Michael Lynch

List of Publications by Year
in descending order

175 papers	29,258 citations	10475 72 h-index	6378 159 g-index
195 all docs	195 docs citations	195 times ranked	27533 citing authors

#	Article	IF	Citations
1	The genome-wide signature of short-term temporal selection. Proceedings of the National Academy of Sciences of the United States of America, 2024, 121, .	7.6	1
2	The fidelity of transcription in human cells. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.6	5
3	Mutation pressure, drift, and the pace of molecular coevolution. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.6	3
4	Evolution of a minimal cell. Nature, 2023, 620, 122-127.	36.2	33
5	Masatoshi Nei (1931 to 2023): Founder of molecular evolutionary genetics. Proceedings of the National Academy of Sciences of the United States of America, 2023, 120, .	7.6	1
6	The divergence of mutation rates and spectra across the Tree of Life. EMBO Reports, 2023, 24, .	5.1	10
7	Rates of Mutations and Transcript Errors in the Foodborne Pathogen<i>Salmonella enterica</i>subsp.<i>enterica</i>. Molecular Biology and Evolution, 2022, 39, .	9.2	11
8	Complex Ecotype Dynamics Evolve in Response to Fluctuating Resources. MBio, 2022, 13, e0346721.	4.4	9
9	Recommendations for improving statistical inference in population genomics. PLoS Biology, 2022, 20, e3001669.	5.4	79
10	Evolutionary bioenergetics of ciliates. Journal of Eukaryotic Microbiology, 2022, 69, .	1.8	3
11	Rapid evolution of mutation rate and spectrum in response to environmental and population-genetic challenges. Nature Communications, 2022, 13, .	13.2	23
12	The insect-killing bacterium Photorhabdus luminescens has the lowest mutation rate among bacteria. Marine Life Science and Technology, 2021, 3, 20-27.	4.6	12
13	The rapid, mass invasion of New Zealand by North American <i>Daphnia</i> â€œ<i>pulex</i>â€. Limnology and Oceanography, 2021, 66, 2672-2683.	3.5	20
14	Physical bioenergetics: Energy fluxes, budgets, and constraints in cells. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.6	67
15	Revisiting the notion of deleterious sweeps. Genetics, 2021, 219, .	2.9	15
16	Unexpected Discovery of Hypermutator Phenotype Sounds the Alarm for Quality Control Strains. Genome Biology and Evolution, 2021, 13, .	2.6	2
17	Evolutionary Dynamics of Asexual Hypermutators Adapting to a Novel Environment. Genome Biology and Evolution, 2021, 13, .	2.6	9
18	Low baseâ€substitution mutation rate and predominance of insertionâ€deletion events in the acidophilic bacterium <i>Acidobacterium capsulatum</i>. Ecology and Evolution, 2021, 11, 17609-17614.	1.9	1

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19	The Rab7 subfamily across <i>Paramecium aurelia</i> species; evidence of high conservation in sequence and function. Small GTPases, 2020, 11, 421-429.	1.9	3
20	Imposed mutational meltdown as an antiviral strategy. Evolution; International Journal of Organic Evolution, 2020, 74, 2549-2559.	2.3	20
21	Enhanced nutrient uptake is sufficient to drive emergent cross-feeding between bacteria in a synthetic community. ISME Journal, 2020, 14, 2816-2828.	10.0	21
22	Low Base-Substitution Mutation Rate but High Rate of Slippage Mutations in the Sequence Repeat-Rich Genome of <i>Dictyostelium discoideum</i>. G3: Genes, Genomes, Genetics, 2020, 10, 3445-3452.	1.9	13
23	Variable Spontaneous Mutation and Loss of Heterozygosity among Heterozygous Genomes in Yeast. Molecular Biology and Evolution, 2020, 37, 3118-3130.	9.2	20
24	Estimation of the Genome-Wide Mutation Rate and Spectrum in the Archaeal Species <i>Haloferax volcanii</i>. Genetics, 2020, 215, 1107-1116.	2.9	13
25	The Limits to Estimating Population-Genetic Parameters with Temporal Data. Genome Biology and Evolution, 2020, 12, 443-455.	2.6	18
26	A Theoretical Framework for Evolutionary Cell Biology. Journal of Molecular Biology, 2020, 432, 1861-1879.	4.3	45
27	The evolutionary scaling of cellular traits imposed by the drift barrier. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10435-10444.	7.6	32
28	Inference of Historical Population-Size Changes with Allele-Frequency Data. G3: Genes, Genomes, Genetics, 2020, 10, 211-223.	1.9	13
29	Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy. Heredity, 2020, 124, 619-620.	2.7	24
30	Universally high transcript error rates in bacteria. ELife, 2020, 9, .	5.9	22
31	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.	7.6	27
32	Joseph Shapiro, an Icon of Applied Limnology. Limnology and Oceanography Bulletin, 2019, 28, 35-37.	0.4	0
33	Population Genetics of Paramecium Mitochondrial Genomes: Recombination, Mutation Spectrum, and Efficacy of Selection. Genome Biology and Evolution, 2019, 11, 1398-1416.	2.6	23
34	The importance of the Neutral Theory in 1968 and 50 years on: A response to Kern and Hahn 2018. Evolution; International Journal of Organic Evolution, 2019, 73, 111-114.	2.3	127
35	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. Nature Ecology and Evolution, 2018, 2, 669-679.	8.0	125
36	Evolutionary determinants of genome-wide nucleotide composition. Nature Ecology and Evolution, 2018, 2, 237-240.	8.0	138

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37	<i>Escherichia coli</i>cultures maintain stable subpopulation structure during long-term evolution. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4642-E4650.	7.6	48
38	Limited Mutation-Rate Variation Within the <i>Paramecium aurelia</i> Species Complex. G3: Genes, Genomes, Genetics, 2018, 8, 2523-2526.	1.9	23
39	Response to Martin and colleagues: mitochondria do not boost the bioenergetic capacity of eukaryotic cells. Biology Direct, 2018, 13, 26.	4.6	4
40	Phylogenetic divergence of cell biological features. ELife, 2018, 7, .	5.9	14
41	An Escherichia coli Nitrogen Starvation Response Is Important for Mutualistic Coexistence with Rhodopseudomonas palustris. Applied and Environmental Microbiology, 2018, 84, .	3.2	9
42	Insertion polymorphisms of mobile genetic elements in sexual and asexual populations of <i>Daphnia pulex</i>. Genome Biology and Evolution, 2017, 9, evw302.	2.6	15
43	Population Genomics of <i>Daphnia pulex</i>. Genetics, 2017, 206, 315-332.	2.9	59
44	Early stages of functional diversification in the Rab GTPase gene family revealed by genomic and localization studies in<i>Paramecium</i>species. Molecular Biology of the Cell, 2017, 28, 1101-1110.	2.5	8
45	Population Genomics of Paramecium Species. Molecular Biology and Evolution, 2017, 34, 1194-1216.	9.2	37
46	Estimating Seven Coefficients of Pairwise Relatedness Using Population-Genomic Data. Genetics, 2017, 206, 105-118.	2.9	37
47	Genotype Calling from Population-Genomic Sequencing Data. G3: Genes, Genomes, Genetics, 2017, 7, 1393-1404.	1.9	86
48	Spontaneous mutations of a model heterotrophic marine bacterium. ISME Journal, 2017, 11, 1713-1718.	10.0	23
49	Catalytic properties of RNA polymerases IV and V: accuracy, nucleotide incorporation and rNTP/dNTP discrimination. Nucleic Acids Research, 2017, 45, 11315-11326.	14.0	24
50	The landscape of transcription errors in eukaryotic cells. Science Advances, 2017, 3, e1701484.	10.9	115
51	Genome-Wide Mutation Rate Response to pH Change in the Coral Reef Pathogen <i>Vibrio shilonii</i> AK1. MBio, 2017, 8, .	4.4	23
52	A New Reference Genome Assembly for the Microcrustacean <i>Daphnia pulex</i>. G3: Genes, Genomes, Genetics, 2017, 7, 1405-1416.	1.9	97
53	The Glyphosate-Based Herbicide Roundup Does Not Elevate Genome-Wide Mutagenesis of<i>Escherichia coli</i>. G3: Genes, Genomes, Genetics, 2017, 7, 3331-3335.	1.9	15
54	Genome-Wide Biases in the Rate and Molecular Spectrum of Spontaneous Mutations in<i>Vibrio cholerae</i>and<i>Vibrio fischeri</i>. Molecular Biology and Evolution, 2017, 34, 93-109.	9.2	85

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55	Membranes, energetics, and evolution across the prokaryote-eukaryote divide. ELife, 2017, 6, .	5.9	65
56	Similar Mutation Rates but Highly Diverse Mutation Spectra in Ascomycete and Basidiomycete Yeasts. Genome Biology and Evolution, 2016, 8, 3815-3821.	2.6	41
57	The Rate and Spectrum of Spontaneous Mutations in <i>Mycobacterium smegmatis</i>, a Bacterium Naturally Devoid of the Postreplicative Mismatch Repair Pathway. G3: Genes, Genomes, Genetics, 2016, 6, 2157-2163.	1.9	54
58	Low Base-Substitution Mutation Rate in the Germline Genome of the Ciliate<i>Tetrahymena thermophil</i>. Genome Biology and Evolution, 2016, 8, evw223.	2.6	40
59	Antibiotic treatment enhances the genome-wide mutation rate of target cells. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2498-505.	7.6	179
60	Addressing ecological effects of radiation on populations and ecosystems to improve protection of the environment against radiation: Agreed statements from a Consensus Symposium. Journal of Environmental Radioactivity, 2016, 158-159, 21-29.	1.8	78
61	Promoter Architecture and Sex-Specific Gene Expression in <i>Daphnia pulex</i>. Genetics, 2016, 204, 593-612.	2.9	20
62	Evolution of the Insertion-Deletion Mutation Rate Across the Tree of Life. G3: Genes, Genomes, Genetics, 2016, 6, 2583-2591.	1.9	94
63	Genetic drift, selection and the evolution of the mutation rate. Nature Reviews Genetics, 2016, 17, 704-714.	16.7	691
64	Mutation, Eugenics, and the Boundaries of Science. Genetics, 2016, 204, 825-827.	2.9	6
65	Diversity and Divergence of Dinoflagellate Histone Proteins. G3: Genes, Genomes, Genetics, 2016, 6, 397-422.	1.9	40
66	Conservation and divergence of the histone code in nucleomorphs. Biology Direct, 2016, 11, 18.	4.6	12
67	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.	7.6	20
68	Mutation and Human Exceptionalism: Our Future Genetic Load. Genetics, 2016, 202, 869-875.	2.9	94
69	High mutational rates of large-scale duplication and deletion in <i>Daphnia pulex</i>. Genome Research, 2016, 26, 60-69.	5.6	103
70	Draft Genome Sequence of Caedibacter varicaedens, a Kappa Killer Endosymbiont Bacterium of the Ciliate <i>Paramecium biaurelia</i>. Genome Announcements, 2015, 3, .	0.8	7
71	Asymmetric Context-Dependent Mutation Patterns Revealed through Mutationâ€“Accumulation Experiments. Molecular Biology and Evolution, 2015, 32, 1672-1683.	9.2	137
72	The Rate and Molecular Spectrum of Spontaneous Mutations in the GC-Rich Multichromosome Genome of <i>Burkholderia cenocepacia</i>. Genetics, 2015, 200, 935-946.	2.9	78

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73	Mutation Rate, Spectrum, Topology, and Context-Dependency in the DNA Mismatch Repair-Deficient Pseudomonas fluorescens ATCC948. Genome Biology and Evolution, 2015, 7, 262-271.	2.6	63
74	Feedforward loop for diversity. Nature, 2015, 523, 414-416.	36.2	10
75	Maintenance and Loss of Duplicated Genes by Dosage Subfunctionalization. Molecular Biology and Evolution, 2015, 32, 2141-2148.	9.2	166
76	Background Mutational Features of the Radiation-Resistant Bacterium<i>Deinococcus radiodurans</i>. Molecular Biology and Evolution, 2015, 32, 2383-2392.	9.2	62
77	The bioenergetic costs of a gene. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15690-15695.	7.6	428
78	The Spontaneous Mutation Rate in the Fission Yeast <i>Schizosaccharomyces pombe</i>. Genetics, 2015, 201, 737-744.	2.9	131
79	Genotype-Frequency Estimation from High-Throughput Sequencing Data. Genetics, 2015, 201, 473-486.	2.9	40
80	A Male-Specific Genetic Map of the Microcrustacean<i>Daphnia pulex</i>Based on Single-Sperm Whole-Genome Sequencing. Genetics, 2015, 201, 31-38.	2.9	52
81	Hybridization and the Origin of Contagious Asexuality in<i>Daphnia pulex</i>. Molecular Biology and Evolution, 2015, 32, msv190.	9.2	51
82	Evolutionary meandering of intermolecular interactions along the drift barrier. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E30-8.	7.6	87
83	Characterization of Newly Gained Introns in Daphnia Populations. Genome Biology and Evolution, 2014, 6, 2218-2234.	2.6	16
84	Population-Genetic Inference from Pooled-Sequencing Data. Genome Biology and Evolution, 2014, 6, 1210-1218.	2.6	105
85	Genome-Wide Linkage-Disequilibrium Profiles from Single Individuals. Genetics, 2014, 198, 269-281.	2.9	31
86	Evolutionary cell biology: Two origins, one objective. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16990-16994.	7.6	111
87	Deciphering the Evolutionary History of Open and Closed Mitosis. Current Biology, 2014, 24, R1099-R1103.	4.0	68
88	Genome-Wide Estimation of Linkage Disequilibrium from Population-Level High-Throughput Sequencing Data. Genetics, 2014, 197, 1303-1313.	2.9	27
89	Insights into Three Whole-Genome Duplications Gleaned from the<i>Paramecium caudatum</i>Genome Sequence. Genetics, 2014, 197, 1417-1428.	2.9	73
90	Differential retention and divergent resolution of duplicate genes following whole-genome duplication. Genome Research, 2014, 24, 1665-1675.	5.6	114

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91	Large-scale detection of in vivo transcription errors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18584-18589.	7.6	100
92	Evolutionary diversification of the multimeric states of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2821-8.	7.6	81
93	Population-genomic insights into the evolutionary origin and fate of obligately asexual<i>Daphnia pulex</i>. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15740-15745.	7.6	162
94	Evolutionary layering and the limits to cellular perfection. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18851-18856.	7.6	46
95	Drift-barrier hypothesis and mutation-rate evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18488-18492.	7.6	365
96	The Evolution of Multimeric Protein Assemblages. Molecular Biology and Evolution, 2012, 29, 1353-1366.	9.2	79
97	THE EFFECT OF VARIABLE FREQUENCY OF SEXUAL REPRODUCTION ON THE GENETIC STRUCTURE OF NATURAL POPULATIONS OF A CYCLICAL PARTHENOGEN. Evolution; International Journal of Organic Evolution, 2012, 66, 919-926.	2.3	24
98	The Repatterning of Eukaryotic Genomes by Random Genetic Drift. Annual Review of Genomics and Human Genetics, 2011, 12, 347-366.	6.3	117
99	The Lower Bound to the Evolution of Mutation Rates. Genome Biology and Evolution, 2011, 3, 1107-1118.	2.6	141
100	Statistical Inference on the Mechanisms of Genome Evolution. PLoS Genetics, 2011, 7, e1001389.	3.4	40
101	Evolution of the mutation rate. Trends in Genetics, 2010, 26, 345-352.	6.9	932
102	mlRho â€“ a program for estimating the population mutation and recombination rates from shotgunâ€sequenced diploid genomes. Molecular Ecology, 2010, 19, 277-284.	3.6	95
103	Rate, molecular spectrum, and consequences of human mutation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 961-968.	7.6	699
104	Scaling expectations for the time to establishment of complex adaptations. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16577-16582.	7.6	54
105	The Rate of Establishment of Complex Adaptations. Molecular Biology and Evolution, 2010, 27, 1404-1414.	9.2	67
106	Patterns of Intraspecific DNA Variation in the Daphnia Nuclear Genome. Genetics, 2009, 182, 325-336.	2.9	33
107	Estimation of Allele Frequencies From High-Coverage Genome-Sequencing Projects. Genetics, 2009, 182, 295-301.	2.9	90
108	Localization of the Genetic Determinants of Meiosis Suppression in <i>Daphnia pulex</i>. Genetics, 2008, 180, 317-327.	2.9	70

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109	A genome-wide view of the spectrum of spontaneous mutations in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9272-9277.	7.6	660
110	Estimation of Nucleotide Diversity, Disequilibrium Coefficients, and Mutation Rates from High-Coverage Genome-Sequencing Projects. Molecular Biology and Evolution, 2008, 25, 2409-2419.	9.2	116
111	The Cellular, Developmental and Population-Genetic Determinants of Mutation-Rate Evolution. Genetics, 2008, 180, 933-943.	2.9	106
112	The frailty of adaptive hypotheses for the origins of organismal complexity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8597-8604.	7.6	704
113	The evolution of genetic networks by non-adaptive processes. Nature Reviews Genetics, 2007, 8, 803-813.	16.7	267
114	Streamlining and Simplification of Microbial Genome Architecture. Annual Review of Microbiology, 2006, 60, 327-349.	7.6	215
115	The Origins of Eukaryotic Gene Structure. Molecular Biology and Evolution, 2006, 23, 450-468.	9.2	354
116	Mutation Pressure and the Evolution of Organelle Genomic Architecture. Science, 2006, 311, 1727-1730.	20.9	502
117	Simple evolutionary pathways to complex proteins. Protein Science, 2005, 14, 2217-2225.	7.8	38
118	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	24
119	Rule-based workflow management for bioinformatics. VLDB Journal, 2005, 14, 318-329.	4.2	14
120	The Evolution of Transcription-Initiation Sites. Molecular Biology and Evolution, 2005, 22, 1137-1146.	9.2	63
121	The altered evolutionary trajectories of gene duplicates. Trends in Genetics, 2004, 20, 544-549.	6.9	272
122	The Origins of Genome Complexity. Science, 2003, 302, 1401-1404.	20.9	1,486
123	The evolutionary demography of duplicate genes. Journal of Structural and Functional Genomics, 2003, 3, 35-44.	1.1	255
124	Messenger RNA Surveillance and the Evolutionary Proliferation of Introns. Molecular Biology and Evolution, 2003, 20, 563-571.	9.2	69
125	Intron evolution as a population-genetic process. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 6118-6123.	7.6	262
126	GENOMICS: Gene Duplication and Evolution. Science, 2002, 297, 945-947.	20.9	160

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127	Captive breeding and the genetic fitness of natural populations. Conservation Genetics, 2001, 2, 363-378.	1.5	269
128	PATTERNS OF GENETIC ARCHITECTURE FOR LIFE-HISTORY TRAITS AND MOLECULAR MARKERS IN A SUBDIVIDED SPECIES. Evolution; International Journal of Organic Evolution, 2001, 55, 1753-1761.	2.3	66
129	PATTERNS OF GENETIC ARCHITECTURE FOR LIFE-HISTORY TRAITS AND MOLECULAR MARKERS IN A SUBDIVIDED SPECIES. Evolution; International Journal of Organic Evolution, 2001, 55, 1753.	2.3	9
130	The Probability of Preservation of a Newly Arisen Gene Duplicate. Genetics, 2001, 159, 1789-1804.	2.9	444
131	THE FITNESS EFFECTS OF SPONTANEOUS MUTATIONS IN CAENORHABDITIS ELEGANS. Evolution; International Journal of Organic Evolution, 2000, 54, 1234-1246.	2.3	178
132	Title is missing!. Conservation Genetics, 2000, 1, 263-269.	1.5	65
133	QUANTITATIVE GENETIC VARIATION IN DAPHNIA: TEMPORAL CHANGES IN GENETIC ARCHITECTURE. Evolution; International Journal of Organic Evolution, 2000, 54, 1502-1509.	2.3	73
134	High Direct Estimate of the Mutation Rate in the Mitochondrial Genome of <i>Caenorhabditis elegans</i>. Science, 2000, 289, 2342-2344.	20.9	263
135	The Probability of Duplicate Gene Preservation by Subfunctionalization. Genetics, 2000, 154, 459-473.	2.9	1,387
136	Perspective: Spontaneous Deleterious Mutation. Evolution; International Journal of Organic Evolution, 1999, 53, 645.	2.3	209
137	THE AGE AND RELATIONSHIPS OF THE MAJOR ANIMAL PHYLA. Evolution; International Journal of Organic Evolution, 1999, 53, 319-325.	2.3	40
138	THE QUANTITATIVE AND MOLECULAR GENETIC ARCHITECTURE OF A SUBDIVIDED SPECIES. Evolution; International Journal of Organic Evolution, 1999, 53, 100-110.	2.3	199
139	PERSPECTIVE: SPONTANEOUS DELETERIOUS MUTATION. Evolution; International Journal of Organic Evolution, 1999, 53, 645-663.	2.3	325
140	Estimating genetic correlations in natural populations. Genetical Research, 1999, 74, 255-264.	0.9	59
141	The Rate of Spontaneous Mutation for Life-History Traits in Caenorhabditis elegans. Genetics, 1999, 151, 119-129.	2.9	143
142	Preservation of Duplicate Genes by Complementary, Degenerative Mutations. Genetics, 1999, 151, 1531-1545.	2.9	3,180
143	Estimation of Pairwise Relatedness With Molecular Markers. Genetics, 1999, 152, 1753-1766.	2.9	978
144	Deleterious mutation accumulation in organelle genomes. Genetica, 1998, 102/103, 29-39.	1.2	127

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145	Inferring the major genomic mode of dominance and overdominance. Genetica, 1998, 102/103, 559-567.	1.2	8
146	MUTATION, SELECTION, AND THE MAINTENANCE OF LIFE-HISTORY VARIATION IN A NATURAL POPULATION. Evolution; International Journal of Organic Evolution, 1998, 52, 727-733.	2.3	69
147	MUTATION AND EXTINCTION: THE ROLE OF VARIABLE MUTATIONAL EFFECTS, SYNERGISTIC EPISTASIS, BENEFICIAL MUTATIONS, AND DEGREE OF OUTCROSSING. Evolution; International Journal of Organic Evolution, 1997, 51, 1363-1371.	2.3	132
148	Allozyme and mtDNA variation in populations of the Daphnia pulex complex from both sides of the Rocky Mountains. Heredity, 1997, 79, 242-251.	2.7	57
149	Allozyme and mtDNA variation in populations of the Daphnia pulex complex from both sides of the Rocky Mountains. Heredity, 1997, 79, 242-251.	2.7	10
150	Estimate of the genomic mutation rate deleterious to overall fitness in E. coll. Nature, 1996, 381, 694-696.	36.2	358
151	Comparing Mutational Variabilities. Genetics, 1996, 143, 1467-1483.	2.9	415
152	MUTATIONAL MELTDOWNS IN SEXUAL POPULATIONS. Evolution; International Journal of Organic Evolution, 1995, 49, 1067-1080.	2.3	303
153	EVOLUTION AND EXTINCTION IN A CHANGING ENVIRONMENT: A QUANTITATIVEâ€GENETIC ANALYSIS. Evolution; International Journal of Organic Evolution, 1995, 49, 151-163.	2.3	482
154	Genetic Slippage in Response to Sex. American Naturalist, 1994, 144, 242-261.	2.2	100
155	The selective advantage of reaction norms for environmental tolerance. Journal of Evolutionary Biology, 1992, 5, 41-59.	1.6	142
156	METHODS FOR THE ANALYSIS OF COMPARATIVE DATA IN EVOLUTIONARY BIOLOGY. Evolution; International Journal of Organic Evolution, 1991, 45, 1065-1080.	2.3	338
157	THE GENETIC INTERPRETATION OF INBREEDING DEPRESSION AND OUTBREEDING DEPRESSION. Evolution; International Journal of Organic Evolution, 1991, 45, 622-629.	2.3	582
158	THE COVARIANCE STRUCTURE OF LIFEâ€HISTORY CHARACTERS IN <i>DAPHNIA PULEX</i>. Evolution; International Journal of Organic Evolution, 1991, 45, 1081-1090.	2.3	94
159	Adaptive and demographic responses of plankton populations to environmental change. Limnology and Oceanography, 1991, 36, 1301-1312.	3.5	107
160	MUTATION LOAD AND THE SURVIVAL OF SMALL POPULATIONS. Evolution; International Journal of Organic Evolution, 1990, 44, 1725-1737.	2.3	400
161	THE DISTRIBUTION OF LIFEâ€HISTORY VARIATION IN THE <i>DAPHNIA PULEX</i> COMPLEX. Evolution; International Journal of Organic Evolution, 1989, 43, 1724-1736.	2.3	71
162	PHYLOGENETIC HYPOTHESES UNDER THE ASSUMPTION OF NEUTRAL QUANTITATIVEâ€GENETIC VARIATION. Evolution; International Journal of Organic Evolution, 1989, 43, 1-17.	2.3	70

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163	The rate of polygenic mutation. Genetical Research, 1988, 51, 137-148.	0.9	273
164	THE DIVERGENCE OF NEUTRAL QUANTITATIVE CHARACTERS AMONG PARTIALLY ISOLATED POPULATIONS. Evolution; International Journal of Organic Evolution, 1988, 42, 455-466.	2.3	31
165	The Consequences of Fluctuating Selection for Isozyme Polymorphisms in Daphnia. Genetics, 1987, 115, 657-669.	2.9	115
166	RANDOM DRIFT, UNIFORM SELECTION, AND THE DEGREE OF POPULATION DIFFERENTIATION. Evolution; International Journal of Organic Evolution, 1986, 40, 640-643.	2.3	9
167	PHENOTYPIC EVOLUTION BY NEUTRAL MUTATION. Evolution; International Journal of Organic Evolution, 1986, 40, 915-935.	2.3	325
168	SPONTANEOUS MUTATIONS FOR LIFEâ€HISTORY CHARACTERS IN AN OBLIGATE PARTHENOGEN. Evolution; International Journal of Organic Evolution, 1985, 39, 804-818.	2.3	143
169	THE GENETIC STRUCTURE OF A CYCLICAL PARTHENOGEN. Evolution; International Journal of Organic Evolution, 1984, 38, 186-203.	2.3	80
170	THE LIMITS TO LIFE HISTORY EVOLUTION IN DAPHNIA. Evolution; International Journal of Organic Evolution, 1984, 38, 465-482.	2.3	99
171	THE SELECTIVE VALUE OF ALLELES UNDERLYING POLYGENIC TRAITS. Genetics, 1984, 108, 1021-1033.	2.9	21
172	Estimation of size-specific mortality rates in zooplankton populations by periodic sampling1. Limnology and Oceanography, 1983, 28, 533-545.	3.5	18
173	ECOLOGICAL GENETICS OF <i>DAPHNIA PULEX</i>. Evolution; International Journal of Organic Evolution, 1983, 37, 358-374.	2.3	175
174	How Well Does the Edmonson-Paloheimo Model Approximate Instantaneous Birth Rates?. Ecology, 1982, 63, 12-18.	3.5	34
175	Predation, competition, and zooplankton community structure: An experimental study1,2. Limnology and Oceanography, 1979, 24, 253-272.	3.5	314