

Michael Lynch

List of Publications by Year in descending order

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173
papers

28,376
citations

10389

72
h-index

6300

158
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186
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186
docs citations

186
times ranked

24524
citing authors

#	ARTICLE	IF	CITATIONS
1	Preservation of Duplicate Genes by Complementary, Degenerative Mutations. <i>Genetics</i> , 1999, 151, 1531-1545.	2.9	3,147
2	The Origins of Genome Complexity. <i>Science</i> , 2003, 302, 1401-1404.	12.6	1,436
3	The Probability of Duplicate Gene Preservation by Subfunctionalization. <i>Genetics</i> , 2000, 154, 459-473.	2.9	1,372
4	The Rate and Molecular Spectrum of Spontaneous Mutations in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2010, 327, 92-94.	12.6	1,004
5	Estimation of Pairwise Relatedness With Molecular Markers. <i>Genetics</i> , 1999, 152, 1753-1766.	2.9	966
6	Evolution of the mutation rate. <i>Trends in Genetics</i> , 2010, 26, 345-352.	6.7	885
7	Rate, molecular spectrum, and consequences of human mutation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 961-968.	7.1	692
8	The frailty of adaptive hypotheses for the origins of organismal complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8597-8604.	7.1	689
9	A genome-wide view of the spectrum of spontaneous mutations in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9272-9277.	7.1	649
10	Genetic drift, selection and the evolution of the mutation rate. <i>Nature Reviews Genetics</i> , 2016, 17, 704-714.	16.3	648
11	THE GENETIC INTERPRETATION OF INBREEDING DEPRESSION AND OUTBREEDING DEPRESSION. <i>Evolution; International Journal of Organic Evolution</i> , 1991, 45, 622-629.	2.3	574
12	Mutation Pressure and the Evolution of Organelle Genomic Architecture. <i>Science</i> , 2006, 311, 1727-1730.	12.6	490
13	EVOLUTION AND EXTINCTION IN A CHANGING ENVIRONMENT: A QUANTITATIVE GENETIC ANALYSIS. <i>Evolution; International Journal of Organic Evolution</i> , 1995, 49, 151-163.	2.3	470
14	Evolution and Selection of Quantitative Traits. , 2018, , .		469
15	The Probability of Preservation of a Newly Arisen Gene Duplicate. <i>Genetics</i> , 2001, 159, 1789-1804.	2.9	440
16	Comparing Mutational Variabilities. <i>Genetics</i> , 1996, 143, 1467-1483.	2.9	413
17	The bioenergetic costs of a gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15690-15695.	7.1	405
18	MUTATION LOAD AND THE SURVIVAL OF SMALL POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 1990, 44, 1725-1737.	2.3	397

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19	Drift-barrier hypothesis and mutation-rate evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18488-18492.	7.1	355
20	Estimate of the genomic mutation rate deleterious to overall fitness in <i>E. coli</i> . Nature, 1996, 381, 694-696.	27.8	352
21	The Origins of Eukaryotic Gene Structure. Molecular Biology and Evolution, 2006, 23, 450-468.	8.9	348
22	METHODS FOR THE ANALYSIS OF COMPARATIVE DATA IN EVOLUTIONARY BIOLOGY. Evolution; International Journal of Organic Evolution, 1991, 45, 1065-1080.	2.3	334
23	PHENOTYPIC EVOLUTION BY NEUTRAL MUTATION. Evolution; International Journal of Organic Evolution, 1986, 40, 915-935.	2.3	325
24	PERSPECTIVE: SPONTANEOUS DELETERIOUS MUTATION. Evolution; International Journal of Organic Evolution, 1999, 53, 645-663.	2.3	317
25	Predation, competition, and zooplankton community structure: An experimental study ^{1,2} . Limnology and Oceanography, 1979, 24, 253-272.	3.1	310
26	MUTATIONAL MELTDOWNS IN SEXUAL POPULATIONS. Evolution; International Journal of Organic Evolution, 1995, 49, 1067-1080.	2.3	300
27	The rate of polygenic mutation. Genetical Research, 1988, 51, 137-148.	0.9	271
28	The altered evolutionary trajectories of gene duplicates. Trends in Genetics, 2004, 20, 544-549.	6.7	267
29	The evolution of genetic networks by non-adaptive processes. Nature Reviews Genetics, 2007, 8, 803-813.	16.3	266
30	Captive breeding and the genetic fitness of natural populations. Conservation Genetics, 2001, 2, 363-378.	1.5	262
31	Intron evolution as a population-genetic process. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6118-6123.	7.1	260
32	High Direct Estimate of the Mutation Rate in the Mitochondrial Genome of <i>Caenorhabditis elegans</i> . Science, 2000, 289, 2342-2344.	12.6	259
33	The evolutionary demography of duplicate genes. Journal of Structural and Functional Genomics, 2003, 3, 35-44.	1.2	249
34	The critical effective size for a genetically secure population. Animal Conservation, 1998, 1, 70-72.	2.9	206
35	Streamlining and Simplification of Microbial Genome Architecture. Annual Review of Microbiology, 2006, 60, 327-349.	7.3	204
36	Perspective: Spontaneous Deleterious Mutation. Evolution; International Journal of Organic Evolution, 1999, 53, 645.	2.3	200

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37	THE QUANTITATIVE AND MOLECULAR GENETIC ARCHITECTURE OF A SUBDIVIDED SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 100-110.	2.3	192
38	THE FITNESS EFFECTS OF SPONTANEOUS MUTATIONS IN <i>CAENORHABDITIS ELEGANS</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1234-1246.	2.3	178
39	ECOLOGICAL GENETICS OF <i>DAPHNIA PULEX</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1983, 37, 358-374.	2.3	175
40	Antibiotic treatment enhances the genome-wide mutation rate of target cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2498-505.	7.1	172
41	Maintenance and Loss of Duplicated Genes by Dosage Subfunctionalization. <i>Molecular Biology and Evolution</i> , 2015, 32, 2141-2148.	8.9	160
42	Population-genomic insights into the evolutionary origin and fate of obligately asexual <i>Daphnia pulex</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15740-15745.	7.1	159
43	GENOMICS: Gene Duplication and Evolution. <i>Science</i> , 2002, 297, 945-947.	12.6	157
44	The evolutionary demography of duplicate genes. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 35-44.	1.2	150
45	SPONTANEOUS MUTATIONS FOR LIFE-HISTORY CHARACTERS IN AN OBLIGATE PARTHENOGEN. <i>Evolution; International Journal of Organic Evolution</i> , 1985, 39, 804-818.	2.3	142
46	The selective advantage of reaction norms for environmental tolerance. <i>Journal of Evolutionary Biology</i> , 1992, 5, 41-59.	1.7	142
47	The Rate of Spontaneous Mutation for Life-History Traits in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 1999, 151, 119-129.	2.9	142
48	The Lower Bound to the Evolution of Mutation Rates. <i>Genome Biology and Evolution</i> , 2011, 3, 1107-1118.	2.5	139
49	MUTATION AND EXTINCTION: THE ROLE OF VARIABLE MUTATIONAL EFFECTS, SYNERGISTIC EPISTASIS, BENEFICIAL MUTATIONS, AND DEGREE OF OUTCROSSING. <i>Evolution; International Journal of Organic Evolution</i> , 1997, 51, 1363-1371.	2.3	132
50	Asymmetric Context-Dependent Mutation Patterns Revealed through Mutation "Accumulation Experiments. <i>Molecular Biology and Evolution</i> , 2015, 32, 1672-1683.	8.9	130
51	The Spontaneous Mutation Rate in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Genetics</i> , 2015, 201, 737-744.	2.9	127
52	Deleterious mutation accumulation in organelle genomes. <i>Genetica</i> , 1998, 102/103, 29-39.	1.1	126
53	Evolutionary determinants of genome-wide nucleotide composition. <i>Nature Ecology and Evolution</i> , 2018, 2, 237-240.	7.8	126
54	The importance of the Neutral Theory in 1968 and 50 years on: A response to Kern and Hahn 2018. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 111-114.	2.3	123

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55	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. <i>Nature Ecology and Evolution</i> , 2018, 2, 669-679.	7.8	117
56	The Repatterning of Eukaryotic Genomes by Random Genetic Drift. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 347-366.	6.2	114
57	The Consequences of Fluctuating Selection for Isozyme Polymorphisms in <i>Daphnia</i> . <i>Genetics</i> , 1987, 115, 657-669.	2.9	113
58	Estimation of Nucleotide Diversity, Disequilibrium Coefficients, and Mutation Rates from High-Coverage Genome-Sequencing Projects. <i>Molecular Biology and Evolution</i> , 2008, 25, 2409-2419.	8.9	112
59	Differential retention and divergent resolution of duplicate genes following whole-genome duplication. <i>Genome Research</i> , 2014, 24, 1665-1675.	5.5	111
60	Evolutionary cell biology: Two origins, one objective. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16990-16994.	7.1	108
61	Adaptive and demographic responses of plankton populations to environmental change. <i>Limnology and Oceanography</i> , 1991, 36, 1301-1312.	3.1	105
62	The Cellular, Developmental and Population-Genetic Determinants of Mutation-Rate Evolution. <i>Genetics</i> , 2008, 180, 933-943.	2.9	102
63	The landscape of transcription errors in eukaryotic cells. <i>Science Advances</i> , 2017, 3, e1701484.	10.3	102
64	Population-Genetic Inference from Pooled-Sequencing Data. <i>Genome Biology and Evolution</i> , 2014, 6, 1210-1218.	2.5	101
65	Genetic Slippage in Response to Sex. <i>American Naturalist</i> , 1994, 144, 242-261.	2.1	100
66	High mutational rates of large-scale duplication and deletion in <i>Daphnia pulex</i> . <i>Genome Research</i> , 2016, 26, 60-69.	5.5	99
67	THE LIMITS TO LIFE HISTORY EVOLUTION IN DAPHNIA. <i>Evolution; International Journal of Organic Evolution</i> , 1984, 38, 465-482.	2.3	98
68	A New Reference Genome Assembly for the Microcrustacean <i>Daphnia pulex</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1405-1416.	1.8	95
69	THE COVARIANCE STRUCTURE OF LIFE-HISTORY CHARACTERS IN <i>DAPHNIA PULEX</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1991, 45, 1081-1090.	2.3	94
70	Large-scale detection of in vivo transcription errors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18584-18589.	7.1	94
71	Mutation and Human Exceptionalism: Our Future Genetic Load. <i>Genetics</i> , 2016, 202, 869-875.	2.9	92
72	Estimation of Allele Frequencies From High-Coverage Genome-Sequencing Projects. <i>Genetics</i> , 2009, 182, 295-301.	2.9	89

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73	Evolution of the Insertion-Deletion Mutation Rate Across the Tree of Life. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2583-2591.	1.8	89
74	mlRho – a program for estimating the population mutation and recombination rates from shotgun-sequenced diploid genomes. <i>Molecular Ecology</i> , 2010, 19, 277-284.	3.9	88
75	Genotype Calling from Population-Genomic Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1393-1404.	1.8	84
76	Evolutionary meandering of intermolecular interactions along the drift barrier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E30-8.	7.1	82
77	Genome-Wide Biases in the Rate and Molecular Spectrum of Spontaneous Mutations in <i>Vibrio cholerae</i> and <i>Vibrio fischeri</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 93-109.	8.9	81
78	THE GENETIC STRUCTURE OF A CYCLICAL PARTHENOGEN. <i>Evolution; International Journal of Organic Evolution</i> , 1984, 38, 186-203.	2.3	80
79	Evolutionary diversification of the multimeric states of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2821-8.	7.1	78
80	The Evolution of Multimeric Protein Assemblages. <i>Molecular Biology and Evolution</i> , 2012, 29, 1353-1366.	8.9	75
81	The Rate and Molecular Spectrum of Spontaneous Mutations in the GC-Rich Multichromosome Genome of <i>Burkholderia cenocepacia</i> . <i>Genetics</i> , 2015, 200, 935-946.	2.9	75
82	Addressing ecological effects of radiation on populations and ecosystems to improve protection of the environment against radiation: Agreed statements from a Consensus Symposium. <i>Journal of Environmental Radioactivity</i> , 2016, 158-159, 21-29.	1.7	75
83	QUANTITATIVE GENETIC VARIATION IN DAPHNIA: TEMPORAL CHANGES IN GENETIC ARCHITECTURE. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1502-1509.	2.3	73
84	THE DISTRIBUTION OF LIFE-HISTORY VARIATION IN THE <i>DAPHNIA PULEX</i> COMPLEX. <i>Evolution; International Journal of Organic Evolution</i> , 1989, 43, 1724-1736.	2.3	71
85	PHYLOGENETIC HYPOTHESES UNDER THE ASSUMPTION OF NEUTRAL QUANTITATIVE GENETIC VARIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1989, 43, 1-17.	2.3	69
86	Messenger RNA Surveillance and the Evolutionary Proliferation of Introns. <i>Molecular Biology and Evolution</i> , 2003, 20, 563-571.	8.9	69
87	Localization of the Genetic Determinants of Meiosis Suppression in <i>Daphnia pulex</i> . <i>Genetics</i> , 2008, 180, 317-327.	2.9	69
88	MUTATION, SELECTION, AND THE MAINTENANCE OF LIFE-HISTORY VARIATION IN A NATURAL POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 1998, 52, 727-733.	2.3	68
89	Insights into Three Whole-Genome Duplications Gleaned from the <i>Paramecium caudatum</i> Genome Sequence. <i>Genetics</i> , 2014, 197, 1417-1428.	2.9	67
90	PATTERNS OF GENETIC ARCHITECTURE FOR LIFE-HISTORY TRAITS AND MOLECULAR MARKERS IN A SUBDIVIDED SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 1753-1761.	2.3	66

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91	The Rate of Establishment of Complex Adaptations. <i>Molecular Biology and Evolution</i> , 2010, 27, 1404-1414.	8.9	66
92	Title is missing!. <i>Conservation Genetics</i> , 2000, 1, 263-269.	1.5	64
93	Deciphering the Evolutionary History of Open and Closed Mitosis. <i>Current Biology</i> , 2014, 24, R1099-R1103.	3.9	64
94	Mutation Rate, Spectrum, Topology, and Context-Dependency in the DNA Mismatch Repair-Deficient <i>Pseudomonas fluorescens</i> ATCC948. <i>Genome Biology and Evolution</i> , 2015, 7, 262-271.	2.5	62
95	The Evolution of Transcription-Initiation Sites. <i>Molecular Biology and Evolution</i> , 2005, 22, 1137-1146.	8.9	60
96	Membranes, energetics, and evolution across the prokaryote-eukaryote divide. <i>ELife</i> , 2017, 6, .	6.0	60
97	Recommendations for improving statistical inference in population genomics. <i>PLoS Biology</i> , 2022, 20, e3001669.	5.6	60
98	Estimating genetic correlations in natural populations. <i>Genetical Research</i> , 1999, 74, 255-264.	0.9	58
99	Background Mutational Features of the Radiation-Resistant Bacterium <i>Deinococcus radiodurans</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 2383-2392.	8.9	58
100	Population Genomics of <i>Daphnia pulex</i> . <i>Genetics</i> , 2017, 206, 315-332.	2.9	55
101	Allozyme and mtDNA variation in populations of the <i>Daphnia pulex</i> complex from both sides of the Rocky Mountains. <i>Heredity</i> , 1997, 79, 242-251.	2.6	53
102	Scaling expectations for the time to establishment of complex adaptations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16577-16582.	7.1	53
103	A Male-Specific Genetic Map of the Microcrustacean <i>Daphnia pulex</i> Based on Single-Sperm Whole-Genome Sequencing. <i>Genetics</i> , 2015, 201, 31-38.	2.9	52
104	Physical bioenergetics: Energy fluxes, budgets, and constraints in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	52
105	Hybridization and the Origin of Contagious Asexuality in <i>Daphnia pulex</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, msv190.	8.9	49
106	The Rate and Spectrum of Spontaneous Mutations in <i>Mycobacterium smegmatis</i> , a Bacterium Naturally Devoid of the Postreplicative Mismatch Repair Pathway. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2157-2163.	1.8	48
107	<i>Escherichia coli</i> cultures maintain stable subpopulation structure during long-term evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4642-E4650.	7.1	46
108	Evolutionary layering and the limits to cellular perfection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18851-18856.	7.1	43

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109	A Theoretical Framework for Evolutionary Cell Biology. <i>Journal of Molecular Biology</i> , 2020, 432, 1861-1879.	4.2	41
110	THE AGE AND RELATIONSHIPS OF THE MAJOR ANIMAL PHYLA. <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 319-325.	2.3	40
111	Similar Mutation Rates but Highly Diverse Mutation Spectra in Ascomycete and Basidiomycete Yeasts. <i>Genome Biology and Evolution</i> , 2016, 8, 3815-3821.	2.5	40
112	Statistical Inference on the Mechanisms of Genome Evolution. <i>PLoS Genetics</i> , 2011, 7, e1001389.	3.5	39
113	Genotype-Frequency Estimation from High-Throughput Sequencing Data. <i>Genetics</i> , 2015, 201, 473-486.	2.9	39
114	Simple evolutionary pathways to complex proteins. <i>Protein Science</i> , 2005, 14, 2217-2225.	7.6	38
115	Low Base-Substitution Mutation Rate in the Germline Genome of the Ciliate <i>Tetrahymena thermophilus</i> . <i>Genome Biology and Evolution</i> , 2016, 8, eww223.	2.5	38
116	Diversity and Divergence of Dinoflagellate Histone Proteins. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 397-422.	1.8	38
117	Population Genomics of Paramecium Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1194-1216.	8.9	35
118	How Well Does the Edmonson-Paloheimo Model Approximate Instantaneous Birth Rates?. <i>Ecology</i> , 1982, 63, 12-18.	3.2	34
119	Estimating Seven Coefficients of Pairwise Relatedness Using Population-Genomic Data. <i>Genetics</i> , 2017, 206, 105-118.	2.9	33
120	The critical effective size for a genetically secure population. <i>Animal Conservation</i> , 1998, 01, 70-72.	2.9	32
121	THE DIVERGENCE OF NEUTRAL QUANTITATIVE CHARACTERS AMONG PARTIALLY ISOLATED POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 1988, 42, 455-466.	2.3	31
122	Patterns of Intraspecific DNA Variation in the Daphnia Nuclear Genome. <i>Genetics</i> , 2009, 182, 325-336.	2.9	31
123	Genome-Wide Linkage-Disequilibrium Profiles from Single Individuals. <i>Genetics</i> , 2014, 198, 269-281.	2.9	30
124	The evolutionary scaling of cellular traits imposed by the drift barrier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10435-10444.	7.1	30
125	Genome-Wide Estimation of Linkage Disequilibrium from Population-Level High-Throughput Sequencing Data. <i>Genetics</i> , 2014, 197, 1303-1313.	2.9	27
126	THE EFFECT OF VARIABLE FREQUENCY OF SEXUAL REPRODUCTION ON THE GENETIC STRUCTURE OF NATURAL POPULATIONS OF A CYCLICAL PARTHENOGEN. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 919-926.	2.3	24

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127	Genetic control of male production in <i>Daphnia pulex</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15602-15609.	7.1	24
128	Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy. Heredity, 2020, 124, 619-620.	2.6	24
129	CONSERVED ONTOGENY AND ALLOMETRIC SCALING OF RESOURCE ACQUISITION AND ALLOCATION IN THE DAPHNIIDAE. Evolution; International Journal of Organic Evolution, 2005, 59, 565-576.	2.3	23
130	Spontaneous mutations of a model heterotrophic marine bacterium. ISME Journal, 2017, 11, 1713-1718.	9.8	22
131	Catalytic properties of RNA polymerases IV and V: accuracy, nucleotide incorporation and rNTP/dNTP discrimination. Nucleic Acids Research, 2017, 45, 11315-11326.	14.5	22
132	Population Genetics of Paramecium Mitochondrial Genomes: Recombination, Mutation Spectrum, and Efficacy of Selection. Genome Biology and Evolution, 2019, 11, 1398-1416.	2.5	22
133	Genome-Wide Mutation Rate Response to pH Change in the Coral Reef Pathogen <i>Vibrio shilonii</i> AK1. MBio, 2017, 8, .	4.1	21
134	Limited Mutation-Rate Variation Within the Paramecium aurelia Species Complex. G3: Genes, Genomes, Genetics, 2018, 8, 2523-2526.	1.8	21
135	THE SELECTIVE VALUE OF ALLELES UNDERLYING POLYGENIC TRAITS. Genetics, 1984, 108, 1021-1033.	2.9	21
136	Promoter Architecture and Sex-Specific Gene Expression in <i>Daphnia pulex</i> . Genetics, 2016, 204, 593-612.	2.9	20
137	Reply to Lane and Martin: Mitochondria do not boost the bioenergetic capacity of eukaryotic cells. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E667-8.	7.1	20
138	Imposed mutational meltdown as an antiviral strategy. Evolution; International Journal of Organic Evolution, 2020, 74, 2549-2559.	2.3	20
139	Estimation of size-specific mortality rates in zooplankton populations by periodic sampling1. Limnology and Oceanography, 1983, 28, 533-545.	3.1	18
140	Enhanced nutrient uptake is sufficient to drive emergent cross-feeding between bacteria in a synthetic community. ISME Journal, 2020, 14, 2816-2828.	9.8	18
141	Variable Spontaneous Mutation and Loss of Heterozygosity among Heterozygous Genomes in Yeast. Molecular Biology and Evolution, 2020, 37, 3118-3130.	8.9	17
142	The Limits to Estimating Population-Genetic Parameters with Temporal Data. Genome Biology and Evolution, 2020, 12, 443-455.	2.5	17
143	Universally high transcript error rates in bacteria. ELife, 2020, 9, .	6.0	17
144	Characterization of Newly Gained Introns in <i>Daphnia</i> Populations. Genome Biology and Evolution, 2014, 6, 2218-2234.	2.5	16

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145	Insertion polymorphisms of mobile genetic elements in sexual and asexual populations of <i>Daphnia pulex</i> . <i>Genome Biology and Evolution</i> , 2017, 9, evw302.	2.5	15
146	The rapid, mass invasion of New Zealand by North American <i>Daphnia pulex</i> . <i>Limnology and Oceanography</i> , 2021, 66, 2672-2683.	3.1	15
147	Rule-based workflow management for bioinformatics. <i>VLDB Journal</i> , 2005, 14, 318-329.	4.1	14
148	The Glyphosate-Based Herbicide Roundup Does Not Elevate Genome-Wide Mutagenesis of <i>Escherichia coli</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3331-3335.	1.8	14
149	Revisiting the notion of deleterious sweeps. <i>Genetics</i> , 2021, 219, .	2.9	14
150	Conservation and divergence of the histone code in nucleomorphs. <i>Biology Direct</i> , 2016, 11, 18.	4.6	12
151	Phylogenetic divergence of cell biological features. <i>ELife</i> , 2018, 7, .	6.0	12
152	Inference of Historical Population-Size Changes with Allele-Frequency Data. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 211-223.	1.8	12
153	Feedforward loop for diversity. <i>Nature</i> , 2015, 523, 414-416.	27.8	10
154	Low Base-Substitution Mutation Rate but High Rate of Slippage Mutations in the Sequence Repeat-Rich Genome of <i>Dictyostelium discoideum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3445-3452.	1.8	10
155	Estimation of the Genome-Wide Mutation Rate and Spectrum in the Archaeal Species <i>Haloferax volcanii</i> . <i>Genetics</i> , 2020, 215, 1107-1116.	2.9	10
156	The insect-killing bacterium <i>Photobacterium luminescens</i> has the lowest mutation rate among bacteria. <i>Marine Life Science and Technology</i> , 2021, 3, 20-27.	4.6	10
157	Allozyme and mtDNA variation in populations of the <i>Daphnia pulex</i> complex from both sides of the Rocky Mountains. <i>Heredity</i> , 1997, 79, 242-251.	2.6	10
158	RANDOM DRIFT, UNIFORM SELECTION, AND THE DEGREE OF POPULATION DIFFERENTIATION. <i>Evolution; International Journal of Organic Evolution</i> , 1986, 40, 640-643.	2.3	9
159	PATTERNS OF GENETIC ARCHITECTURE FOR LIFE-HISTORY TRAITS AND MOLECULAR MARKERS IN A SUBDIVIDED SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2001, 55, 1753.	2.3	9
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