741	3.1	1
182	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	11.5	11
181	Pinetree: a step-wise gene expression simulator with codon-specific translation rates. <i>Bioinformatics</i> , 2019 , 35, 4176-4178	7.2	3
180	Influenza passaging annotations: what they tell us and why we should listen. <i>Virus Evolution</i> , 2019 , 5, vez016	3.7	6
179	Welcome to the Tidyverse. <i>Journal of Open Source Software</i> , 2019 , 4, 1686	5.2	2985
178	Evolutionary couplings detect side-chain interactions. <i>PeerJ</i> , 2019 , 7, e7280	3.1	8
177	More than efficacy revealed by single-cell analysis of antiviral therapeutics. <i>Science Advances</i> , 2019 , 5, eaax4761	14.3	8

176	Phylogenetic weighting does little to improve the accuracy of evolutionary coupling analyses. <i>Entropy</i> , 2019 , 21,	2.8	6
175	Transcript degradation and codon usage regulate gene expression in a lytic phage. <i>Virus Evolution</i> , 2019 , 5, vez055	3.7	5
174	The Many Nuanced Evolutionary Consequences of Duplicated Genes. <i>Molecular Biology and Evolution</i> , 2019 , 36, 304-314	8.3	13
173	Beyond Thermodynamic Constraints: Evolutionary Sampling Generates Realistic Protein Sequence Variation. <i>Genetics</i> , 2018 , 208, 1387-1395	4	6
172	Discovery of Next-Generation Antimicrobials through Bacterial Self-Screening of Surface-Displayed Peptide Libraries. <i>Cell</i> , 2018 , 172, 618-628.e13	56.2	79
171	Within-Genes Shine-Dalgarno Sequences Are Not Selected for Function. <i>Molecular Biology and Evolution</i> , 2018 , 35, 2487-2498	8.3	6
170	Combinatorial Approaches to Viral Attenuation. <i>MSystems</i> , 2018 , 3,	7.6	3
169	Limitations of alignment-free tools in total RNA-seq quantification. <i>BMC Genomics</i> , 2018 , 19, 510	4.5	42
168	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,	7.8	21
167	Using the Mutation-Selection Framework to Characterize Selection on Protein Sequences. <i>Genes</i> , 2018 , 9,	4.2	6
166	Predicting bacterial growth conditions from mRNA and protein abundances. <i>PLoS ONE</i> , 2018 , 13, e0206634	9.7	3
165	Sicegar: R package for sigmoidal and double-sigmoidal curve fitting. <i>PeerJ</i> , 2018 , 6, e4251	3.1	18
164	Accelerated simulation of evolutionary trajectories in origin-fixation models. <i>Journal of the Royal Society Interface</i> , 2017 , 14,	4.1	10
163	The E. coli molecular phenotype under different growth conditions. <i>Scientific Reports</i> , 2017 , 7, 45303	4.9	18
162	Biophysical Models of Protein Evolution: Understanding the Patterns of Evolutionary Sequence Divergence. <i>Annual Review of Biophysics</i> , 2017 , 46, 85-103	21.1	68
161	Computational prediction of the tolerance to amino-acid deletion in green-fluorescent protein. <i>PLoS ONE</i> , 2017 , 12, e0164905	3.7	8
160	Single-Cell Virology: On-Chip Investigation of Viral Infection Dynamics. <i>Cell Reports</i> , 2017 , 21, 1692-1704	10.6	41
159	Reduced Protein Expression in a Virus Attenuated by Codon Deoptimization. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2957-2968	3.2	11

158	Large-scale analysis of post-translational modifications in <i>E. coli</i> under glucose-limiting conditions. <i>BMC Genomics</i> , 2017 , 18, 301	4.5	26
157	A new twist in measuring mutation rates. <i>ELife</i> , 2017 , 6,	8.9	4
156	Measuring evolutionary rates of proteins in a structural context. <i>F1000Research</i> , 2017 , 6, 1845	3.6	9
155	Measuring evolutionary rates of proteins in a structural context. <i>F1000Research</i> , 2017 , 6, 1845	3.6	9
154	The evolution of logic circuits for the purpose of protein contact map prediction. <i>PeerJ</i> , 2017 , 5, e3139	3.1	5
153	Calculating site-specific evolutionary rates at the amino-acid or codon level yields similar rate estimates. <i>PeerJ</i> , 2017 , 5, e3391	3.1	8
152	Extensively Parameterized Mutation-Selection Models Reliably Capture Site-Specific Selective Constraint. <i>Molecular Biology and Evolution</i> , 2016 , 33, 2990-3002	8.3	16
151	Dissecting the roles of local packing density and longer-range effects in protein sequence evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 841-54	4.2	11
150	Intermediate divergence levels maximize the strength of structure-sequence correlations in enzymes and viral proteins. <i>Protein Science</i> , 2016 , 25, 1341-53	6.3	4
149	Causes of evolutionary rate variation among protein sites. <i>Nature Reviews Genetics</i> , 2016 , 17, 109-21	30.1	162
148	At the mercy of viruses. <i>ELife</i> , 2016 , 5,	8.9	8
147	Viral factors in influenza pandemic risk assessment. <i>ELife</i> , 2016 , 5,	8.9	61
146	Reproducibility of SNV-calling in multiple sequencing runs from single tumors. <i>PeerJ</i> , 2016 , 4, e1508	3.1	2
145	Functional Sites Induce Long-Range Evolutionary Constraints in Enzymes. <i>PLoS Biology</i> , 2016 , 14, e1002452	4.7	65
144	A Comparison of One-Rate and Two-Rate Inference Frameworks for Site-Specific dN/dS Estimation. <i>Genetics</i> , 2016 , 204, 499-511	4	14
143	Sequence amplification via cell passaging creates spurious signals of positive adaptation in influenza virus H3N2 hemagglutinin. <i>Virus Evolution</i> , 2016 , 2,	3.7	28
142	The relationship between dN/dS and scaled selection coefficients. <i>Molecular Biology and Evolution</i> , 2015 , 32, 1097-108	8.3	63
141	Geometric Constraints Dominate the Antigenic Evolution of Influenza H3N2 Hemagglutinin. <i>PLoS Pathogens</i> , 2015 , 11, e1004940	7.6	34

140	Relationship between protein thermodynamic constraints and variation of evolutionary rates among sites. <i>Physical Biology</i> , 2015 , 12, 025002	3	34
139	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	4.1	7
138	Evolutionary paths of least resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 12553-4	11.5	4
137	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, 11643-53	6.6	12
136	Pyvolve: A Flexible Python Module for Simulating Sequences along Phylogenies. <i>PLoS ONE</i> , 2015 , 10, e0139047	3.7	54
135	Evolution. Systematic humanization of yeast genes reveals conserved functions and genetic modularity. <i>Science</i> , 2015 , 348, 921-5	33.3	227
134	Time dependence of evolutionary metrics during the 2009 pandemic influenza virus outbreak. <i>Virus Evolution</i> , 2015 , 1,	3.7	20
133	Controlled Measurement and Comparative Analysis of Cellular Components in E. coli Reveals Broad Regulatory Changes in Response to Glucose Starvation. <i>PLoS Computational Biology</i> , 2015 , 11, e1004400 ⁵		27
132	Comprehensive, structurally-informed alignment and phylogeny of vertebrate biogenic amine receptors. <i>PeerJ</i> , 2015 , 3, e773	3.1	14
131	Predicting evolutionary site variability from structure in viral proteins: buriedness, packing, flexibility, and design. <i>Journal of Molecular Evolution</i> , 2014 , 79, 130-42	3.1	31
130	Socioeconomic disparities in the presentation of acute bacterial sinusitis complications in children. <i>Laryngoscope</i> , 2014 , 124, 1700-6	3.6	43
129	Limited utility of residue masking for positive-selection inference. <i>Molecular Biology and Evolution</i> , 2014 , 31, 2496-500	8.3	7
128	Fitting outbreak models to data from many small norovirus outbreaks. <i>Epidemics</i> , 2014 , 6, 18-29	5.1	15
127	Predicting growth conditions from internal metabolic fluxes in an in-silico model of E. coli. <i>PLoS ONE</i> , 2014 , 9, e114608	3.7	10
126	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, 511-3	1.6	2
125	Analyzing machupo virus-receptor binding by molecular dynamics simulations. <i>PeerJ</i> , 2014 , 2, e266	3.1	7
124	RNaseIII and T4 polynucleotide Kinase sequence biases and solutions during RNA-seq library construction. <i>Biology Direct</i> , 2013 , 8, 16	7.2	9
123	Membrane environment imposes unique selection pressures on transmembrane domains of G protein-coupled receptors. <i>Journal of Molecular Evolution</i> , 2013 , 76, 172-82	3.1	18

122	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	5.8	18
121	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	4.9	3
120	Integrating sequence variation and protein structure to identify sites under selection. <i>Molecular Biology and Evolution</i> , 2013 , 30, 36-44	8.3	36
119	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	11.5	55
118	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, 755-61	6.3	37
117	Congruent evolution of fitness and genetic robustness in vesicular stomatitis virus. <i>Journal of Virology</i> , 2013 , 87, 4923-8	6.6	7
116	PeptideBuilder: A simple Python library to generate model peptides. <i>PeerJ</i> , 2013 , 1, e80	3.1	39
115	Maximum allowed solvent accessibilities of residues in proteins. <i>PLoS ONE</i> , 2013 , 8, e80635	3.7	190
114	Amino-acid site variability among natural and designed proteins. <i>PeerJ</i> , 2013 , 1, e211	3.1	13
113	Interactions between evolutionary processes at high mutation rates. <i>Evolution; International Journal of Organic Evolution</i> , 2012 , 66, 2303-14	3.8	4
112	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, 430-7	3	3
111	Modeling coding-sequence evolution within the context of residue solvent accessibility. <i>BMC Evolutionary Biology</i> , 2012 , 12, 179	3	30
110	Slow fitness recovery in a codon-modified viral genome. <i>Molecular Biology and Evolution</i> , 2012 , 29, 2997-3004	3.9	49
109	Risk factors for development of chronic rhinosinusitis in patients with allergic rhinitis. <i>International Forum of Allergy and Rhinology</i> , 2012 , 2, 370-5	6.3	42
108	Bringing molecules back into molecular evolution. <i>PLoS Computational Biology</i> , 2012 , 8, e1002572	5	45
107	Reduced mRNA secondary-structure stability near the start codon indicates functional genes in prokaryotes. <i>Genome Biology and Evolution</i> , 2012 , 4, 80-8	3.9	25
106	Principal-oscillation-pattern analysis of gene expression. <i>PLoS ONE</i> , 2012 , 7, e28805	3.7	7
105	The phenotype-fitness map in experimental evolution of phages. <i>PLoS ONE</i> , 2011 , 6, e27796	3.7	28

104	Kinetics of the viral cycle influence pharmacodynamics of antiretroviral therapy. <i>Biology Direct</i> , 2011 , 6, 42	7.2	4
103	Reduced stability of mRNA secondary structure near the translation-initiation site in dsDNA viruses. <i>BMC Evolutionary Biology</i> , 2011 , 11, 59	3	17
102	Temporal and spatial alterations in mutant swarm size of St. Louis encephalitis virus in mosquito hosts. <i>Infection, Genetics and Evolution</i> , 2011 , 11, 460-8	4.5	13
101	The relationship between relative solvent accessibility and evolutionary rate in protein evolution. <i>Genetics</i> , 2011 , 188, 479-88	4	84
100	Specific and nonspecific host adaptation during arboviral experimental evolution. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011 , 21, 71-81	0.9	17
99	Short communication: dynamic constraints on the second phase compartment of HIV-infected cells. <i>AIDS Research and Human Retroviruses</i> , 2011 , 27, 759-61	1.6	19
98	Transcriptional robustness complements nonsense-mediated decay in humans. <i>PLoS Genetics</i> , 2011 , 7, e1002296	6	4
97	Contact heterogeneity and phylodynamics: how contact networks shape parasite evolutionary trees. <i>Interdisciplinary Perspectives on Infectious Diseases</i> , 2011 , 2011, 238743	1.7	18
96	Reply to Torre. <i>Clinical Infectious Diseases</i> , 2010 , 50, 1425-1426	11.6	1
95	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, 1931-41	5.8	17
94	Genomic evolution of vesicular stomatitis virus strains with differences in adaptability. <i>Journal of Virology</i> , 2010 , 84, 4960-8	6.6	16
93	Incongruent fitness landscapes, not tradeoffs, dominate the adaptation of vesicular stomatitis virus to novel host types. <i>Journal of General Virology</i> , 2010 , 91, 1484-93	4.9	20
92	Detecting positive and purifying selection at synonymous sites in yeast and worm. <i>Molecular Biology and Evolution</i> , 2010 , 27, 1912-22	8.3	50
91	A universal trend of reduced mRNA stability near the translation-initiation site in prokaryotes and eukaryotes. <i>PLoS Computational Biology</i> , 2010 , 6, e1000664	5	208
90	Does mutational robustness inhibit extinction by lethal mutagenesis in viral populations?. <i>PLoS Computational Biology</i> , 2010 , 6, e1000811	5	18
89	Signatures of protein biophysics in coding sequence evolution. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 385-9	8.1	38
88	Phenotypic differences in viral immune escape explained by linking within-host dynamics to host-population immunity. <i>Journal of Theoretical Biology</i> , 2010 , 265, 501-10	2.3	20
87	Translationally optimal codons associate with aggregation-prone sites in proteins. <i>Proteomics</i> , 2010 , 10, 4163-71	4.8	36

86	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, 8470-81	6.6	108
85	T cell dynamics and the response to HAART in a cohort of HIV-1-infected elite suppressors. <i>Clinical Infectious Diseases</i> , 2009 , 49, 1763-6	11.6	46
84	Lethal mutagenesis in a structured environment. <i>Journal of Theoretical Biology</i> , 2009 , 261, 67-73	2.3	11
83	The evolutionary consequences of erroneous protein synthesis. <i>Nature Reviews Genetics</i> , 2009 , 10, 715-24	36.1	334
82	Translationally optimal codons associate with structurally sensitive sites in proteins. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1571-80	8.3	146
81	Constraints on the dominant mechanism for HIV viral dynamics in patients on raltegravir. <i>Antiviral Therapy</i> , 2009 , 14, 263-71	1.6	21
80	Avida 2009 , 3-35		23
79	Constraints on the dominant mechanism for HIV viral dynamics in patients on raltegravir. <i>Antiviral Therapy</i> , 2009 , 14, 263-271	1.6	23
78	The traveling-wave approach to asexual evolution: Muller's ratchet and speed of adaptation. <i>Theoretical Population Biology</i> , 2008 , 73, 24-46	1.2	115
77	The look-ahead effect of phenotypic mutations. <i>Biology Direct</i> , 2008 , 3, 18	7.2	49
76	Mistranslation-induced protein misfolding as a dominant constraint on coding-sequence evolution. <i>Cell</i> , 2008 , 134, 341-52	56.2	763
75	Rapid adaptive amplification of preexisting variation in an RNA virus. <i>Journal of Virology</i> , 2008 , 82, 4354-62	6.7	15
74	The stochastic edge in adaptive evolution. <i>Genetics</i> , 2008 , 179, 603-20	4	52
73	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, 4832-7	11.5	105
72	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, 12589-90	6.6	7
71	Lethal mutagenesis of bacteria. <i>Genetics</i> , 2008 , 180, 1061-70	4	35
70	Lethal Mutagenesis 2008 , 207-218		6
69	Detecting clusters of mutations. <i>PLoS ONE</i> , 2008 , 3, e3765	3.7	7

68	Contact density affects protein evolutionary rate from bacteria to animals. <i>Journal of Molecular Evolution</i> , 2008 , 66, 395-404	3.1	44
67	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	4	43
66	Frequency-Dependent Selection in a Periodic Environment. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 381, 255-264	3.3	1
65	Effects of population size and mutation rate on the evolution of mutational robustness. <i>Evolution; International Journal of Organic Evolution</i> , 2007 , 61, 666-74	3.8	41
64	Limits on replenishment of the resting CD4+ T cell reservoir for HIV in patients on HAART. <i>PLoS Pathogens</i> , 2007 , 3, e122	7.6	57
63	Theory of lethal mutagenesis for viruses. <i>Journal of Virology</i> , 2007 , 81, 2930-9	6.6	197
62	Thermodynamics of neutral protein evolution. <i>Genetics</i> , 2007 , 175, 255-66	4	120
61	Selection for mutational robustness in finite populations. <i>Journal of Theoretical Biology</i> , 2006 , 243, 181-203		31
60	Structural determinants of the rate of protein evolution in yeast. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1751-61	8.3	138
59	Robustness and Evolvability in Living Systems. <i>BioScience</i> , 2006 , 56, 695	5.7	5
58	Population genetics of translational robustness. <i>Genetics</i> , 2006 , 173, 473-81	4	44
57	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, 6441-57	6.6	321
56	Density-Dependent Selection in Vesicular Stomatitis Virus. <i>Journal of Virology</i> , 2006 , 80, 4207-4207	6.6	78
55	A single determinant dominates the rate of yeast protein evolution. <i>Molecular Biology and Evolution</i> , 2006 , 23, 327-37	8.3	317
54	Quasispecies in time-dependent environments. <i>Current Topics in Microbiology and Immunology</i> , 2006 , 299, 33-50	3.3	11
53	Tradeoff between short-term and long-term adaptation in a changing environment. <i>Physical Review E</i> , 2005 , 72, 041922	2.4	3
52	Predicting the tolerance of proteins to random amino acid substitution. <i>Biophysical Journal</i> , 2005 , 89, 3714-20	2.9	36
51	Quasispecies theory in the context of population genetics. <i>BMC Evolutionary Biology</i> , 2005 , 5, 44	3	192

50	On the conservative nature of intragenic recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 5380-5	11.5	79
49	Why highly expressed proteins evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 14338-43	11.5	590
48	Thermodynamic prediction of protein neutrality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 606-11	11.5	272
47	Avida: Evolution Experiments with Self-Replicating Computer Programs 2005 , 3-35		2
46	Density-dependent selection in vesicular stomatitis virus. <i>Journal of Virology</i> , 2004 , 78, 5799-804	6.6	69
45	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	3.8	2
44	Co-infection weakens selection against epistatic mutations in RNA viruses. <i>Genetics</i> , 2004 , 168, 9-19	4	67
43	The speed of adaptation in large asexual populations. <i>Genetics</i> , 2004 , 167, 2045-53	4	108
42	Adaptive radiation from resource competition in digital organisms. <i>Science</i> , 2004 , 305, 84-6	33.3	97
41	Avida: a software platform for research in computational evolutionary biology. <i>Artificial Life</i> , 2004 , 10, 191-229	1.4	205
40	Experiments in Digital Evolution (Editors Introduction to the Special Issue). <i>Artificial Life</i> , 2004 , 10, 117-122		7
39	Evolution of resource competition between mutually dependent digital organisms. <i>Artificial Life</i> , 2004 , 10, 145-56	1.4	6
38	Digital evolution in time-dependent fitness landscapes. <i>Artificial Life</i> , 2004 , 10, 123-34	1.4	8
37	Replication at periodically changing multiplicity of infection promotes stable coexistence of competing viral populations. <i>Evolution; International Journal of Organic Evolution</i> , 2004 , 58, 900-5	3.8	30
36	Supplementary materials need the right format. <i>Nature</i> , 2004 , 430, 291	50.4	
35	Molecular clock in neutral protein evolution. <i>BMC Genetics</i> , 2004 , 5, 25	2.6	38
34	Stability and the evolvability of function in a model protein. <i>Biophysical Journal</i> , 2004 , 86, 2758-64	2.9	80
33	Modelling Stochastic Clonal Interference. <i>Natural Computing Series</i> , 2004 , 21-38	2.5	2

32	Does the Red Queen Reign in the Kingdom of Digital Organisms?. <i>Lecture Notes in Computer Science</i> , 2003 , 405-414	0.9	
31	Compensatory mutations cause excess of antagonistic epistasis in RNA secondary structure folding. <i>BMC Evolutionary Biology</i> , 2003 , 3, 3	3	56
30	Phenotypic mixing and hiding may contribute to memory in viral quasispecies. <i>BMC Microbiology</i> , 2003 , 3, 11	4.5	48
29	Evolution of mutational robustness. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2003 , 522, 3-11	3.3	95
28	Probability of fixation of an advantageous mutant in a viral quasispecies. <i>Genetics</i> , 2003 , 163, 467-74	4	33
27	Genealogical process on a correlated fitness landscape. <i>The Journal of Experimental Zoology</i> , 2002 , 294, 274-84		13
26	Viral evolution under the pressure of an adaptive immune system: Optimal mutation rates for viral escape. <i>Complexity</i> , 2002 , 8, 28-33	1.6	41
25	Optimal adaptive performance and delocalization in NK fitness landscapes. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2002 , 304, 495-506	3.3	25
24	Maternal effects in molecular evolution. <i>Physical Review Letters</i> , 2002 , 88, 078101	7.4	15
23	The biology of digital organisms. <i>Trends in Ecology and Evolution</i> , 2002 , 17, 528-532	10.9	68
22	Dynamic fitness landscapes in molecular evolution. <i>Physics Reports</i> , 2001 , 349, 395-446	27.7	94
21	Dynamic fitness landscapes: expansions for small mutation rates. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2001 , 290, 475-490	3.3	10
20	Adaptive evolution on neutral networks. <i>Bulletin of Mathematical Biology</i> , 2001 , 63, 715-30	2.1	98
19	Selection for fitness versus selection for robustness in RNA secondary structure folding. <i>Evolution; International Journal of Organic Evolution</i> , 2001 , 55, 2412-20	3.8	69
18	Evolution of digital organisms at high mutation rates leads to survival of the flattest. <i>Nature</i> , 2001 , 412, 331-3	50.4	446
17	SELECTION FOR FITNESS VERSUS SELECTION FOR ROBUSTNESS IN RNA SECONDARY STRUCTURE FOLDING. <i>Evolution; International Journal of Organic Evolution</i> , 2001 , 55, 2412	3.8	8
16	Interaction between directional epistasis and average mutational effects. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001 , 268, 1469-74	4.4	92
15	Lifetimes of agents under external stress. <i>Physical Review E</i> , 1999 , 59, R2512-R2515	2.4	1

14	Adaptive walks on time-dependent fitness landscapes. <i>Physical Review E</i> , 1999 , 60, 2154-9	2.4	13
13	Molecular Evolution in Time-Dependent Environments. <i>Lecture Notes in Computer Science</i> , 1999 , 417-421	6.9	
12	Aftershocks in coherent-noise models. <i>Physica D: Nonlinear Phenomena</i> , 1998 , 120, 401-417	3.3	13
11	Hierarchical noise in large systems of independent agents. <i>Physical Review E</i> , 1998 , 58, 7101-7108	2.4	1
10	Axion cyclotron emissivity of magnetized white dwarfs and neutron stars. <i>Physical Review D</i> , 1997 , 56, 1313-1319	4.9	13
9	Simple model of evolution with variable system size. <i>Physical Review E</i> , 1997 , 56, 7128-7131	2.4	15
8	Uncovering modeling features of viral replication dynamics from high-throughput single-cell virology experiments		1
7	A systematic analysis of the beta hairpin motif in the Protein Data Bank		1
6	Relationship between protein thermodynamic constraints and variation of evolutionary rates among sites		1
5	Sequence amplification via cell passaging creates spurious signals of positive adaptation in influenza H3N2 hemagglutinin		2
4	BACPHLIP: Predicting bacteriophage lifestyle from conserved protein domains		1
3	Theory of measurement for site-specific evolutionary rates in amino-acid sequences		2
2	Transcript degradation and codon usage regulate gene expression in a lytic phage		1
1	Humanization of yeast genes with multiple human orthologs reveals principles of functional divergence between paralogs		4