

Nicolas Galtier

List of Publications by Year in descending order

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Version: 2024-02-01

102
papers

9,757
citations

44069

48
h-index

45317

90
g-index

110
all docs

110
docs citations

110
times ranked

10648
citing authors

#	ARTICLE	IF	CITATIONS
1	Convergent consequences of parthenogenesis on stick insect genomes. <i>Science Advances</i> , 2022, 8, eabg3842.	10.3	27
2	Purging of deleterious burden in the endangered Iberian lynx. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2110614119.	7.1	32
3	Detection of F1 Hybrids from Single-genome Data Reveals Frequent Hybridization in Hymenoptera and Particularly Ants. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	2
4	The Multilocus Multispecies Coalescent: A Flexible New Model of Gene Family Evolution. <i>Systematic Biology</i> , 2021, 70, 822-837.	5.6	9
5	First annotated draft genomes of nonmarine ostracods (Ostracoda, Crustacea) with different reproductive modes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	9
6	DILS: Demographic inferences with linked selection by using ABC. <i>Molecular Ecology Resources</i> , 2021, 21, 2629-2644.	4.8	32
7	Haplotype divergence supports long-term asexuality in the oribatid mite <i>Oppiella nova</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	23
8	Prevalence and Implications of Contamination in Public Genomic Resources: A Case Study of 43 Reference Arthropod Assemblies. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 721-730.	1.8	25
9	How Much Does $\langle i \rangle Ne \langle /i \rangle$ Vary Among Species?. <i>Genetics</i> , 2020, 216, 559-572.	2.9	38
10	Is adaptation limited by mutation? A timescale-dependent effect of genetic diversity on the adaptive substitution rate in animals. <i>PLoS Genetics</i> , 2020, 16, e1008668.	3.5	55
11	Title is missing!. , 2020, 16, e1008668.		0
12	Title is missing!. , 2020, 16, e1008668.		0
13	Title is missing!. , 2020, 16, e1008668.		0
14	Title is missing!. , 2020, 16, e1008668.		0
15	Title is missing!. , 2020, 16, e1008668.		0
16	Genome Evolution in Outcrossing vs. Selfing vs. Asexual Species. <i>Methods in Molecular Biology</i> , 2019, 1910, 331-369.	0.9	51
17	Influence of Recombination and GC-biased Gene Conversion on the Adaptive and Nonadaptive Substitution Rate in Mammals versus Birds. <i>Molecular Biology and Evolution</i> , 2019, 36, 458-471.	8.9	41
18	Sexually dimorphic gene expression and transcriptome evolution provide mixed evidence for a fast effect in <i>Heliconius</i> . <i>Journal of Evolutionary Biology</i> , 2019, 32, 194-204.	1.7	31

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19	Delineating species in the speciation continuum: A proposal. <i>Evolutionary Applications</i> , 2019, 12, 657-663.	3.1	61
20	Consequences of Asexuality in Natural Populations: Insights from Stick Insects. <i>Molecular Biology and Evolution</i> , 2018, 35, 1668-1677.	8.9	63
21	Codon Usage Bias in Animals: Disentangling the Effects of Natural Selection, Effective Population Size, and GC-Biased Gene Conversion. <i>Molecular Biology and Evolution</i> , 2018, 35, 1092-1103.	8.9	111
22	Illumina Library Preparation for Sequencing the GC-Rich Fraction of Heterogeneous Genomic DNA. <i>Genome Biology and Evolution</i> , 2018, 10, 616-622.	2.5	32
23	Patterns of Genome-Wide Nucleotide Diversity in the Gynodioecious Plant <i>Thymus vulgaris</i> Are Compatible with Recent Sweeps of Cytoplasmic Genes. <i>Genome Biology and Evolution</i> , 2018, 10, 239-248.	2.5	8
24	Overestimation of the adaptive substitution rate in fluctuating populations. <i>Biology Letters</i> , 2018, 14, 20180055.	2.3	44
25	Incomplete Lineage Sorting in Mammalian Phylogenomics. <i>Systematic Biology</i> , 2017, 66, syw082.	5.6	88
26	Patterns of cross-contamination in a multispecies population genomic project: detection, quantification, impact, and solutions. <i>BMC Biology</i> , 2017, 15, 25.	3.8	100
27	Avian Genomes Revisited: Hidden Genes Uncovered and the Rates versus Traits Paradox in Birds. <i>Molecular Biology and Evolution</i> , 2017, 34, 3123-3131.	8.9	90
28	Large Variation in the Ratio of Mitochondrial to Nuclear Mutation Rate across Animals: Implications for Genetic Diversity and the Use of Mitochondrial DNA as a Molecular Marker. <i>Molecular Biology and Evolution</i> , 2017, 34, 2762-2772.	8.9	240
29	Hemizyosity Enhances Purifying Selection: Lack of Fast-Z Evolution in Two Satyrine Butterflies. <i>Genome Biology and Evolution</i> , 2016, 8, 3108-3119.	2.5	31
30	Shedding Light on the Grey Zone of Speciation along a Continuum of Genomic Divergence. <i>PLoS Biology</i> , 2016, 14, e2000234.	5.6	381
31	Population genomics of sexual and asexual lineages in fissiparous ribbon worms (<i>Lineus</i> , <i>Nemertea</i>): hybridization, polyploidy and the Meselson effect. <i>Molecular Ecology</i> , 2016, 25, 3356-3369.	3.9	58
32	Determinants of genetic diversity. <i>Nature Reviews Genetics</i> , 2016, 17, 422-433.	16.3	587
33	A replicated climate change field experiment reveals rapid evolutionary response in an ecologically important soil invertebrate. <i>Global Change Biology</i> , 2016, 22, 2370-2379.	9.5	15
34	Life History Traits, Protein Evolution, and the Nearly Neutral Theory in Amniotes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1517-1527.	8.9	75
35	Adaptive Protein Evolution in Animals and the Effective Population Size Hypothesis. <i>PLoS Genetics</i> , 2016, 12, e1005774.	3.5	176
36	Molecular Evolution of Freshwater Snails with Contrasting Mating Systems. <i>Molecular Biology and Evolution</i> , 2015, 32, 2403-2416.	8.9	54

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37	Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , 2015, 25, 1215-1228.	5.5	127
38	Biased Gene Conversion and GC-Content Evolution in the Coding Sequences of Reptiles and Vertebrates. <i>Genome Biology and Evolution</i> , 2015, 7, 240-250.	2.5	67
39	Gene expression, chromosome heterogeneity and the fast-X effect in mammals. <i>Biology Letters</i> , 2015, 11, 20150010.	2.3	12
40	Comparative Analysis of Transcriptomes from Secondary Reproductives of Three Reticulitermes Termite Species. <i>PLoS ONE</i> , 2015, 10, e0145596.	2.5	14
41	Population genomics of eusocial insects: the costs of a vertebrate-like effective population size. <i>Journal of Evolutionary Biology</i> , 2014, 27, 593-603.	1.7	89
42	Mutation-Driven Evolution. <i>Systematic Biology</i> , 2014, 63, 113-114.	5.6	0
43	OrthoMaM v8: A Database of Orthologous Exons and Coding Sequences for Comparative Genomics in Mammals. <i>Molecular Biology and Evolution</i> , 2014, 31, 1923-1928.	8.9	77
44	The Rate of Molecular Adaptation in a Changing Environment. <i>Molecular Biology and Evolution</i> , 2013, 30, 1292-1301.	8.9	51
45	Less Is More in Mammalian Phylogenomics: AT-Rich Genes Minimize Tree Conflicts and Unravel the Root of Placental Mammals. <i>Molecular Biology and Evolution</i> , 2013, 30, 2134-2144.	8.9	158
46	Population genomics of the endangered giant Galápagos tortoise. <i>Genome Biology</i> , 2013, 14, R136.	9.6	32
47	Genomic Evidence for Large, Long-Lived Ancestors to Placental Mammals. <i>Molecular Biology and Evolution</i> , 2013, 30, 5-13.	8.9	56
48	Bio++: Efficient Extensible Libraries and Tools for Computational Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2013, 30, 1745-1750.	8.9	163
49	Reference-Free Population Genomics from Next-Generation Transcriptome Data and the Vertebrate-Invertebrate Gap. <i>PLoS Genetics</i> , 2013, 9, e1003457.	3.5	157
50	Crossing the Species Barrier: Genomic Hotspots of Introgression between Two Highly Divergent <i>Ciona intestinalis</i> Species. <i>Molecular Biology and Evolution</i> , 2013, 30, 1574-1587.	8.9	148
51	Evidence for Widespread Positive and Purifying Selection Across the European Rabbit (<i>Oryctolagus cuniculus</i>). <i>Molecular Biology and Evolution</i> , 2013, 30, 1843-1851.	8.9	71
52	Efficient Selection of Branch-Specific Models of Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 1861-1874.	8.9	56
53	Dating cryptodiran nodes: Origin and diversification of the turtle superfamily Testudinoidea. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 496-507.	2.7	63
54	The Population Genomics of a Fast Evolver: High Levels of Diversity, Functional Constraint, and Molecular Adaptation in the Tunicate <i>Ciona intestinalis</i> . <i>Genome Biology and Evolution</i> , 2012, 4, 852-861.	2.5	116

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55	Fast and Robust Characterization of Time-Heterogeneous Sequence Evolutionary Processes Using Substitution Mapping. <i>PLoS ONE</i> , 2012, 7, e33852.	2.5	47
56	Next-generation sequencing of transcriptomes: a guide to RNA isolation in nonmodel animals. <i>Molecular Ecology Resources</i> , 2011, 11, 650-661.	4.8	92
57	COMPLEXITY, PLEIOTROPY, AND THE FITNESS EFFECT OF MUTATIONS. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 1559-1571.	2.3	57
58	GC-Biased Gene Conversion Impacts Ribosomal DNA Evolution in Vertebrates, Angiosperms, and Other Eukaryotes. <i>Molecular Biology and Evolution</i> , 2011, 28, 2561-2575.	8.9	53
59	RNA extraction from sauropsids blood: evaluation and improvement of methods. <i>Amphibia - Reptilia</i> , 2011, 32, 136-139.	0.5	24
60	Accelerated Evolutionary Rate of Housekeeping Genes in Tunicates. <i>Journal of Molecular Evolution</i> , 2010, 71, 153-167.	1.8	40
61	Detecting positive selection within genomes: the problem of biased gene conversion. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 2571-2580.	4.0	130
62	Contrasting GC-content dynamics across 33 mammalian genomes: Relationship with life-history traits and chromosome sizes. <i>Genome Research</i> , 2010, 20, 1001-1009.	5.5	195
63	An Evolutionary Genome Scan for Longevity-Related Natural Selection in Mammals. <i>Molecular Biology and Evolution</i> , 2010, 27, 840-847.	8.9	62
64	Apparent longevity-related adaptation of mitochondrial amino acid content is due to nucleotide compositional shifts. <i>Mitochondrion</i> , 2010, 10, 540-547.	3.4	18
65	Mitochondrial whims: metabolic rate, longevity and the rate of molecular evolution. <i>Biology Letters</i> , 2009, 5, 413-416.	2.3	90
66	Comment on "Human-Specific Gain of Function in a Developmental Enhancer". <i>Science</i> , 2009, 323, 714-714.	12.6	30
67	GC-biased gene conversion promotes the fixation of deleterious amino acid changes in primates. <i>Trends in Genetics</i> , 2009, 25, 1-5.	6.7	167
68	Inverse relationship between longevity and evolutionary rate of mitochondrial proteins in mammals and birds. <i>Mitochondrion</i> , 2009, 9, 51-57.	3.4	36
69	Biased Gene Conversion and the Evolution of Mammalian Genomic Landscapes. <i>Annual Review of Genomics and Human Genetics</i> , 2009, 10, 285-311.	6.2	607
70	Determination of Mitochondrial Genetic Diversity in Mammals. <i>Genetics</i> , 2008, 178, 351-361.	2.9	107
71	Evolutionary Modeling of Rate Shifts Reveals Specificity Determinants in HIV-1 Subtypes. <i>PLoS Computational Biology</i> , 2008, 4, e1000214.	3.2	30
72	A Model of Horizontal Gene Transfer and the Bacterial Phylogeny Problem. <i>Systematic Biology</i> , 2007, 56, 633-642.	5.6	73

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73	Strong Variations of Mitochondrial Mutation Rate across Mammals--the Longevity Hypothesis. <i>Molecular Biology and Evolution</i> , 2007, 25, 120-130.	8.9	394
74	Adaptation or biased gene conversion? Extending the null hypothesis of molecular evolution. <i>Trends in Genetics</i> , 2007, 23, 273-277.	6.7	214
75	Population Size Does Not Influence Mitochondrial Genetic Diversity in Animals. <i>Science</i> , 2006, 312, 570-572.	12.6	773
76	A new perspective on isochore evolution. <i>Gene</i> , 2006, 385, 71-74.	2.2	88
77	Bio++: a set of C++ libraries for sequence analysis, phylogenetics, molecular evolution and population genetics. <i>BMC Bioinformatics</i> , 2006, 7, 188.	2.6	101
78	GC-Biased Segregation of Noncoding Polymorphisms in <i>Drosophila</i> . <i>Genetics</i> , 2006, 172, 221-228.	2.9	55
79	A Model-Based Approach for Detecting Coevolving Positions in a Molecule. <i>Molecular Biology and Evolution</i> , 2005, 22, 1919-1928.	8.9	131
80	Mutation hot spots in mammalian mitochondrial DNA. <i>Genome Research</i> , 2005, 16, 215-222.	5.5	116
81	Sampling Properties of the Bootstrap Support in Molecular Phylogeny: Influence of Nonindependence Among Sites. <i>Systematic Biology</i> , 2004, 53, 38-46.	5.6	29
82	Recombination, GC-content and the human pseudoautosomal boundary paradox. <i>Trends in Genetics</i> , 2004, 20, 347-349.	6.7	36
83	The Decline of Isochores in Mammals: An Assessment of the GC Content Variation Along the Mammalian Phylogeny. <i>Journal of Molecular Evolution</i> , 2004, 58, 653-660.	1.8	63
84	Molecular Adaptation in Plant Hemoglobin, a Duplicated Gene Involved in Plant-Bacteria Symbiosis. <i>Journal of Molecular Evolution</i> , 2004, 59, 416-425.	1.8	9
85	Sex chromosomes: how X-Y recombination stops. <i>Current Biology</i> , 2003, 13, R641-R643.	3.9	59
86	Gene conversion drives GC content evolution in mammalian histones. <i>Trends in Genetics</i> , 2003, 19, 65-68.	6.7	136
87	Recombination explains isochores in mammalian genomes. <i>Trends in Genetics</i> , 2003, 19, 128-130.	6.7	111
88	BAGE genes generated by juxtacentromeric reshuffling in the hominidae lineage are under selective pressure. <i>Genomics</i> , 2003, 81, 391-399.	2.9	21
89	The influence of demography, population structure and selection on molecular diversity in the selfing freshwater snail <i>Biomphalaria pfeifferi</i> . <i>Genetical Research</i> , 2003, 81, 193-204.	0.9	14
90	Vanishing GC-Rich Isochores in Mammalian Genomes. <i>Genetics</i> , 2002, 162, 1837-1847.	2.9	157

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91	Maximum-Likelihood Phylogenetic Analysis Under a Covarion-like Model. <i>Molecular Biology and Evolution</i> , 2001, 18, 866-873.	8.9	260
92	The Covariation Between TpA Deficiency, CpG Deficiency, and G+C Content of Human Isochores Is Due to a Mathematical Artifact. <i>Molecular Biology and Evolution</i> , 2000, 17, 1620-1625.	8.9	77
93	Title is missing!. <i>Conservation Genetics</i> , 2000, 1, 299-308.	1.5	43
94	A New Method for Locating Changes in a Tree Reveals Distinct Nucleotide Polymorphism vs Divergence Patterns in Mouse Mitochondrial Control Region. <i>Journal of Molecular Evolution</i> , 2000, 50, 224-231.	1.8	13
95	Detecting Bottlenecks and Selective Sweeps From DNA Sequence Polymorphism. <i>Genetics</i> , 2000, 155, 981-987.	2.9	173
96	Molecular Phylogeny of Cyprinidae Inferred from cytochrome b DNA Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 100-108.	2.7	241
97	Isochore Evolution in Mammals: A Human-Like Ancestral Structure. <i>Genetics</i> , 1998, 150, 1577-1584.	2.9	45
98	Relationships Between Genomic G+C Content, RNA Secondary Structures, and Optimal Growth Temperature in Prokaryotes. <i>Journal of Molecular Evolution</i> , 1997, 44, 632-636.	1.8	370
99	Phylogenetic Relationships within Genus <i>Leuciscus</i> (Pisces, Cyprinidae) in Portuguese Fresh Waters, Based on Mitochondrial DNA Cytochrome b Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1997, 8, 435-442.	2.7	97
100	Reconstruction of body mass evolution in the Cetartiodactyla and mammals using phylogenomic data. , 0, 1, .		1
101	Lacking conservation genomics in the giant Galápagos tortoise. , 0, 1, .		0
102	Fine-scale quantification of GC-biased gene conversion intensity in mammals. , 0, 1, .		6