

Michael Lynch

List of Publications by Year in descending order

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173
papers

28,376
citations

11908

72
h-index

7427

157
g-index

186
all docs

186
docs citations

186
times ranked

27664
citing authors

#	ARTICLE	IF	CITATIONS
1	Rates of Mutations and Transcript Errors in the Foodborne Pathogen <i>Salmonella enterica</i> subsp. <i>enterica</i> . <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	9
2	Complex Ecotype Dynamics Evolve in Response to Fluctuating Resources. <i>MBio</i> , 2022, 13, e0346721.	1.8	7
3	Recommendations for improving statistical inference in population genomics. <i>PLoS Biology</i> , 2022, 20, e3001669.	2.6	60
4	Evolutionary bioenergetics of ciliates. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, .	0.8	3
5	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.	1.8	10
6	The rapid, mass invasion of New Zealand by North American <i>Daphnia pulex</i> . <i>Limnology and Oceanography</i> , 2021, 66, 2672-2683.	1.6	15
7	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, .	3.3	52
8	Revisiting the notion of deleterious sweeps. <i>Genetics</i> , 2021, 219, .	1.2	14
9	Unexpected Discovery of Hypermutator Phenotype Sounds the Alarm for Quality Control Strains. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	2
10	Evolutionary Dynamics of Asexual Hypermutators Adapting to a Novel Environment. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	8
11	Low base substitution mutation rate and predominance of insertion-deletion events in the acidophilic bacterium <i>Acidobacterium capsulatum</i> . <i>Ecology and Evolution</i> , 2021, 11, 17609-17614.	0.8	0
12	The Rab7 subfamily across <i>Paramecium aurelia</i> species; evidence of high conservation in sequence and function. <i>Small GTPases</i> , 2020, 11, 421-429.	0.7	2
13	Imposed mutational meltdown as an antiviral strategy. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 2549-2559.	1.1	20
14	Enhanced nutrient uptake is sufficient to drive emergent cross-feeding between bacteria in a synthetic community. <i>ISME Journal</i> , 2020, 14, 2816-2828.	4.4	18
15	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.	0.8	10
16	Variable Spontaneous Mutation and Loss of Heterozygosity among Heterozygous Genomes in Yeast. <i>Molecular Biology and Evolution</i> , 2020, 37, 3118-3130.	3.5	17
17	Estimation of the Genome-Wide Mutation Rate and Spectrum in the Archaeal Species <i>Haloferax volcanii</i> . <i>Genetics</i> , 2020, 215, 1107-1116.	1.2	10
18	The Limits to Estimating Population-Genetic Parameters with Temporal Data. <i>Genome Biology and Evolution</i> , 2020, 12, 443-455.	1.1	17

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19	A Theoretical Framework for Evolutionary Cell Biology. <i>Journal of Molecular Biology</i> , 2020, 432, 1861-1879.	2.0	41
20	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.	3.3	30
21	Inference of Historical Population-Size Changes with Allele-Frequency Data. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 211-223.	0.8	12
22	Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy. <i>Heredity</i> , 2020, 124, 619-620.	1.2	24
23	Universally high transcript error rates in bacteria. <i>ELife</i> , 2020, 9, .	2.8	17
24	Genetic control of male production in <i>Daphnia pulex</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15602-15609.	3.3	24
25	Joseph Shapiro, an Icon of Applied Limnology. <i>Limnology and Oceanography Bulletin</i> , 2019, 28, 35-37.	0.2	0
26	Population Genetics of <i>Paramecium</i> Mitochondrial Genomes: Recombination, Mutation Spectrum, and Efficacy of Selection. <i>Genome Biology and Evolution</i> , 2019, 11, 1398-1416.	1.1	22
27	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.	1.1	123
28	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. <i>Nature Ecology and Evolution</i> , 2018, 2, 669-679.	3.4	117
29	Evolutionary determinants of genome-wide nucleotide composition. <i>Nature Ecology and Evolution</i> , 2018, 2, 237-240.	3.4	126
30	<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.	3.3	46
31	Limited Mutation-Rate Variation Within the <i>Paramecium aurelia</i> Species Complex. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2523-2526.	0.8	21
32	Response to Martin and colleagues: mitochondria do not boost the bioenergetic capacity of eukaryotic cells. <i>Biology Direct</i> , 2018, 13, 26.	1.9	4
33	Phylogenetic divergence of cell biological features. <i>ELife</i> , 2018, 7, .	2.8	12
34	An <i>Escherichia coli</i> Nitrogen Starvation Response Is Important for Mutualistic Coexistence with <i>Rhodospseudomonas palustris</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	7
35	Evolution and Selection of Quantitative Traits. , 2018, , .		469
36	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.	1.1	15

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37	Population Genomics of <i>Daphnia pulex</i> . <i>Genetics</i> , 2017, 206, 315-332.	1.2	55
38	Early stages of functional diversification in the Rab GTPase gene family revealed by genomic and localization studies in <i>Paramecium</i> species. <i>Molecular Biology of the Cell</i> , 2017, 28, 1101-1110.	0.9	7
39	Population Genomics of <i>Paramecium</i> Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1194-1216.	3.5	35
40	Estimating Seven Coefficients of Pairwise Relatedness Using Population-Genomic Data. <i>Genetics</i> , 2017, 206, 105-118.	1.2	33
41	Genotype Calling from Population-Genomic Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1393-1404.	0.8	84
42	Spontaneous mutations of a model heterotrophic marine bacterium. <i>ISME Journal</i> , 2017, 11, 1713-1718.	4.4	22
43	Catalytic properties of RNA polymerases IV and V: accuracy, nucleotide incorporation and rNTP/dNTP discrimination. <i>Nucleic Acids Research</i> , 2017, 45, 11315-11326.	6.5	22
44	The landscape of transcription errors in eukaryotic cells. <i>Science Advances</i> , 2017, 3, e1701484.	4.7	102
45	Genome-Wide Mutation Rate Response to pH Change in the Coral Reef Pathogen <i>Vibrio shilonii</i> AK1. <i>MBio</i> , 2017, 8, .	1.8	21
46	A New Reference Genome Assembly for the Microcrustacean <i>Daphnia pulex</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1405-1416.	0.8	95
47	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.	0.8	14
48	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.	3.5	81
49	Membranes, energetics, and evolution across the prokaryote-eukaryote divide. <i>ELife</i> , 2017, 6, .	2.8	60
50	Similar Mutation Rates but Highly Diverse Mutation Spectra in Ascomycete and Basidiomycete Yeasts. <i>Genome Biology and Evolution</i> , 2016, 8, 3815-3821.	1.1	40
51	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.	0.8	48
52	Low Base-Substitution Mutation Rate in the Germline Genome of the Ciliate <i>Tetrahymena thermophil</i> . <i>Genome Biology and Evolution</i> , 2016, 8, eww223.	1.1	38
53	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.	3.3	172
54	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.	0.9	75

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55	Promoter Architecture and Sex-Specific Gene Expression in <i>Daphnia pulex</i> . <i>Genetics</i> , 2016, 204, 593-612.	1.2	20
56	Evolution of the Insertion-Deletion Mutation Rate Across the Tree of Life. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2583-2591.	0.8	89
57	Genetic drift, selection and the evolution of the mutation rate. <i>Nature Reviews Genetics</i> , 2016, 17, 704-714.	7.7	648
58	Mutation, Eugenics, and the Boundaries of Science. <i>Genetics</i> , 2016, 204, 825-827.	1.2	6
59	Diversity and Divergence of Dinoflagellate Histone Proteins. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 397-422.	0.8	38
60	Conservation and divergence of the histone code in nucleomorphs. <i>Biology Direct</i> , 2016, 11, 18.	1.9	12
61	Reply to Lane and Martin: Mitochondria do not boost the bioenergetic capacity of eukaryotic cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E667-8.	3.3	20
62	Mutation and Human Exceptionalism: Our Future Genetic Load. <i>Genetics</i> , 2016, 202, 869-875.	1.2	92
63	High mutational rates of large-scale duplication and deletion in <i>Daphnia pulex</i> . <i>Genome Research</i> , 2016, 26, 60-69.	2.4	99
64	Draft Genome Sequence of <i>Caedibacter varicaedens</i> , a Kappa Killer Endosymbiont Bacterium of the Ciliate <i>Paramecium biaurelia</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	7
65	Asymmetric Context-Dependent Mutation Patterns Revealed through Mutation Accumulation Experiments. <i>Molecular Biology and Evolution</i> , 2015, 32, 1672-1683.	3.5	130
66	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.	1.2	75
67	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.	1.1	62
68	Feedforward loop for diversity. <i>Nature</i> , 2015, 523, 414-416.	13.7	10
69	Maintenance and Loss of Duplicated Genes by Dosage Subfunctionalization. <i>Molecular Biology and Evolution</i> , 2015, 32, 2141-2148.	3.5	160
70	Background Mutational Features of the Radiation-Resistant Bacterium <i>Deinococcus radiodurans</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 2383-2392.	3.5	58
71	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.	3.3	405
72	The Spontaneous Mutation Rate in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Genetics</i> , 2015, 201, 737-744.	1.2	127

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73	Genotype-Frequency Estimation from High-Throughput Sequencing Data. <i>Genetics</i> , 2015, 201, 473-486.	1.2	39
74	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.	1.2	52
75	Hybridization and the Origin of Contagious Asexuality in <i>Daphnia pulex</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, msv190.	3.5	49
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.	3.3	82
77	Characterization of Newly Gained Introns in <i>Daphnia</i> Populations. <i>Genome Biology and Evolution</i> , 2014, 6, 2218-2234.	1.1	16
78	Population-Genetic Inference from Pooled-Sequencing Data. <i>Genome Biology and Evolution</i> , 2014, 6, 1210-1218.	1.1	101
79	Genome-Wide Linkage-Disequilibrium Profiles from Single Individuals. <i>Genetics</i> , 2014, 198, 269-281.	1.2	30
80	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.	3.3	108
81	Deciphering the Evolutionary History of Open and Closed Mitosis. <i>Current Biology</i> , 2014, 24, R1099-R1103.	1.8	64
82	Genome-Wide Estimation of Linkage Disequilibrium from Population-Level High-Throughput Sequencing Data. <i>Genetics</i> , 2014, 197, 1303-1313.	1.2	27
83	Insights into Three Whole-Genome Duplications Gleaned from the <i>Paramecium caudatum</i> Genome Sequence. <i>Genetics</i> , 2014, 197, 1417-1428.	1.2	67
84	Differential retention and divergent resolution of duplicate genes following whole-genome duplication. <i>Genome Research</i> , 2014, 24, 1665-1675.	2.4	111
85	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.	3.3	94
86	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.	3.3	78
87	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.	3.3	159
88	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.	3.3	43
89	Drift-barrier hypothesis and mutation-rate evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 18488-18492.	3.3	355
90	The Evolution of Multimeric Protein Assemblages. <i>Molecular Biology and Evolution</i> , 2012, 29, 1353-1366.	3.5	75

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91	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.	1.1	24
92	The Repatterning of Eukaryotic Genomes by Random Genetic Drift. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 347-366.	2.5	114
93	The Lower Bound to the Evolution of Mutation Rates. <i>Genome Biology and Evolution</i> , 2011, 3, 1107-1118.	1.1	139
94	Statistical Inference on the Mechanisms of Genome Evolution. <i>PLoS Genetics</i> , 2011, 7, e1001389.	1.5	39
95	Evolution of the mutation rate. <i>Trends in Genetics</i> , 2010, 26, 345-352.	2.9	885
96	mlRho â€” a program for estimating the population mutation and recombination rates from shotgunâ€”sequenced diploid genomes. <i>Molecular Ecology</i> , 2010, 19, 277-284.	2.0	88
97	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.	3.3	692
98	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.	3.3	53
99	The Rate of Establishment of Complex Adaptations. <i>Molecular Biology and Evolution</i> , 2010, 27, 1404-1414.	3.5	66
100	The Rate and Molecular Spectrum of Spontaneous Mutations in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2010, 327, 92-94.	6.0	1,004
101	Patterns of Intraspecific DNA Variation in the <i>Daphnia</i> Nuclear Genome. <i>Genetics</i> , 2009, 182, 325-336.	1.2	31
102	Estimation of Allele Frequencies From High-Coverage Genome-Sequencing Projects. <i>Genetics</i> , 2009, 182, 295-301.	1.2	89
103	Localization of the Genetic Determinants of Meiosis Suppression in <i>Daphnia pulex</i> . <i>Genetics</i> , 2008, 180, 317-327.	1.2	69
104	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.	3.3	649
105	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.	3.5	112
106	The Cellular, Developmental and Population-Genetic Determinants of Mutation-Rate Evolution. <i>Genetics</i> , 2008, 180, 933-943.	1.2	102
107	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.	3.3	689
108	The evolution of genetic networks by non-adaptive processes. <i>Nature Reviews Genetics</i> , 2007, 8, 803-813.	7.7	266

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109	Streamlining and Simplification of Microbial Genome Architecture. <i>Annual Review of Microbiology</i> , 2006, 60, 327-349.	2.9	204
110	The Origins of Eukaryotic Gene Structure. <i>Molecular Biology and Evolution</i> , 2006, 23, 450-468.	3.5	348
111	Mutation Pressure and the Evolution of Organelle Genomic Architecture. <i>Science</i> , 2006, 311, 1727-1730.	6.0	490
112	Simple evolutionary pathways to complex proteins. <i>Protein Science</i> , 2005, 14, 2217-2225.	3.1	38
113	CONSERVED ONTOGENY AND ALLOMETRIC SCALING OF RESOURCE ACQUISITION AND ALLOCATION IN THE DAPHNIIDAE. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 565-576.	1.1	23
114	Rule-based workflow management for bioinformatics. <i>VLDB Journal</i> , 2005, 14, 318-329.	2.7	14
115	The Evolution of Transcription-Initiation Sites. <i>Molecular Biology and Evolution</i> , 2005, 22, 1137-1146.	3.5	60
116	The altered evolutionary trajectories of gene duplicates. <i>Trends in Genetics</i> , 2004, 20, 544-549.	2.9	267
117	The Origins of Genome Complexity. <i>Science</i> , 2003, 302, 1401-1404.	6.0	1,436
118	The evolutionary demography of duplicate genes. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 35-44.	1.2	249
119	Messenger RNA Surveillance and the Evolutionary Proliferation of Introns. <i>Molecular Biology and Evolution</i> , 2003, 20, 563-571.	3.5	69
120	The evolutionary demography of duplicate genes. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 35-44.	1.2	150
121	Intron evolution as a population-genetic process. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6118-6123.	3.3	260
122	GENOMICS: Gene Duplication and Evolution. <i>Science</i> , 2002, 297, 945-947.	6.0	157
123	Captive breeding and the genetic fitness of natural populations. <i>Conservation Genetics</i> , 2001, 2, 363-378.	0.8	262
124	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.	1.1	66
125	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.	1.1	9
126	The Probability of Preservation of a Newly Arisen Gene Duplicate. <i>Genetics</i> , 2001, 159, 1789-1804.	1.2	440

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127	THE FITNESS EFFECTS OF SPONTANEOUS MUTATIONS IN CAENORHABDITIS ELEGANS. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1234-1246.	1.1	178
128	Title is missing!. <i>Conservation Genetics</i> , 2000, 1, 263-269.	0.8	64
129	QUANTITATIVE GENETIC VARIATION IN DAPHNIA: TEMPORAL CHANGES IN GENETIC ARCHITECTURE. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1502-1509.	1.1	73
130	High Direct Estimate of the Mutation Rate in the Mitochondrial Genome of <i>Caenorhabditis elegans</i> . <i>Science</i> , 2000, 289, 2342-2344.	6.0	259
131	The Probability of Duplicate Gene Preservation by Subfunctionalization. <i>Genetics</i> , 2000, 154, 459-473.	1.2	1,372
132	Perspective: Spontaneous Deleterious Mutation. <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 645.	1.1	200
133	THE AGE AND RELATIONSHIPS OF THE MAJOR ANIMAL PHYLA. <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 319-325.	1.1	40
134	THE QUANTITATIVE AND MOLECULAR GENETIC ARCHITECTURE OF A SUBDIVIDED SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 100-110.	1.1	192
135	PERSPECTIVE: SPONTANEOUS DELETERIOUS MUTATION. <i>Evolution; International Journal of Organic Evolution</i> , 1999, 53, 645-663.	1.1	317
136	Estimating genetic correlations in natural populations. <i>Genetical Research</i> , 1999, 74, 255-264.	0.3	58
137	The Rate of Spontaneous Mutation for Life-History Traits in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 1999, 151, 119-129.	1.2	142
138	Preservation of Duplicate Genes by Complementary, Degenerative Mutations. <i>Genetics</i> , 1999, 151, 1531-1545.	1.2	3,147
139	Estimation of Pairwise Relatedness With Molecular Markers. <i>Genetics</i> , 1999, 152, 1753-1766.	1.2	966
140	Deleterious mutation accumulation in organelle genomes. <i>Genetica</i> , 1998, 102/103, 29-39.	0.5	126
141	Inferring the major genomic mode of dominance and overdominance. <i>Genetica</i> , 1998, 102/103, 559-567.	0.5	8
142	The critical effective size for a genetically secure population. <i>Animal Conservation</i> , 1998, 1, 70-72.	1.5	206
143	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.	1.1	68
144	The critical effective size for a genetically secure population. , 1998, 1, 70.		32

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145	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.	1.1	132
146	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.	1.2	53
147	Estimate of the genomic mutation rate deleterious to overall fitness in <i>E. coli</i> . <i>Nature</i> , 1996, 381, 694-696.	13.7	352
148	Comparing Mutational Variabilities. <i>Genetics</i> , 1996, 143, 1467-1483.	1.2	413
149	MUTATIONAL MELTDOWNS IN SEXUAL POPULATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 1995, 49, 1067-1080.	1.1	300
150	EVOLUTION AND EXTINCTION IN A CHANGING ENVIRONMENT: A QUANTITATIVEâ€œGENETIC ANALYSIS. <i>Evolution; International Journal of Organic Evolution</i> , 1995, 49, 151-163.	1.1	470
151	Genetic Slippage in Response to Sex. <i>American Naturalist</i> , 1994, 144, 242-261.	1.0	100
152	The selective advantage of reaction norms for environmental tolerance. <i>Journal of Evolutionary Biology</i> , 1992, 5, 41-59.	0.8	142
153	METHODS FOR THE ANALYSIS OF COMPARATIVE DATA IN EVOLUTIONARY BIOLOGY. <i>Evolution; International Journal of Organic Evolution</i> , 1991, 45, 1065-1080.	1.1	334
154	THE GENETIC INTERPRETATION OF INBREEDING DEPRESSION AND OUTBREEDING DEPRESSION. <i>Evolution; International Journal of Organic Evolution</i> , 1991, 45, 622-629.	1.1	574
155	THE COVARIANCE STRUCTURE OF LIFEâ€œHISTORY CHARACTERS IN <i>DAPHNIA PULEX</i> . <i>Evolution; International Journal of Organic Evolution</i> , 1991, 45, 1081-1090.	1.1	94
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