

John Gatesy

List of Publications by Year in descending order

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71102

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times ranked

8818
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#	ARTICLE	IF	CITATIONS
1	Theoretical and Practical Considerations when using Retroelement Insertions to Estimate Species Trees in the Anomaly Zone. <i>Systematic Biology</i> , 2022, 71, 721-740.	5.6	10
2	Gene-tree misrooting drives conflicts in phylogenomic coalescent analyses of palaeognath birds. <i>Molecular Phylogenetics and Evolution</i> , 2022, 167, 107344.	2.7	16
3	Molecular evolutionary analyses of tooth genes support sequential loss of enamel and teeth in baleen whales (Mysticeti). <i>Molecular Phylogenetics and Evolution</i> , 2022, 171, 107463.	2.7	12
4	Phylogenomic Coalescent Analyses of Avian Retroelements Infer Zero-Length Branches at the Base of Neoaves, Emergent Support for Controversial Clades, and Ancient Introgressive Hybridization in Afroaves. <i>Genes</i> , 2022, 13, 1167.	2.4	2
5	Higher level phylogeny of baleen whales. , 2021, , 3-10.		1
6	Phylogenomics and the Genetic Architecture of the Placental Mammal Radiation. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 29-53.	7.4	32
7	Collapsing dubiously resolved gene-tree branches in phylogenomic coalescent analyses. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107092.	2.7	24
8	Genomic and anatomical comparisons of skin support independent adaptation to life in water by cetaceans and hippos. <i>Current Biology</i> , 2021, 31, 2124-2139.e3.	3.9	30
9	Speciation in the deep: genomics and morphology reveal a new species of beaked whale <i>Mesoplodon eueu</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2021, 288, 20211213.	2.6	18
10	ILS-Aware Analysis of Low-Homoplasy Retroelement Insertions: Inference of Species Trees and Introgression Using Quartets. <i>Journal of Heredity</i> , 2020, 111, 147-168.	2.4	30
11	Phylogenomics reveals novel relationships among Neotropical crocodiles (<i>Crocodylus</i> spp.). <i>Molecular Phylogenetics and Evolution</i> , 2020, 152, 106924.	2.7	11
12	Evolutionary Models for the Diversification of Placental Mammals Across the KPg Boundary. <i>Frontiers in Genetics</i> , 2019, 10, 1241.	2.3	41
13	Genes lost during the transition from land to water in cetaceans highlight genomic changes associated with aquatic adaptations. <i>Science Advances</i> , 2019, 5, eaaw6671.	10.3	100
14	Odontogenic ameloblast-associated (ODAM) is inactivated in toothless/enamelless placental mammals and toothed whales. <i>BMC Evolutionary Biology</i> , 2019, 19, 31.	3.2	22
15	Partitioned coalescence support reveals biases in species-tree methods and detects gene trees that determine phylogenomic conflicts. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106539.	2.7	31
16	Gene-wise resampling outperforms site-wise resampling in phylogenetic coalescence analyses. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 80-92.	2.7	33
17	Evolution of the MC5R gene in placental mammals with evidence for its inactivation in multiple lineages that lack sebaceous glands. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 364-374.	2.7	35
18	Pinniped Diphyle and Bat Triphyle: More Homology Errors Drive Conflicts in the Mammalian Tree. <i>Journal of Heredity</i> , 2018, 109, 297-307.	2.4	13

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19	On the importance of homology in the age of phylogenomics. <i>Systematics and Biodiversity</i> , 2018, 16, 210-228.	1.2	78
20	Delimiting Coalescence Genes (C-Genes) in Phylogenomic Data Sets. <i>Genes</i> , 2018, 9, 123.	2.4	30
21	Microstructure and mechanical properties of different keratinous horns. <i>Journal of the Royal Society Interface</i> , 2018, 15, 20180093.	3.4	33
22	On the Illogic of Coalescence Simulations for Distinguishing the Causes of Conflict among Gene Trees. <i>Journal of Phylogenetics & Evolutionary Biology</i> , 2018, 06, .	0.2	3
23	Inactivation of the olfactory marker protein (OMP) gene in river dolphins and other odontocete cetaceans. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 375-387.	2.7	19
24	Phylogenomic red flags: Homology errors and zombie lineages in the evolutionary diversification of placental mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9431-E9432.	7.1	50
25	Resolution of a concatenation/coalescence kerfuffle: partitioned coalescence support and a robust family-level tree for Mammalia. <i>Cladistics</i> , 2017, 33, 295-332.	3.3	70
26	Lineage diversification of fringe-toed lizards (Phrynosomatidae: <i>Uma notata</i> complex) in the Colorado Desert: Delimiting species in the presence of gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 103-117.	2.7	28
27	Inactivation of Cone-Specific Phototransduction Genes in Rod Monochromatic Cetaceans. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	2.2	27
28	Biases of tree-independent-character-subsampling methods. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 424-443.	2.7	11
29	Inactivation of C4orf26 in toothless placental mammals. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 34-45.	2.7	45
30	The effects of subsampling gene trees on coalescent methods applied to ancient divergences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 76-89.	2.7	45
31	The gene tree delusion. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 1-33.	2.7	259
32	Interordinal gene capture, the phylogenetic position of Steller's sea cow based on molecular and morphological data, and the macroevolutionary history of Sirenia. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 178-193.	2.7	75
33	Coalescence vs. concatenation: Sophisticated analyses vs. first principles applied to rooting the angiosperms. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 98-122.	2.7	77
34	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
35	Land plant origins and coalescence confusion. <i>Trends in Plant Science</i> , 2014, 19, 267-269.	8.8	61
36	Molecular evolution tracks macroevolutionary transitions in Cetacea. <i>Trends in Ecology and Evolution</i> , 2014, 29, 336-346.	8.7	105

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37	Phylogenetic analysis at deep timescales: Unreliable gene trees, bypassed hidden support, and the coalescence/concatalescence conundrum. <i>Molecular Phylogenetics and Evolution</i> , 2014, 80, 231-266.	2.7	286
38	Molecular decay of enamel matrix protein genes in turtles and other edentulous amniotes. <i>BMC Evolutionary Biology</i> , 2013, 13, 20.	3.2	53
39	A phylogenetic blueprint for a modern whale. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 479-506.	2.7	200
40	THE EVOLUTIONARY HISTORY OF CETACEAN BRAIN AND BODY SIZE. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 3339-3353.	2.3	94
41	Rod Monochromacy and the Coevolution of Cetacean Retinal Opsins. <i>PLoS Genetics</i> , 2013, 9, e1003432.	3.5	118
42	Concatenation versus coalescence versus "concatalescence". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1179.	7.1	95
43	Response to Comment on "Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification". <i>Science</i> , 2012, 337, 34-34.	12.6	2
44	Macroevolutionary Dynamics and Historical Biogeography of Primate Diversification Inferred from a Species Supermatrix. <i>PLoS ONE</i> , 2012, 7, e49521.	2.5	447
45	Pseudogenization of the tooth gene <i>enamelysin</i> (<i>MMP20</i>) in the common ancestor of extant baleen whales. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 993-1002.	2.6	79
46	A phylogenetic hypothesis for <i>Crocodylus</i> (<i>Crocodylia</i>) based on mitochondrial DNA: Evidence for a trans-Atlantic voyage from Africa to the New World. <i>Molecular Phylogenetics and Evolution</i> , 2011, 60, 183-191.	2.7	82
47	Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification. <i>Science</i> , 2011, 334, 521-524.	12.6	1,264
48	A supermatrix analysis of genomic, morphological, and paleontological data from crown Cetacea. <i>BMC Evolutionary Biology</i> , 2011, 11, 112.	3.2	171
49	Phylogeny and adaptive evolution of the brain-development gene <i>microcephalin</i> (<i>MCPH1</i>) in cetaceans. <i>BMC Evolutionary Biology</i> , 2011, 11, 98.	3.2	24
50	Nuclear "Mitochondrial Sequences as Witnesses of Past Interbreeding and Population Diversity in the Jumping Bristletail <i>Mesomachilis</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 195-210.	8.9	30
51	Molecular Decay of the Tooth Gene <i>Enamelin</i> (<i>ENAM</i>) Mirrors the Loss of Enamel in the Fossil Record of Placental Mammals. <i>PLoS Genetics</i> , 2009, 5, e1000634.	3.5	133
52	Evolution and phylogenetic utility of the melanocortin-1 receptor gene (<i>MC1R</i>) in Cetartiodactyla. <i>Molecular Phylogenetics and Evolution</i> , 2009, 52, 550-557.	2.7	18
53	Divergence date estimation and a comprehensive molecular tree of extant cetaceans. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 891-906.	2.7	337
54	Relationships of Cetacea (<i>Artiodactyla</i>) Among Mammals: Increased Taxon Sampling Alters Interpretations of Key Fossils and Character Evolution. <i>PLoS ONE</i> , 2009, 4, e7062.	2.5	166

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55	The rapid accumulation of consistent molecular support for intergeneric crocodylian relationships. <i>Molecular Phylogenetics and Evolution</i> , 2008, 48, 1232-1237.	2.7	21
56	Impact of increased character sampling on the phylogeny of Cetartiodactyla (Mammalia): combined analysis including fossils. <i>Cladistics</i> , 2008, 24, 397-442.	3.3	95
57	Morphological and Molecular Evidence for a Stepwise Evolutionary Transition from Teeth to Baleen in Mysticete Whales. <i>Systematic Biology</i> , 2008, 57, 15-37.	5.6	238
58	The Vestigial Olfactory Receptor Subgenome of Odontocete Whales: Phylogenetic Congruence between Gene-Tree Reconciliation and Supermatrix Methods. <i>Systematic Biology</i> , 2008, 57, 574-590.	5.6	82
59	How Many Genes Should a Systematist Sample? Conflicting Insights from a Phylogenomic Matrix Characterized by Replicated Incongruence. <i>Systematic Biology</i> , 2007, 56, 355-363.	5.6	80
60	The supermatrix approach to systematics. <i>Trends in Ecology and Evolution</i> , 2007, 22, 34-41.	8.7	375
61	Adaptive Evolution and Phylogenetic Utility of Acr(Acrosin), a Rapidly Evolving Mammalian Fertilization Gene. <i>Journal of Mammalogy</i> , 2007, 88, 32-42.	1.3	10
62	Hidden Likelihood Support in Genomic Data: Can Forty-Five Wrongs Make a Right?. <i>Systematic Biology</i> , 2005, 54, 483-492.	5.6	136
63	A Critique of Matrix Representation with Parsimony Supertrees. <i>Computational Biology</i> , 2004, , 369-388.	0.2	42
64	Inconsistencies in Arguments for the Supertree Approach: Supermatrices versus Supertrees of Crocodylia. <i>Systematic Biology</i> , 2004, 53, 342-355.	5.6	101
65	Combined Support for Wholesale Taxic Atavism in Gavialine Crocodylians. <i>Systematic Biology</i> , 2003, 52, 403-422.	5.6	176
66	Are the Dental Data Really at Odds with the Molecular Data? Morphological Evidence for Whale Phylogeny (Re)Reexamined. <i>Systematic Biology</i> , 2003, 52, 853-864.	5.6	32
67	Resolution of a Supertree/Supermatrix Paradox. <i>Systematic Biology</i> , 2002, 51, 652-664.	5.6	190
68	Is morphology still relevant?. , 2002, , 163-174.		46
69	Relative quality of different systematic datasets for cetartiodactyl mammals: assessments within a combined analysis framework. , 2002, , 45-67.		9
70	Deciphering whale origins with molecules and fossils. <i>Trends in Ecology and Evolution</i> , 2001, 16, 562-570.	8.7	103
71	Hidden Morphological Support for the Phylogenetic Placement of <i>Pseudoryx nghetinhensis</i> with Bovine Bovids: A Combined Analysis of Gross Anatomical Evidence and DNA Sequences from Five Genes. <i>Systematic Biology</i> , 2000, 49, 515-538.	5.6	76
72	Linked Branch Support and Tree Stability. <i>Systematic Biology</i> , 2000, 49, 800-807.	5.6	24

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73	Stability of Cladistic Relationships between Cetacea and Higher-Level Artiodactyl Taxa. <i>Systematic Biology</i> , 1999, 48, 6-20.	5.6	164
74	Corroboration among Data Sets in Simultaneous Analysis: Hidden Support for Phylogenetic Relationships among Higher Level Artiodactyl Taxa. <i>Cladistics</i> , 1999, 15, 271-313.	3.3	288
75	Corroboration among Data Sets in Simultaneous Analysis: Hidden Support for Phylogenetic Relationships among Higher Level Artiodactyl Taxa. <i>Cladistics</i> , 1999, 15, 271-313.	3.3	69
76	Molecular Evidence for the Phylogenetic Affinities of Cetacea. , 1998, , 63-111.		54
77	PCR assays of variable nucleotide sites for identification of conservation units: n example from Caiman. , 1998, , 177-190.		8
78	A Cladistic Analysis of Mitochondrial Ribosomal DNA from the Bovidae. <i>Molecular Phylogenetics and Evolution</i> , 1997, 7, 303-319.	2.7	134
79	Elision: A Method for Accommodating Multiple Molecular Sequence Alignments with Alignment-Ambiguous Sites. <i>Molecular Phylogenetics and Evolution</i> , 1995, 4, 1-9.	2.7	145
80	Rate Limits for Mispairing and Compensatory Change: The Mitochondrial Ribosomal DNA of Antelopes. <i>Evolution; International Journal of Organic Evolution</i> , 1994, 48, 188.	2.3	8
81	Alignment-Ambiguous Nucleotide Sites and the Exclusion of Systematic Data. <i>Molecular Phylogenetics and Evolution</i> , 1993, 2, 152-157.	2.7	323
82	Sequence Similarity of 12S Ribosomal Segment of Mitochondrial DNAs of Gharial and False Gharial. <i>Copeia</i> , 1992, 1992, 241.	1.3	40
83	Genomic evidence for the parallel regression of melatonin synthesis and signaling pathways in placental mammals. <i>Open Research Europe</i> , 0, 1, 75.	2.0	3
84	Genomic evidence for the parallel regression of melatonin synthesis and signaling pathways in placental mammals. <i>Open Research Europe</i> , 0, 1, 75.	2.0	2