

Resolving conflict in eutherian mammal phylogeny using multispecies coalescent model

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Evolution and divergence of the mammalian SAMD9/SAMD9L gene family. <i>BMC Evolutionary Biology</i> , 2013, 13, 121.	3.2	43
2	Origin of land plants using the multispecies coalescent model. <i>Trends in Plant Science</i> , 2013, 18, 492-495.	4.3	109
3	Ciliary Regulation: Disassembly Takes the Spotlight. <i>Current Biology</i> , 2013, 23, R1001-R1003.	1.8	8
4	Naive binning improves phylogenomic analyses. <i>Bioinformatics</i> , 2013, 29, 2277-2284.	1.8	156
5	Addressing Gene Tree Discordance and Non-Stationarity to Resolve a Multi-Locus Phylogeny of the Flatfishes (Teleostei: Pleuronectiformes). <i>Systematic Biology</i> , 2013, 62, 763-785.	2.7	116
6	Phylogenomic Analyses Elucidate the Evolutionary Relationships of Bats. <i>Current Biology</i> , 2013, 23, 2262-2267.	1.8	139
7	Phylogenetics: Bats United, Microbats Divided. <i>Current Biology</i> , 2013, 23, R999-R1001.	1.8	19
8	An archaeal origin of eukaryotes supports only two primary domains of life. <i>Nature</i> , 2013, 504, 231-236.	13.7	456
9	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.	3.5	158
10	MICROEVOLUTIONARY PROCESSES GENERATE PHYLOGENOMIC DISCORDANCE AT ANCIENT DIVERGENCES. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 1823-1830.	1.1	89
11	A Versatile and Highly Efficient Toolkit Including 102 Nuclear Markers for Vertebrate Phylogenomics, Tested by Resolving the Higher Level Relationships of the Caudata. <i>Molecular Biology and Evolution</i> , 2013, 30, 2235-2248.	3.5	76
12	One Thousand Two Hundred Ninety Nuclear Genes from a Genome-Wide Survey Support Lungfishes as the Sister Group of Tetrapods. <i>Molecular Biology and Evolution</i> , 2013, 30, 1803-1807.	3.5	45
13	Heterogeneous Models Place the Root of the Placental Mammal Phylogeny. <i>Molecular Biology and Evolution</i> , 2013, 30, 2145-2156.	3.5	115
14	Making the Impossible Possible: Rooting the Tree of Placental Mammals. <i>Molecular Biology and Evolution</i> , 2013, 30, 1999-2000.	3.5	38
15	Rewriting Evolutionâ€”â€œBeen There, Done Thatâ€• <i>Genome Biology and Evolution</i> , 2013, 5, 819-821.	1.1	7
16	Retrophylogenomics Place Tarsiers on the Evolutionary Branch of Anthropoids. <i>Scientific Reports</i> , 2013, 3, 1756.	1.6	47
17	STRAW: Species TRee Analysis Web server. <i>Nucleic Acids Research</i> , 2013, 41, W238-W241.	6.5	93
18	Concatenation versus coalescence versus â€œconcatalenceâ€• <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1179.	3.3	95

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19	Modeling Transformations of Neurodevelopmental Sequences across Mammalian Species. <i>Journal of Neuroscience</i> , 2013, 33, 7368-7383.	1.7	687
20	Reply to Gatesy and Springer: The multispecies coalescent model can effectively handle recombination and gene tree heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1180.	3.3	26
21	Old genes and new genes: The evolution of the kallikrein locus. <i>Thrombosis and Haemostasis</i> , 2013, 110, 469-475.	1.8	19
22	Phylogenomic Analyses of Nuclear Genes Reveal the Evolutionary Relationships within the BEP Clade and the Evidence of Positive Selection in Poaceae. <i>PLoS ONE</i> , 2013, 8, e64642.	1.1	37
23	Phylogenomics and Coalescent Analyses Resolve Extant Seed Plant Relationships. <i>PLoS ONE</i> , 2013, 8, e80870.	1.1	69
24	ASTRAL: genome-scale coalescent-based species tree estimation. <i>Bioinformatics</i> , 2014, 30, i541-i548.	1.8	1,002
25	Phylogenetic distinction of iNOS and IDO function in mesenchymal stem cell-mediated immunosuppression in mammalian species. <i>Cell Death and Differentiation</i> , 2014, 21, 388-396.	5.0	193
26	High-level systematics of placental mammals: Current status of the problem. <i>Biology Bulletin</i> , 2014, 41, 801-816.	0.1	3
27	Evolution of Visual and Non-visual Pigments. , 2014, , .		33
28	Scaling the primate lateral geniculate nucleus: Niche and neurodevelopment in the regulation of magnocellular and parvocellular cell number and nucleus volume. <i>Journal of Comparative Neurology</i> , 2014, 522, 1839-1857.	0.9	9
29	Statistical binning enables an accurate coalescent-based estimation of the avian tree. <i>Science</i> , 2014, 346, 1250-1253.	6.0	225
30	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254-1257.	6.0	300
31	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	6.0	1,583
32	Multispecies Coalescent Analysis of the Early Diversification of Neotropical Primates: Phylogenetic Inference under Strong Gene Trees/Species Tree Conflict. <i>Genome Biology and Evolution</i> , 2014, 6, 3105-3114.	1.1	15
33	The multispecies coalescent model and land plant origins: a reply to Springer and Gatesy. <i>Trends in Plant Science</i> , 2014, 19, 270-272.	4.3	20
34	Primate phylogenetic relationships and divergence dates inferred from complete mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , 2014, 75, 165-183.	1.2	260
35	One hundred new universal exonic markers for birds developed from a genomic pipeline. <i>Journal of Ornithology</i> , 2014, 155, 561-569.	0.5	7
36	Comparative methods offer powerful insights into social evolution in bees. <i>Apidologie</i> , 2014, 45, 289-305.	0.9	74

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37	The Use (and Misuse) of Phylogenetic Trees in Comparative Behavioral Analyses. <i>International Journal of Primatology</i> , 2014, 35, 32-54.	0.9	8
38	Land plant origins and coalescence confusion. <i>Trends in Plant Science</i> , 2014, 19, 267-269.	4.3	61
39	Global Biodiversity Assessment and Hyper-Cryptic Species Complexes: More Than One Species of Elephant in the Room?. <i>Systematic Biology</i> , 2014, 63, 518-533.	2.7	157
40	Robustness to Divergence Time Underestimation When Inferring Species Trees from Estimated Gene Trees. <i>Systematic Biology</i> , 2014, 63, 66-82.	2.7	54
41	Phylogenetic affinity of tree shrews to Glires is attributed to fast evolution rate. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 193-200.	1.2	24
42	Disentangling Methodological and Biological Sources of Gene Tree Discordance on <i>Oryza</i> (Poaceae) Chromosome 3. <i>Systematic Biology</i> , 2014, 63, 645-659.	2.7	43
43	Evolution of <i>Klk4</i> and enamel maturation in eutherians. <i>Biological Chemistry</i> , 2014, 395, 1003-1013.	1.2	22
44	Coalescent versus Concatenation Methods and the Placement of Amborella as Sister to Water Lilies. <i>Systematic Biology</i> , 2014, 63, 919-932.	2.7	166
45	Effectiveness of phylogenomic data and coalescent species-tree methods for resolving difficult nodes in the phylogeny of advanced snakes (Serpentes: Caenophidia). <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 221-231.	1.2	86
46	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.	1.2	286
47	An Introduction to Supertree Construction (and Partitioned Phylogenetic Analyses) with a View Toward the Distinction Between Gene Trees and Species Trees. , 2014, , 49-76.		10
48	Novel Information Theory-Based Measures for Quantifying Incongruence among Phylogenetic Trees. <i>Molecular Biology and Evolution</i> , 2014, 31, 1261-1271.	3.5	259
49	L.U.St: a tool for approximated maximum likelihood supertree reconstruction. <i>BMC Bioinformatics</i> , 2014, 15, 183.	1.2	14
50	A multilocus phylogeny reveals deep lineages within African galagids (Primates: Galagidae). <i>BMC Evolutionary Biology</i> , 2014, 14, 72.	3.2	80
51	A time-calibrated, multi-locus phylogeny of piranhas and pacus (Characiformes: Serrasalminidae) and a comparison of species tree methods. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 242-257.	1.2	64
52	A comprehensive multilocus phylogeny of the Neotropical cotingas (Cotingidae, Aves) with a comparative evolutionary analysis of breeding system and plumage dimorphism and a revised phylogenetic classification. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 120-136.	1.2	35
53	An empirical evaluation of two-stage species tree inference strategies using a multilocus dataset from North American pines. <i>BMC Evolutionary Biology</i> , 2014, 14, 67.	3.2	21
54	Torpor during Reproduction in Mammals and Birds: Dealing with an Energetic Conundrum. <i>Integrative and Comparative Biology</i> , 2014, 54, 516-532.	0.9	74

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55	Molecular phylogenetic analysis of the Papionina using concatenation and species tree methods. <i>Journal of Human Evolution</i> , 2014, 66, 18-28.	1.3	17
56	Importance of synonymous substitutions under dense taxon sampling and appropriate modeling in reconstructing the mitogenomic tree of Eutheria. <i>Genes and Genetic Systems</i> , 2014, 89, 237-251.	0.2	8
57	Radiation of the <i>Drosophila</i> nannoptera species group in Mexico. <i>Journal of Evolutionary Biology</i> , 2014, 27, 575-584.	0.8	13
58	BBCA: Improving the scalability of *BEAST using random binning. <i>BMC Genomics</i> , 2014, 15, S11.	1.2	38
59	Disk covering methods improve phylogenomic analyses. <i>BMC Genomics</i> , 2014, 15, S7.	1.2	24
60	Coalescent methods for estimating species trees from phylogenomic data. <i>Journal of Systematics and Evolution</i> , 2015, 53, 380-390.	1.6	89
61	Ancient collagen reveals evolutionary history of the endemic South American ungulates™. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20142671.	1.2	106
62	Neuron Types in the Presumptive Primary Somatosensory Cortex of the Florida Manatee (<i>Trichechus</i>)	0.9	7
63	Phylotranscriptomic Analysis Based on Coalescence was Less Influenced by the Evolving Rates and the Number of Genes: A Case Study in Ericales. <i>Evolutionary Bioinformatics</i> , 2015, 11s1, EBO.S22448.	0.6	8
64	A comparative study of SVDquartets and other coalescent-based species tree estimation methods. <i>BMC Genomics</i> , 2015, 16, S2.	1.2	128
65	ASTRID: Accurate Species Trees from Internode Distances. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	143
66	Estimating phylogenetic trees from genome-scale data. <i>Annals of the New York Academy of Sciences</i> , 2015, 1360, 36-53.	1.8	165
67	A Guide to Phylogenetic Reconstruction Using Heterogeneous Models™ A Case Study from the Root of the Placental Mammal Tree. <i>Computation</i> , 2015, 3, 177-196.	1.0	17
68	Alternatives to the Use of Nonhuman Primates in Regulatory Toxicology. , 2015, , 337-355.		5
69	The SKINT1-Like Gene Is Inactivated in Hominoids But Not in All Primate Species: Implications for the Origin of Dendritic Epidermal T Cells. <i>PLoS ONE</i> , 2015, 10, e0123258.	1.1	12
70	Mapping of Post-translational Modifications of Transition Proteins, TP1 and TP2, and Identification of Protein Arginine Methyltransferase 4 and Lysine Methyltransferase 7 as Methyltransferase for TP2. <i>Journal of Biological Chemistry</i> , 2015, 290, 12101-12122.	1.6	24
71	Multilocus phylogeny and taxonomic revision of the <i>Hemidactylus robustus</i> species group (Reptilia, Gekkonidae) with descriptions of three new species from Yemen and Ethiopia. <i>Systematics and Biodiversity</i> , 2015, 13, 346-368.	0.5	26
72	The Inference of Gene Trees with Species Trees. <i>Systematic Biology</i> , 2015, 64, e42-e62.	2.7	226

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73	The Challenges of Resolving a Rapid, Recent Radiation: Empirical and Simulated Phylogenomics of Philippine Shrews. <i>Systematic Biology</i> , 2015, 64, 727-740.	2.7	140
74	A Genome-Scale Investigation of Incongruence in Culicidae Mosquitoes. <i>Genome Biology and Evolution</i> , 2015, 7, 3463-3471.	1.1	8
76	A species-level phylogeny of all extant and late Quaternary extinct mammals using a novel heuristic-hierarchical Bayesian approach. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 14-26.	1.2	116
77	Resolving phylogenetic relationships of the recently radiated carnivorous plant genus <i>Sarracenia</i> using target enrichment. <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 76-87.	1.2	108
78	Multilocus species tree analyses resolve the ancient radiation of the subtribe <i>Zizaniinae</i> (Poaceae). <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 232-239.	1.2	18
79	Likelihood-based tree reconstruction on a concatenation of aligned sequence data sets can be statistically inconsistent. <i>Theoretical Population Biology</i> , 2015, 100, 56-62.	0.5	218
80	The <i>Tetramerium</i> lineage (Acanthaceae: Justiceae) does not support the Pleistocene Arc hypothesis for South American seasonally dry forests. <i>American Journal of Botany</i> , 2015, 102, 992-1007.	0.8	24
81	Sequence diversity of the MHC α ; DRB gene in Chinese tree shrews (<i>Tupaia belangeri chinensis</i>). <i>Biochemical Systematics and Ecology</i> , 2015, 61, 417-423.	0.6	1
82	Positive selection effects on the biochemical properties of mammal pyroglutamylated RFamide peptide receptor (QRFPR). <i>Italian Journal of Zoology</i> , 2015, 82, 309-326.	0.6	4
83	Genes with minimal phylogenetic information are problematic for coalescent analyses when gene tree estimation is biased. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 63-71.	1.2	104
84	Multilocus Species Trees Show the Recent Adaptive Radiation of the Mimetic <i>Heliconius</i> Butterflies. <i>Systematic Biology</i> , 2015, 64, 505-524.	2.7	204
85	Species tree estimation of diploid <i>Helianthus</i> (Asteraceae) using target enrichment. <i>American Journal of Botany</i> , 2015, 102, 910-920.	0.8	61
86	Convergence of multiple markers and analysis methods defines the genetic distinctiveness of cryptic pitvipers. <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 266-279.	1.2	9
87	The evolutionary history of ferns inferred from 25 low-copy nuclear genes. <i>American Journal of Botany</i> , 2015, 102, 1089-1107.	0.8	157
88	Mammalian genome evolution is governed by multiple pacemakers. <i>Bioinformatics</i> , 2015, 31, 2061-2065.	1.8	17
89	On the Robustness to Gene Tree Estimation Error (or lack thereof) of Coalescent-Based Species Tree Methods. <i>Systematic Biology</i> , 2015, 64, 663-676.	2.7	161
90	Phylogenomic analysis uncovers the evolutionary history of nutrition and infection mode in rice blast fungus and other Magnaporthales. <i>Scientific Reports</i> , 2015, 5, 9448.	1.6	32
91	Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015, 522, 81-84.	13.7	273

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92	A composite genome approach to identify phylogenetically informative data from next-generation sequencing. <i>BMC Bioinformatics</i> , 2015, 16, 193.	1.2	26
93	Selecting Question-Specific Genes to Reduce Incongruence in Phylogenomics: A Case Study of Jawed Vertebrate Backbone Phylogeny. <i>Systematic Biology</i> , 2015, 64, 1104-1120.	2.7	105
94	Tupaia small RNAs provide insights into function and evolution of RNAi-based transposon defense in mammals. <i>Rna</i> , 2015, 21, 911-922.	1.6	19
95	Coalescent Methods Are Robust to the Simultaneous Effects of Long Branches and Incomplete Lineage Sorting. <i>Molecular Biology and Evolution</i> , 2015, 32, 791-805.	3.5	69
96	An analysis of von Economo neurons in the cerebral cortex of cetaceans, artiodactyls, and perissodactyls. <i>Brain Structure and Function</i> , 2015, 220, 2303-2314.	1.2	43
97	Deep phylogenetic incongruence in the angiosperm clade Rosidae. <i>Molecular Phylogenetics and Evolution</i> , 2015, 83, 156-166.	1.2	125
98	The Effects of Inference Method, Population Sampling, and Gene Sampling on Species Tree Inferences: An Empirical Study in Slender Salamanders (Plethodontidae: Batrachoseps). <i>Systematic Biology</i> , 2015, 64, 66-83.	2.7	18
99	Evaluating Summary Methods for Multilocus Species Tree Estimation in the Presence of Incomplete Lineage Sorting. <i>Systematic Biology</i> , 2016, 65, 366-380.	2.7	242
100	A Genome-Scale Investigation of How Sequence, Function, and Tree-Based Gene Properties Influence Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 2565-2580.	1.1	70
101	Oxytocin and arginine vasopressin receptor evolution: implications for adaptive novelties in placental mammals. <i>Genetics and Molecular Biology</i> , 2016, 39, 646-657.	0.6	15
102	Never Ending Analysis of a Century Old Evolutionary Debate: "Unringing" the Urmetazoon Bell. <i>Frontiers in Ecology and Evolution</i> , 2016, 4, .	1.1	15
103	Genomic data reveal ancient microendemism in forest scorpions across the California Floristic Province. <i>Molecular Ecology</i> , 2016, 25, 3731-3751.	2.0	23
104	RAD-seq phylogenomics recovers a well-resolved phylogeny of a rapid radiation of mutualistic and antagonistic yucca moths. <i>Systematic Entomology</i> , 2016, 41, 672-682.	1.7	17
105	Phylogenetic analysis of RAD-seq data: examining the influence of gene genealogy conflict on analysis of concatenated data. <i>Cladistics</i> , 2016, 32, 672-681.	1.5	39
106	Phylogenomic subsampling: a brief review. <i>Zoologica Scripta</i> , 2016, 45, 63-74.	0.7	49
107	Inconsistency of Species Tree Methods under Gene Flow. <i>Systematic Biology</i> , 2016, 65, 843-851.	2.7	146
108	Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies. <i>Molecular Biology and Evolution</i> , 2016, 33, 1654-1668.	3.5	650
109	Golgi Analysis of Neuron Morphology in the Presumptive Somatosensory Cortex and Visual Cortex of the Florida Manatee (<i>Trichechus manatus latirostris</i>). <i>Brain, Behavior and Evolution</i> , 2016, 87, 105-116.	0.9	6

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110	Incomplete Lineage Sorting in Mammalian Phylogenomics. <i>Systematic Biology</i> , 2017, 66, syw082.	2.7	88
111	Unusual Diversity of Myoglobin Genes in the Lungfish. <i>Molecular Biology and Evolution</i> , 2016, 33, 3033-3041.	3.5	22
112	Species Trees, Inference of. , 2016, , 236-244.		5
113	Multilocus inference of species trees and DNA barcoding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150335.	1.8	67
114	Cis-Regulatory Evolution of Forkhead Box O1 (FOXO1), a Terminal Selector Gene for Decidual Stromal Cell Identity. <i>Molecular Biology and Evolution</i> , 2016, 33, 3161-3169.	3.5	29
115	Ancestral Gene Flow and Parallel Organellar Genome Capture Result in Extreme Phylogenomic Discord in a Lineage of Angiosperms. <i>Systematic Biology</i> , 2017, 66, syw083.	2.7	132
116	Reticulation, divergence, and the phylogeographyâ€“phylogenetics continuum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8025-8032.	3.3	130
117	The Identification of the Closest Living Relative(s) of Tetrapods: Phylogenomic Lessons for Resolving Short Ancient Internodes. <i>Systematic Biology</i> , 2016, 65, 1057-1075.	2.7	45
118	Displayed Trees Do Not Determine Distinguishability Under the Network Multispecies Coalescent. <i>Systematic Biology</i> , 2017, 66, syw097.	2.7	34
119	Consensus Methods, Phylogenetic. , 2016, , 341-346.		0
120	Phylogenomic analyses of bat subordinal relationships based on transcriptome data. <i>Scientific Reports</i> , 2016, 6, 27726.	1.6	69
121	Reconstructing the Backbone of the Saccharomycotina Yeast Phylogeny Using Genome-Scale Data. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3927-3939.	0.8	187
122	Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. <i>BMC Genomics</i> , 2016, 17, 783.	1.2	24
123	Somatosensory brainstem, thalamus, and cortex of the California sea lion (<i>Zalophus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock_10 Tf 50 2 0.9 30		
125	Mammal madness: is the mammal tree of life not yet resolved?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150140.	1.8	216
126	Phylogeny, Genes, and Hearing: Implications for the Evolution of Echolocation in Bats. <i>Springer Handbook of Auditory Research</i> , 2016, , 25-54.	0.3	35
127	Assessing parallel gene histories in viral genomes. <i>BMC Evolutionary Biology</i> , 2016, 16, 32.	3.2	10
128	LSÂ³: A Method for Improving Phylogenomic Inferences When Evolutionary Rates Are Heterogeneous among Taxa. <i>Molecular Biology and Evolution</i> , 2016, 33, 1625-1634.	3.5	18

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129	An introduction to plant phylogenomics with a focus on palms. <i>Botanical Journal of the Linnean Society</i> , 2016, 182, 234-255.	0.8	42
130	A Bayesian Supertree Model for Genome-Wide Species Tree Reconstruction. <i>Systematic Biology</i> , 2016, 65, 397-416.	2.7	40
131	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 330-344.	1.1	195
132	Phylogenomic analyses resolve an ancient trichotomy at the base of Ischyropsalidoidea (Arachnida). <i>Tj ETQq1 1 0.784314 rgBT /Overl</i> <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 171-182.	1.2	23
133	Euarchontan Opsin Variation Brings New Focus to Primate Origins. <i>Molecular Biology and Evolution</i> , 2016, 33, 1029-1041.	3.5	22
134	The effects of subsampling gene trees on coalescent methods applied to ancient divergences. <i>Molecular Phylogenetics and Evolution</i> , 2016, 97, 76-89.	1.2	45
135	Detecting the Anomaly Zone in Species Trees and Evidence for a Misleading Signal in Higher-Level Skink Phylogeny (Squamata: Scincidae).. <i>Systematic Biology</i> , 2016, 65, 465-477.	2.7	85
136	Expanded phylogenetic analyses of the class Heterotrichea (Ciliophora, Postciliodesmatophora) using five molecular markers and morphological data. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 229-246.	1.2	56
137	Shotgun Mitogenomics Provides a Reference Phylogenetic Framework and Timescale for Living Xenarthrans. <i>Molecular Biology and Evolution</i> , 2016, 33, 621-642.	3.5	167
138	Molecular signatures that are distinctive characteristics of the vertebrates and chordates and supporting a grouping of vertebrates with the tunicates. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 383-391.	1.2	15
139	Speciation of two gobioid species, <i>Pterogobius elapoides</i> and <i>Pterogobius zonoleucus</i> revealed by multi-locus nuclear and mitochondrial DNA analyses. <i>Gene</i> , 2016, 576, 593-602.	1.0	8
140	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 447-462.	1.2	321
141	Micro-computed tomography and microdissection of the temporal bone of tree shrews. <i>Annals of Anatomy</i> , 2016, 208, 69-77.	1.0	8
142	The gene tree delusion. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 1-33.	1.2	259
143	Oxidative shielding and the cost of reproduction. <i>Biological Reviews</i> , 2016, 91, 483-497.	4.7	143
144	Resolving the relationships of Paleocene placental mammals. <i>Biological Reviews</i> , 2017, 92, 521-550.	4.7	75
145	Genome-wide interrogation advances resolution of recalcitrant groups in the tree of life. <i>Nature Ecology and Evolution</i> , 2017, 1, 20.	3.4	193
146	Multiple measures could alleviate long-branch attraction in phylogenomic reconstruction of Cupressoideae (Cupressaceae). <i>Scientific Reports</i> , 2017, 7, 41005.	1.6	45

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147	<i>De Novo</i> Genome and Transcriptome Assembly of the Canadian Beaver (<i>Castor canadensis</i>). G3: Genes, Genomes, Genetics, 2017, 7, 755-773.	0.8	18
148	Macrosystematics of eutherian mammals combining HTS data to expand taxon coverage. Molecular Phylogenetics and Evolution, 2017, 113, 76-83.	1.2	8
149	The effects of Pleistocene climate change on biotic differentiation in a montane songbird clade from Wallacea. Molecular Phylogenetics and Evolution, 2017, 114, 353-366.	1.2	18
150	Species Tree Estimation from Genome-Wide Data with guenomu. Methods in Molecular Biology, 2017, 1525, 461-478.	0.4	14
151	More on the Best Evolutionary Rate for Phylogenetic Analysis. Systematic Biology, 2017, 66, 769-785.	2.7	48
152	Transcriptome sequencing and phylogenetic analysis of four species of luminescent beetles. Scientific Reports, 2017, 7, 1814.	1.6	30
153	Inferring Rates and Length-Distributions of Indels Using Approximate Bayesian Computation. Genome Biology and Evolution, 2017, 9, 1280-1294.	1.1	7
154	STELLS2: fast and accurate coalescent-based maximum likelihood inference of species trees from gene tree topologies. Bioinformatics, 2017, 33, 1789-1797.	1.8	14
155	Whence river blindness? The domestication of mammals and host-parasite co-evolution in the nematode genus Onchocerca. International Journal for Parasitology, 2017, 47, 457-470.	1.3	36
156	A novel set of single-copy nuclear gene markers in white oak and implications for species delimitation. Tree Genetics and Genomes, 2017, 13, 1.	0.6	6
157	Speciation network in Laurasiatheria: retrophylogenomic signals. Genome Research, 2017, 27, 997-1003.	2.4	38
158	Systematics and biogeography of the Automolus infuscatus complex (Aves; Furnariidae): Cryptic diversity reveals western Amazonia as the origin of a transcontinental radiation. Molecular Phylogenetics and Evolution, 2017, 107, 503-515.	1.2	22
159	In the shadows: Phylogenomics and coalescent species delimitation unveil cryptic diversity in a Cerrado endemic lizard (Squamata: Tropicurus). Molecular Phylogenetics and Evolution, 2017, 107, 455-465.	1.2	37
160	TreeShrink: Efficient Detection of Outlier Tree Leaves. Lecture Notes in Computer Science, 2017, , 116-140.	1.0	7
161	ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. Lecture Notes in Computer Science, 2017, , 53-75.	1.0	129
162	Rates of Molecular Evolution Suggest Natural History of Life History Traits and a Post-K-Pg Nocturnal Bottleneck of Placentals. Current Biology, 2017, 27, 3025-3033.e5.	1.8	51
163	Investigating Difficult Nodes in the Placental Mammal Tree with Expanded Taxon Sampling and Thousands of Ultraconserved Elements. Genome Biology and Evolution, 2017, 9, 2308-2321.	1.1	102
164	IDXL: Species Tree Inference Using Internode Distance and Excess Gene Leaf Count. Journal of Molecular Evolution, 2017, 85, 57-78.	0.8	1

#	ARTICLE	IF	CITATIONS
165	Phylogenomic Resolution of the Phylogeny of Laurasiatherian Mammals: Exploring Phylogenetic Signals within Coding and Noncoding Sequences. <i>Genome Biology and Evolution</i> , 2017, 9, 1998-2012.	1.1	65
166	Genomic evidence reveals a radiation of placental mammals uninterrupted by the KPg boundary. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7282-E7290.	3.3	119
167	Phylotranscriptomic consolidation of the jawed vertebrate timetree. <i>Nature Ecology and Evolution</i> , 2017, 1, 1370-1378.	3.4	247
168	Genomic Analysis Reveals Genetic Distinctiveness of the Paiute Cutthroat Trout <i>Oncorhynchus clarkii seleniris</i> . <i>Transactions of the American Fisheries Society</i> , 2017, 146, 1291-1302.	0.6	8
169	Maximizing Power in Phylogenetics and Phylogenomics: A Perspective Illuminated by Fungal Big Data. <i>Advances in Genetics</i> , 2017, 100, 1-47.	0.8	28
170	The Genomes of Two Bat Species with Long Constant Frequency Echolocation Calls. <i>Molecular Biology and Evolution</i> , 2017, 34, 20-34.	3.5	38
171	Mutually exclusive phylogenomic inferences at the root of the angiosperms: <i>Amborella</i> is supported as sister and Observed Variability is biased. <i>Cladistics</i> , 2017, 33, 488-512.	1.5	16
172	Resolution of a concatenation/coalescence keruffle: partitioned coalescence support and a robust family-level tree for Mammalia. <i>Cladistics</i> , 2017, 33, 295-332.	1.5	70
173	The evolution of the macrophage-specific enhancer (Fms intronic regulatory element) within the CSF1R locus of vertebrates. <i>Scientific Reports</i> , 2017, 7, 17115.	1.6	10
174	Simulation-Based Evaluation of Hybridization Network Reconstruction Methods in the Presence of Incomplete Lineage Sorting. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431769193.	0.6	15
175	Evolutionary Genetic Analysis Uncovers Multiple Species with Distinct Habitat Preferences and Antibiotic Resistance Phenotypes in the <i>Stenotrophomonas maltophilia</i> Complex. <i>Frontiers in Microbiology</i> , 2017, 8, 1548.	1.5	47
176	Comparative analysis estimates the relative frequencies of co-divergence and cross-species transmission within viral families. <i>PLoS Pathogens</i> , 2017, 13, e1006215.	2.1	224
177	Comparative Structure of the Cerebral Cortex in Large Mammals. , 2017, , 267-289.		4
178	Climate change and body size trends in aquatic and terrestrial endotherms: Does habitat matter?. <i>PLoS ONE</i> , 2017, 12, e0183051.	1.1	17
179	FOXP in Tetrapoda: Intrinsically Disordered Regions, Short Linear Motifs and their evolutionary significance. <i>Genetics and Molecular Biology</i> , 2017, 40, 181-190.	0.6	3
180	âˆˆâˆ†âŠˆç‰©æˆˆjâžˆç,ä,â½/2•ä,çˆˆæ´é¼¼ ©â´ç?. <i>Zoological Research</i> , 2017, 38, 118-126.	0.9	74
181	A phylotranscriptomic backbone of the orb-weaving spider family Araneidae (Arachnida, Araneae) supported by multiple methodological approaches. <i>Molecular Phylogenetics and Evolution</i> , 2018, 126, 129-140.	1.2	35
182	Integrating genomic and phenotypic data to evaluate alternative phylogenetic and species delimitation hypotheses in a recent evolutionary radiation of grasshoppers. <i>Molecular Ecology</i> , 2018, 27, 1229-1244.	2.0	27

#	ARTICLE	IF	CITATIONS
183	Evaluating Fast Maximum Likelihood-Based Phylogenetic Programs Using Empirical Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2018, 35, 486-503.	3.5	147
184	Species Tree Estimation Using ASTRAL: How Many Genes Are Enough?. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1738-1747.	1.9	19
185	Impact of long-term chromosomal shuffling on the multispecies coalescent analysis of two anthropoid primate lineages. <i>Ecology and Evolution</i> , 2018, 8, 1206-1216.	0.8	2
186	PHYLOGENETIC ANALYSIS OF THE GENOME OF AN ENTERITIS-ASSOCIATED BOTTLENOSE DOLPHIN MASTADENOVIRUS SUPPORTS A CLADE INFECTING THE CETARTIODACTYLA. <i>Journal of Wildlife Diseases</i> , 2018, 54, 112.	0.3	8
187	Diversity of microbial communities potentially involved in mercury methylation in rice paddies surrounding typical mercury mining areas in China. <i>MicrobiologyOpen</i> , 2018, 7, e00577.	1.2	20
188	SVDquest: Improving SVDquartets species tree estimation using exact optimization within a constrained search space. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 122-136.	1.2	32
189	The <i>Microtus</i> voles: Resolving the phylogeny of one of the most speciose mammalian genera using genomics. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 85-92.	1.2	28
190	Variation Across Mitochondrial Gene Trees Provides Evidence for Systematic Error: How Much Gene Tree Variation Is Biological?. <i>Systematic Biology</i> , 2018, 67, 847-860.	2.7	51
191	Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (<i>Vitaceae</i>). <i>Cladistics</i> , 2018, 34, 57-77.	1.5	44
192	Analysis of Phylogenomic Tree Space Resolves Relationships Among Marsupial Families. <i>Systematic Biology</i> , 2018, 67, 400-412.	2.7	85
193	Pinniped Diphyly and Bat Triphyly: More Homology Errors Drive Conflicts in the Mammalian Tree. <i>Journal of Heredity</i> , 2018, 109, 297-307.	1.0	13
194	Phylogenomic support for evolutionary relationships of New World direct-developing frogs (Anura: Tj ETQq1 1 0.784314 rgBT / Overl	1.2	74
195	On the importance of homology in the age of phylogenomics. <i>Systematics and Biodiversity</i> , 2018, 16, 210-228.	0.5	78
196	Resolving taxonomic turbulence and uncovering cryptic diversity in the musk turtles (<i>Sternotherus</i>) using robust demographic modeling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 1-15.	1.2	23
198	Global Rate Variation in Bony Vertebrates. <i>Genome Biology and Evolution</i> , 2018, 10, 1803-1815.	1.1	28
199	Population genomics of wild Chinese rhesus macaques reveals a dynamic demographic history and local adaptation, with implications for biomedical research. <i>GigaScience</i> , 2018, 7, .	3.3	27
200	TreeShrink: fast and accurate detection of outlier long branches in collections of phylogenetic trees. <i>BMC Genomics</i> , 2018, 19, 272.	1.2	225
201	Phylogenomics resolves evolutionary relationships and provides insights into floral evolution in the tribe Shoreaeae (<i>Dipterocarpaceae</i>). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 1-13.	1.2	29

#	ARTICLE	IF	CITATIONS
202	Modeling Hybridization Under the Network Multispecies Coalescent. <i>Systematic Biology</i> , 2018, 67, 786-799.	2.7	97
203	Incomplete lineage sorting impacts the inference of macroevolutionary regimes from molecular phylogenies when concatenation is employed: An analysis based on Cetacea. <i>Ecology and Evolution</i> , 2018, 8, 6965-6971.	0.8	5
204	Multispecies coalescent analysis confirms standing phylogenetic instability in Hexapoda. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1623-1631.	0.8	7
205	Neural Progenitors in the Developing Neocortex of the Northern Tree Shrew (<i>Tupaia belangeri</i>) Show a Closer Relationship to Gyrencephalic Primates Than to Lissencephalic Rodents. <i>Frontiers in Neuroanatomy</i> , 2018, 12, 29.	0.9	14
206	Creating diversity in mammalian facial morphology: a review of potential developmental mechanisms. <i>EvoDevo</i> , 2018, 9, 15.	1.3	28
207	Delimiting Coalescence Genes (C-Genes) in Phylogenomic Data Sets. <i>Genes</i> , 2018, 9, 123.	1.0	30
208	SIESTA: enhancing searches for optimal supertrees and species trees. <i>BMC Genomics</i> , 2018, 19, 252.	1.2	4
209	ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. <i>BMC Bioinformatics</i> , 2018, 19, 153.	1.2	1,451
210	Oxytocin and arginine vasopressin systems in the domestication process. <i>Genetics and Molecular Biology</i> , 2018, 41, 235-242.	0.6	14
211	Visualization of Biomedical Networks. , 2019, , 1016-1035.		2
212	A Novel Test for Absolute Fit of Evolutionary Models Provides a Means to Correctly Identify the Substitution Model and the Model Tree. <i>Genome Biology and Evolution</i> , 2019, 11, 2403-2419.	1.1	2
213	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019, 6, 151.	2.4	34
214	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.4	30
215	A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera <i>Aspergillus</i> and <i>Penicillium</i> . <i>MBio</i> , 2019, 10, .	1.8	106
216	OMA standalone: orthology inference among public and custom genomes and transcriptomes. <i>Genome Research</i> , 2019, 29, 1152-1163.	2.4	111
217	The anatomy of an unstable node: a Levantine relict precipitates phylogenomic dissolution of higher-level relationships of the armoured harvestmen (Arachnida: Opiliones: Laniatores). <i>Invertebrate Systematics</i> , 2019, , .	0.5	12
218	Treehouse: a user-friendly application to obtain subtrees from large phylogenies. <i>BMC Research Notes</i> , 2019, 12, 541.	0.6	14
219	Evolution of Termite Symbiosis Informed by Transcriptome-Based Phylogenies. <i>Current Biology</i> , 2019, 29, 3728-3734.e4.	1.8	110

#	ARTICLE	IF	CITATIONS
220	Evolutionary Models for the Diversification of Placental Mammals Across the KPg Boundary. <i>Frontiers in Genetics</i> , 2019, 10, 1241.	1.1	41
221	The effect of alignment uncertainty, substitution models and priors in building and dating the mammal tree of life. <i>BMC Evolutionary Biology</i> , 2019, 19, 203.	3.2	11
222	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. <i>Science</i> , 2019, 364, .	6.0	266
223	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.	1.2	31
224	Diversification of Hawaiian <i>Cyrtandra</i> (Gesneriaceae) under the influence of incomplete lineage sorting and hybridization. <i>Journal of Systematics and Evolution</i> , 2019, 57, 561-578.	1.6	32
225	Early primate evolution: insights into the functional significance of grasping from motion analyses of extant mammals. <i>Biological Journal of the Linnean Society</i> , 2019, 127, 611-631.	0.7	20
226	Whole-Genome Analyses Resolve the Phylogeny of Flightless Birds (Palaeognathae) in the Presence of an Empirical Anomaly Zone. <i>Systematic Biology</i> , 2019, 68, 937-955.	2.7	88
227	Gene Selection and Evolutionary Modeling Affect Phylogenomic Inference of Neuropterida Based on Transcriptome Data. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1072.	1.8	8
228	Quantifying the completeness of the bat fossil record. <i>Palaeontology</i> , 2019, 62, 757-776.	1.0	35
229	Digging for the spiny rat and hutia phylogeny using a gene capture approach, with the description of a new mammal subfamily. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 241-253.	1.2	32
230	Assessing Combinability of Phylogenomic Data Using Bayes Factors. <i>Systematic Biology</i> , 2019, 68, 744-754.	2.7	6
231	Impacts of Inference Method and Data set Filtering on Phylogenomic Resolution in a Rapid Radiation of Ground Squirrels (Xerinae: Marmotini). <i>Systematic Biology</i> , 2019, 68, 298-316.	2.7	33
232	Phylogenomic incongruence, hypothesis testing, and taxonomic sampling: The monophyly of characiform fishes*. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 329-345.	1.1	78
233	Phylogenomics of the adaptive radiation of <i>Triturus</i> newts supports gradual ecological niche expansion towards an incrementally aquatic lifestyle. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 120-127.	1.2	38
234	Evolution and Development of the Atrial Septum. <i>Anatomical Record</i> , 2019, 302, 32-48.	0.8	34
235	Gene-wise resampling outperforms site-wise resampling in phylogenetic coalescence analyses. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 80-92.	1.2	33
236	Hybrid capture data unravel a rapid radiation of pimpliform parasitoid wasps (Hymenoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 T	1.7	43
237	Reconstructing the phylogeny of new world monkeys (platyrrhini): evidence from multiple non-coding loci. <i>Environmental Epigenetics</i> , 2019, 65, 579-588.	0.9	18

#	ARTICLE	IF	CITATIONS
238	Gene Golden Age paradox and its partial solution. <i>Genomics</i> , 2019, 111, 115-126.	1.3	8
239	Phylogenomics Uncovers Confidence and Conflict in the Rapid Radiation of Australo-Papuan Rodents. <i>Systematic Biology</i> , 2020, 69, 431-444.	2.7	44
240	Quartet-Based Computations of Internode Certainty Provide Robust Measures of Phylogenetic Incongruence. <i>Systematic Biology</i> , 2020, 69, 308-324.	2.7	38
241	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.	1.0	30
242	Irisin is expressed by undifferentiated spermatogonia and modulates gene expression in organotypic primate testis cultures. <i>Molecular and Cellular Endocrinology</i> , 2020, 504, 110670.	1.6	11
243	Human Embryogenesis: A Comparative Perspective. <i>Annual Review of Cell and Developmental Biology</i> , 2020, 36, 411-440.	4.0	39
244	Machine learning based imputation techniques for estimating phylogenetic trees from incomplete distance matrices. <i>BMC Genomics</i> , 2020, 21, 497.	1.2	15
245	Intragenic Conflict in Phylogenomic Data Sets. <i>Molecular Biology and Evolution</i> , 2020, 37, 3380-3388.	3.5	5
246	Is Phylotranscriptomics as Reliable as Phylogenomics?. <i>Molecular Biology and Evolution</i> , 2020, 37, 3672-3683.	3.5	52
247	Patterns of genetic partitioning and gene flow in the endangered San Bernardino kangaroo rat (<i>Dipodomys merriami parvus</i>) and implications for conservation management. <i>Conservation Genetics</i> , 2020, 21, 819-833.	0.8	5
248	Megaherbivore browsers vs. tannins: is being big enough?. <i>Oecologia</i> , 2020, 194, 383-390.	0.9	3
249	An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). <i>BMC Evolutionary Biology</i> , 2020, 20, 64.	3.2	48
250	Maximum Likelihood Estimation of Species Trees from Gene Trees in the Presence of Ancestral Population Structure. <i>Genome Biology and Evolution</i> , 2020, 12, 3977-3995.	1.1	5
251	Whole genome phylogeny of <i>Gallus</i> : introgression and data-type effects. <i>Avian Research</i> , 2020, 11, .	0.5	17
252	Elaboration of the Corticosteroid Synthesis Pathway in Primates through a Multistep Enzyme. <i>Molecular Biology and Evolution</i> , 2020, 37, 2257-2267.	3.5	6
253	A transcriptome-based study on the phylogeny and evolution of the taxonomically controversial subfamily Apioideae (Apiaceae). <i>Annals of Botany</i> , 2020, 125, 937-953.	1.4	35
254	Conflicting signal in transcriptomic markers leads to a poorly resolved backbone phylogeny of chalcidoid wasps. <i>Systematic Entomology</i> , 2020, 45, 783-802.	1.7	23
255	STELAR: a statistically consistent coalescent-based species tree estimation method by maximizing triplet consistency. <i>BMC Genomics</i> , 2020, 21, 136.	1.2	17

#	ARTICLE	IF	CITATIONS
256	Phylogeny and highland adaptation of Chinese species in <i>Allium</i> section <i>Daghestanica</i> (Amaryllidaceae) revealed by transcriptome sequencing. <i>Molecular Phylogenetics and Evolution</i> , 2020, 146, 106737.	1.2	10
257	A Characteristic Expression Pattern of Core Circadian Genes in the Diurnal Tree Shrew. <i>Neuroscience</i> , 2020, 437, 145-160.	1.1	2
258	Factors influencing customer satisfaction: The case of Facebook Chabot Vietnam. <i>International Journal of Data and Network Science</i> , 2020, , 167-178.	3.4	3
259	Phylogenomics and the Genetic Architecture of the Placental Mammal Radiation. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 29-53.	3.6	32
260	Phylogenomics of manakins (Aves: Pipridae) using alternative locus filtering strategies based on informativeness. <i>Molecular Phylogenetics and Evolution</i> , 2021, 155, 107013.	1.2	20
261	The Perfect Storm: Gene Tree Estimation Error, Incomplete Lineage Sorting, and Ancient Gene Flow Explain the Most Recalcitrant Ancient Angiosperm Clade, Malpighiales. <i>Systematic Biology</i> , 2021, 70, 491-507.	2.7	61
262	The role of linguistic experience in the development of the consonant bias. <i>Animal Cognition</i> , 2021, 24, 419-431.	0.9	1
263	Bayesian Inference of Species Trees using Diffusion Models. <i>Systematic Biology</i> , 2021, 70, 145-161.	2.7	21
264	Genome-Scale Profiling Reveals Noncoding Loci Carry Higher Proportions of Concordant Data. <i>Molecular Biology and Evolution</i> , 2021, 38, 2306-2318.	3.5	12
265	Gene Tree Discord, Simplex Plots, and Statistical Tests under the Coalescent. <i>Systematic Biology</i> , 2022, 71, 929-942.	2.7	14
266	Integrating Sequence Capture and Restriction Site-Associated DNA Sequencing to Resolve Recent Radiations of Pelagic Seabirds. <i>Systematic Biology</i> , 2021, 70, 976-996.	2.7	12
267	Jaw shape and mechanical advantage are indicative of diet in Mesozoic mammals. <i>Communications Biology</i> , 2021, 4, 242.	2.0	22
268	Infectious recombinant Senecavirus A expressing novel reporter proteins. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2385-2397.	1.7	11
269	Ultraconserved Elements Improve the Resolution of Difficult Nodes within the Rapid Radiation of Neotropical Sigmodontine Rodents (Cricetidae: Sigmodontinae). <i>Systematic Biology</i> , 2021, 70, 1090-1100.	2.7	17
270	Species Tree Estimation from Gene Trees by Minimizing Deep Coalescence and Maximizing Quartet Consistency: A Comparative Study and the Presence of Pseudo Species Tree Terraces. <i>Systematic Biology</i> , 2021, 70, 1213-1231.	2.7	5
271	Diverse phylogenomic datasets uncover a concordant scenario of laurasiatherian interordinal relationships. <i>Molecular Phylogenetics and Evolution</i> , 2021, 157, 107065.	1.2	4
272	Phylogenomic conflict coincides with rapid morphological innovation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	40
273	Gene Duplication and Loss of <i>AANAT</i> in Mammals Driven by Rhythmic Adaptations. <i>Molecular Biology and Evolution</i> , 2021, 38, 3925-3937.	3.5	10

#	ARTICLE	IF	CITATIONS
274	Enhancing mitogenomic phylogeny and resolving the relationships of extinct megafaunal placental mammals. <i>Molecular Phylogenetics and Evolution</i> , 2021, 158, 107082.	1.2	7
275	Testing the Utility of Alternative Metrics of Branch Support to Address the Ancient Evolutionary Radiation of Tunas, Stromateoids, and Allies (Teleostei: Pelagiaria). <i>Systematic Biology</i> , 2021, 70, 1123-1144.	2.7	19
276	Physcraper: a Python package for continually updated phylogenetic trees using the Open Tree of Life. <i>BMC Bioinformatics</i> , 2021, 22, 355.	1.2	2
277	Defining Coalescent Genes: Theory Meets Practice in Organelle Phylogenomics. <i>Systematic Biology</i> , 2022, 71, 476-489.	2.7	47
278	wQFM: highly accurate genome-scale species tree estimation from weighted quartets. <i>Bioinformatics</i> , 2021, 37, 3734-3743.	1.8	17
279	Concordance-Based Approaches for the Inference of Relationships and Molecular Rates with Phylogenomic Data Sets. <i>Systematic Biology</i> , 2022, 71, 943-958.	2.7	11
280	Out of Africa: A New Afrotheria Lineage Rises From Extinct South American Mammals. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	4
282	Phylogenetics of mud snakes (Squamata: Serpentes: Homalopsidae): A paradox of both undescribed diversity and taxonomic inflation. <i>Molecular Phylogenetics and Evolution</i> , 2021, 160, 107109.	1.2	17
283	Rapid Radiation and Rampant Reticulation: Phylogenomics of South American <i>Liolaemus</i> Lizards. <i>Systematic Biology</i> , 2022, 71, 286-300.	2.7	20
285	Gene tree quality affects empirical coalescent branch length estimation. <i>Zoologica Scripta</i> , 0, , .	0.7	9
286	Low-Coverage Whole Genomes Reveal the Higher Phylogeny of Green Lacewings. <i>Insects</i> , 2021, 12, 857.	1.0	4
287	Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps. <i>Nature Computational Science</i> , 2021, 1, 573-577.	3.8	10
288	The Evolution of Photoreceptors and Visual Photopigments in Vertebrates. , 2014, , 163-217.		17
289	Accumulated Coalescence Rank and Excess Gene Count for Species Tree Inference. <i>Lecture Notes in Computer Science</i> , 2016, , 93-105.	1.0	1
291	Testis-enriched heat shock protein A2 (HSPA2): Adaptive advantages of the birds with internal testes over the mammals with testicular descent. <i>Scientific Reports</i> , 2016, 6, 18770.	1.6	8
292	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	2.7	47
310	Red Algal Phylogenomics Provides a Robust Framework for Inferring Evolution of Key Metabolic Pathways. <i>PLOS Currents</i> , 2016, 8, .	1.4	14
311	Coalescent-Based Genome Analyses Resolve the Early Branches of the Euarchontoglires. <i>PLoS ONE</i> , 2013, 8, e60019.	1.1	43

#	ARTICLE	IF	CITATIONS
312	Weighted Statistical Binning: Enabling Statistically Consistent Genome-Scale Phylogenetic Analyses. PLoS ONE, 2015, 10, e0129183.	1.1	98
313	The Value of Molecular vs. Morphometric and Acoustic Information for Species Identification Using Sympatric Molossid Bats. PLoS ONE, 2016, 11, e0150780.	1.1	30
314	Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction. PLoS ONE, 2017, 12, e0182238.	1.1	71
315	Conserved sequences identify the closest living relatives of primates. Zoological Research, 2019, 40, 532-540.	0.9	8
316	Summary of Laurasiatheria (Mammalia) Phylogeny. Zoological Research, 2013, 33, 65-74.	0.6	10
317	Error in Phylogenetic Estimation for Bushes in the Tree of Life. Journal of Phylogenetics & Evolutionary Biology, 2013, 01, .	0.2	75
318	On the Illogic of Coalescence Simulations for Distinguishing the Causes of Conflict among Gene Trees. Journal of Phylogenetics & Evolutionary Biology, 2018, 06, .	0.2	3
320	Phylogenomics of white-eyes, a "great speciator", reveals Indonesian archipelago as the center of lineage diversity. ELife, 2020, 9, .	2.8	17
321	Ten genes and two topologies: an exploration of higher relationships in skipper butterflies (Hesperiidae). PeerJ, 2016, 4, e2653.	0.9	44
322	Evolution of the patellar sesamoid bone in mammals. PeerJ, 2017, 5, e3103.	0.9	39
324	Molecular Evidence of Primate Origins and Evolution. , 2013, , 1-47.		0
326	Molecular Evidence on Primate Origins and Evolution. , 2015, , 1083-1135.		3
327	Couplet Supertree Based Species Tree Estimation. Lecture Notes in Computer Science, 2015, , 48-59.	1.0	0
332	Preliminary Behavioral, Pathological and Transcriptome Studies of Tree Shrew: Evidence for a Complementary Small-Animal Alzheimer's Disease Model. Pakistan Journal of Zoology, 2017, 49, 1231-1241.	0.1	1
342	The Evolutionary History of Vertebrate Adhesion GPCRs and Its Implication on Their Classification. International Journal of Molecular Sciences, 2021, 22, 11803.	1.8	7
347	Gene-tree misrooting drives conflicts in phylogenomic coalescent analyses of palaeognath birds. Molecular Phylogenetics and Evolution, 2022, 167, 107344.	1.2	16
352	How challenging RADseq data turned out to favor coalescent-based species tree inference. A case study in Aichryson (Crassulaceae). Molecular Phylogenetics and Evolution, 2022, 167, 107342.	1.2	14
354	Comparing Partitioned Models to Mixture Models: Do Information Criteria Apply?. Systematic Biology, 2022, 71, 1541-1548.	2.7	11

#	ARTICLE	IF	CITATIONS
355	How to Tackle Phylogenetic Discordance in Recent and Rapidly Radiating Groups? Developing a Workflow Using Loricaria (Asteraceae) as an Example. <i>Frontiers in Plant Science</i> , 2021, 12, 765719.	1.7	12
356	Rocks and clocks revised: New promises and challenges in dating the primate tree of life. <i>Evolutionary Anthropology</i> , 2022, , .	1.7	8
357	StarBeast3: Adaptive Parallelized Bayesian Inference under the Multispecies Coalescent. <i>Systematic Biology</i> , 2022, 71, 901-916.	2.7	29
358	Champagne: Automated Whole-Genome Phylogenomic Character Matrix Method Using Large Genomic Indels for Homoplasy-Free Inference. <i>Genome Biology and Evolution</i> , 2022, 14, .	1.1	3
359	Scalable Species Tree Inference with External Constraints. <i>Journal of Computational Biology</i> , 2022, 29, 664-678.	0.8	1
361	Phylotranscriptomic insights into a Mesoproterozoicâ€“Neoproterozoic origin and early radiation of green seaweeds (Ulvophyceae). <i>Nature Communications</i> , 2022, 13, 1610.	5.8	21
362	Investigating Phylogenetic Placement and Species-Level Relationships in a Recent Radiation of <i>Mentzelia</i> section <i>Bartonia</i> (Loasaceae) from the Mojave Desert. <i>Systematic Botany</i> , 2022, 47, 140-151.	0.2	3
363	Quintet Rooting: rooting species trees under the multi-species coalescent model. <i>Bioinformatics</i> , 2022, 38, i109-i117.	1.8	6
366	Advances in phylogenomics. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2014, 36, 669-78.	0.1	0
367	Contradictory Phylogenetic Signals in the Laurasiatheria Anomaly Zone. <i>Genes</i> , 2022, 13, 766.	1.0	7
368	Euarchontoglires Challenged by Incomplete Lineage Sorting. <i>Genes</i> , 2022, 13, 774.	1.0	2
370	Alterations of Dopamine Receptors and the Adaptive Changes of L-Type Calcium Channel Subtypes Regulate Cocaine-Seeking Habit in Tree Shrew. <i>Life</i> , 2022, 12, 984.	1.1	0
371	Simultaneously collecting coding and non-coding phylogenomic data using homemade full-length cDNA probes, tested by resolving the high-level relationships of Colubridae. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
372	The complete mitochondrial genome of <i>Talpa martinorum</i> (Mammalia: Talpidae), a mole species endemic to Thrace: genome content and phylogenetic considerations. <i>Genetica</i> , 2022, 150, 317-325.	0.5	2
373	Molecular insights on the conflicting generic boundaries in the <i>Carduncellus</i> â€“ <i>Carthamus</i> complex (Compositae). <i>Taxon</i> , 2022, 71, 1268-1286.	0.4	2
375	Exploring Conflicts in Whole Genome Phylogenetics: A Case Study Within Manakins (Aves: Pipridae). <i>Systematic Biology</i> , 2023, 72, 161-178.	2.7	2
376	The evolution and polymorphism of mono-amino acid repeats in androgen receptor and their regulatory role in health and disease. <i>Frontiers in Medicine</i> , 0, 9, .	1.2	2
377	OrthoSNAP: A tree splitting and pruning algorithm for retrieving single-copy orthologs from gene family trees. <i>PLoS Biology</i> , 2022, 20, e3001827.	2.6	10

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378	Taming the selection of optimal substitution models in Phylogenomics by site subsampling and upsampling. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	0
379	The Sourp Genome (<i>Annona muricata</i> L., Annonaceae). <i>Compendium of Plant Genomes</i> , 2022, , 149-174.	0.3	0
380	Concordance and Discordance in the Phylogenomics of the Wrasses and Parrotfishes (Teleostei): Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50 6	2.7	9
381	Did some extinct South American native ungulates arise from an afrothere ancestor? A critical appraisal of Avilla and MothÃ©â€™s (2021) Sudamericungulata â€“ Panameridiungulata hypothesis. <i>Journal of Mammalian Evolution</i> , 0, , .	1.0	0
382	Diversification of Amazonian spiny tree rats in genus <i>Makalata</i> (Rodentia, Echimyidae): Cryptic diversity, geographic structure and drivers of speciation. <i>PLoS ONE</i> , 2022, 17, e0276475.	1.1	1
384	Effects of discordance between species and gene trees on phylogenetic diversity conservation. <i>Journal of Mathematical Biology</i> , 2023, 86, .	0.8	1
386	A new entelodont (Artiodactyla, Mammalia) from the late Eocene of China and its phylogenetic implications. <i>Journal of Systematic Palaeontology</i> , 2023, 21, .	0.6	1
387	Phylogenomics reveal extensive phylogenetic discordance due to incomplete lineage sorting following the rapid radiation of alpine butterflies (Papilionidae: <i>Parnassius</i>). <i>Systematic Entomology</i> , 2023, 48, 585-599.	1.7	2
388	Phylogenomic analyses of <i>Camellia</i> support reticulate evolution among major clades. <i>Molecular Phylogenetics and Evolution</i> , 2023, 182, 107744.	1.2	3
389	Evaluating Compression-Based Phylogeny Estimation in the Presence of Incomplete Lineage Sorting. <i>Journal of Computational Biology</i> , 2023, 30, 250-260.	0.8	1
390	The Sacro-Iliac Joint of the Felidae and Canidae and Their Large Ungulate Prey: An Example of Divergence and Convergence. <i>Fascinating Life Sciences</i> , 2023, , 79-114.	0.5	1
391	Evolutionary relationships of mitogenomes in a recently radiated Old World avian family. <i>Avian Research</i> , 2023, 14, 100097.	0.5	2
399	How Visualizations Have Revolutionized Taxonomy: From Macroscopic, to Microscopic, to Genetic. , 2023, , 55-88.		0