

Gene Trees in Species Trees

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Index to American Botanical Literature. <i>Brittonia</i> , 1997, 49, 406-430.	0.8	0
2	Who's related to whom? Recent results from molecular systematic studies. <i>Current Opinion in Plant Biology</i> , 1998, 1, 149-158.	3.5	17
3	Duplicate Genes and the Root of Angiosperms, with an Example Using Phytochrome Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 489-500.	1.2	31
4	Index to American Botanical Literature. <i>Brittonia</i> , 1998, 50, 129-154.	0.8	0
5	Trees within trees: phylogeny and historical associations. <i>Trends in Ecology and Evolution</i> , 1998, 13, 356-359.	4.2	261
6	Changing perspectives on the origin of eukaryotes. <i>Trends in Ecology and Evolution</i> , 1998, 13, 493-497.	4.2	34
7	Enigmatic phylogeny of skuas: an alternative hypothesis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1998, 265, 995-999.	1.2	19
8	Individuality and the Existence of Species Through Time. <i>Systematic Biology</i> , 1998, 47, 641-653.	2.7	81
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10	GeneTree: comparing gene and species phylogenies using reconciled trees. <i>Bioinformatics</i> , 1998, 14, 819-820.	1.8	221
11	The Systematics of Chuckwallas (<i>Sauromalus</i>) with a Phylogenetic Analysis of Other Iguanid Lizards. <i>Herpetological Monographs</i> , 1998, 12, 38.	1.1	36
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15	<i>Escherichia coli</i> molecular phylogeny using the incongruence length difference test. <i>Molecular Biology and Evolution</i> , 1998, 15, 1685-1695.	3.5	186
16	Partial β -tubulin gene sequences for evolutionary studies in the Basidiomycotina. <i>Mycologia</i> , 1999, 91, 468-474.	0.8	63
17	RAPDs and noncoding chloroplast DNA reveal a single origin of the cultivated <i>Allium fistulosum</i> from <i>A. altaicum</i> (Alliaceae). <i>American Journal of Botany</i> , 1999, 86, 554-562.	0.8	48
18	The Tangled Web: Gene Genealogies and the Origin of Eukaryotes. <i>American Naturalist</i> , 1999, 154, S137-S145.	1.0	33

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20	Phylogenetic Aspects of the Evolution of C4 Photosynthesis. , 1999, , 411-444.		84
21	Delimitation of Phylogenetic Species with DNA Sequences: A Critique of Davis and Nixon's Population Aggregation Analysis. <i>Systematic Biology</i> , 1999, 48, 199-213.	2.7	99
22	Hybridization and skua phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 1579-1585.	1.2	37
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26	What do we know about chrysidoid (Hymenoptera) relationships?. <i>Zoologica Scripta</i> , 1999, 28, 215-231.	0.7	64
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34	Phylogenetic reconstruction based on low copy DNA sequence data in an allopolyploid: The B genome of wheat. <i>Genome</i> , 1999, 42, 351-360.	0.9	89
35	Phylogenetic relationships of two anomalous species of <i>Pultenaea</i> (Fabaceae: Mirbelieae), and description of a new genus. <i>Taxon</i> , 1999, 48, 701-714.	0.4	18
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38	Phylogeny and Divergence Times in Pinaceae: Evidence from Three Genomes. <i>Molecular Biology and Evolution</i> , 2000, 17, 773-781.	3.5	226
39	Actin Gene Family Evolution and the Phylogeny of Coleoid Cephalopods (Mollusca: Cephalopoda). <i>Molecular Biology and Evolution</i> , 2000, 17, 1353-1370.	3.5	82
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41	Phylogenetic Relationships of Mormyrid Electric Fishes (Mormyridae; Teleostei) Inferred from Cytochrome b Sequences. <i>Molecular Phylogenetics and Evolution</i> , 2000, 14, 1-10.	1.2	58
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45	Phylogenetic relationships of the family Axinellidae (Porifera: Demospongiae) using morphological and molecular data. <i>Zoologica Scripta</i> , 2000, 29, 169-198.	0.7	66
46	TESTS OF PLEISTOCENE SPECIATION IN MONTANE GRASSHOPPERS (GENUS <i>MELANOPLUS</i>) FROM THE SKY ISLANDS OF WESTERN NORTH AMERICA. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1337-1348.	1.1	229
47	CLADISTS IN WONDERLAND. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1828-1832.	1.1	10
48	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE IN COALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1839-1854.	1.1	757
49	A plastid DNA phylogeny of the genus <i>Acacia</i> Miller (Acacieae, Leguminoseae). <i>Botanical Journal of the Linnean Society</i> , 2000, 132, 195-222.	0.8	53
50	Phylogenetic Species, Nested Hierarchies, and Character Fixation. <i>Cladistics</i> , 2000, 16, 364-384.	1.5	56
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52	Biology and conservation of sturgeon and paddlefish. <i>Reviews in Fish Biology and Fisheries</i> , 2000, 10, 355-392.	2.4	368
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54	The Current State Of Insect Molecular Systematics: A Thriving Tower of Babel. <i>Annual Review of Entomology</i> , 2000, 45, 1-54.	5.7	477

#	ARTICLE	IF	CITATIONS
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56	Morphometric Variation as an Indicator of Genetic Interactions Between Black-Capped and Carolina Chickadees at a Contact Zone in the Appalachian Mountains. <i>Auk</i> , 2000, 117, 427-444.	0.7	8
57	TESTS OF PLEISTOCENE SPECIATION IN MONTANE GRASSHOPPERS (GENUS MELANOPLUS) FROM THE SKY ISLANDS OF WESTERN NORTH AMERICA. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1337.	1.1	17
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63	Basal Angiosperm Phylogeny Inferred from Duplicate Phytochromes A and C. <i>International Journal of Plant Sciences</i> , 2000, 161, S41-S55.	0.6	98
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65	PERSPECTIVE: GENE DIVERGENCE, POPULATION DIVERGENCE, AND THE VARIANCE IN COALESCENCE TIME IN PHYLOGEOGRAPHIC STUDIES. <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 1839.	1.1	604
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68	Phylogenetic Species, Reproductive Mode, and Specificity of the Green Alga <i>Trebouxia</i> Forming Lichens with the Fungal Genus <i>Letharia</i> . <i>Bryologist</i> , 2000, 103, 645-660.	0.1	201
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#	ARTICLE	IF	CITATIONS
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74	Female Fertility and Single Nucleotide Polymorphism Comparisons in <i>Cylindrocladium pauciramsum</i> . <i>Plant Disease</i> , 2001, 85, 941-946.	0.7	20
75	Phylogenetic Utility and Evidence for Multiple Copies of Elongation Factor-1 α in the Spider Genus <i>Habronattus</i> (Araneae: Salticidae). <i>Molecular Biology and Evolution</i> , 2001, 18, 1512-1521.	3.5	31
76	A genealogical view of geographical variation. <i>Molecular Ecology</i> , 2001, 10, 2569-2576.	2.0	12
77	Phylogeny of <i>Bicyclus</i> (Lepidoptera: Nymphalidae) Inferred from COI, COII, and EF-1 α Gene Sequences. <i>Molecular Phylogenetics and Evolution</i> , 2001, 18, 264-281.	1.2	200
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83	Molecular Phylogeny of <i>Larrea</i> and Its Allies (Zygophyllaceae): Reticulate Evolution and the Probable Time of Creosote Bush Arrival to North America. <i>Molecular Phylogenetics and Evolution</i> , 2001, 21, 309-320.	1.2	75
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86	Difficulties in Detecting Hybridization. <i>Systematic Biology</i> , 2001, 50, 978-982.	2.7	157
87	Molecular and Morphological Phylogenetic Analysis of an Insular Radiation in Pacific Black Flies (<i>Simulium</i>). <i>Systematic Biology</i> , 2001, 50, 18-38.	2.7	19
88	Phylogenetic Relationships of Fig Wasps Pollinating Functionally Dioecious <i>Ficus</i> Based on Mitochondrial DNA Sequences and Morphology. <i>Systematic Biology</i> , 2001, 50, 243-267.	2.7	58
89	Phylogeny of Saxifragales (Angiosperms, Eudicots): Analysis of a Rapid, Ancient Radiation. <i>Systematic Biology</i> , 2001, 50, 817-847.	2.7	163
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91	Molecular and Morphological Phylogenetic Analysis of an Insular Radiation in Pacific Black Flies (<i>Simulium</i>). <i>Systematic Biology</i> , 2001, 50, 18-38.	2.7	37
92	Exploring Data Interaction and Nucleotide Alignment in a Multiple Gene Analysis of <i>Ips</i> (Coleoptera: Tj ETQq1 1 0.784314 rgBT ₁ /Over 141	2.7	141
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104	Recombination in Evolutionary Genomics. <i>Annual Review of Genetics</i> , 2002, 36, 75-97.	3.2	266
105	Utility of Low-Copy Nuclear Gene Sequences in Plant Phylogenetics. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2002, 37, 121-147.	2.3	319
106	Troubleshooting Molecular Phylogenetic Analyses. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2002, 33, 49-72.	6.7	270
107	Estimating Divergence Times from Molecular Data on Phylogenetic and Population Genetic Timescales. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2002, 33, 707-740.	6.7	521
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#	ARTICLE	IF	CITATIONS
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110	One hundred and seventeen clades of euagarics. <i>Molecular Phylogenetics and Evolution</i> , 2002, 23, 357-400.	1.2	583
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114	Molecular evolution of Holarctic martens (genus <i>Martes</i> , Mammalia: Carnivora: Mustelidae). <i>Molecular Phylogenetics and Evolution</i> , 2002, 24, 169-179.	1.2	68
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128	Molecular systematics of armadillos (<i>Xenarthra</i> , Dasypodidae): contribution of maximum likelihood and Bayesian analyses of mitochondrial and nuclear genes. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 261-275.	1.2	76
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130	Incongruent nuclear and mitochondrial phylogeographic patterns in the <i>Timarcha goettingensis</i> species complex (Coleoptera, Chrysomelidae). <i>Journal of Evolutionary Biology</i> , 2003, 16, 833-843.	0.8	41
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133	Genome-scale approaches to resolving incongruence in molecular phylogenies. <i>Nature</i> , 2003, 425, 798-804.	13.7	1,366
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1089	Coalescent Histories for Lodgepole Species Trees. <i>Journal of Computational Biology</i> , 2015, 22, 918-929.	0.8	15
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1317	Reticulate Evolution in <i>Elatine</i> L. (Elatinaceae), a Predominantly Autogamous Genus of Aquatic Plants. <i>Systematic Botany</i> , 2017, 42, 87-95.	0.2	10
1318	Evolutionary and domestication history of <i>Cucurbita</i> (pumpkin and squash) species inferred from 44 nuclear loci. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 98-109.	1.2	67
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#	ARTICLE	IF	CITATIONS
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1339	Genetic studies in the recently divergent <i>Eligmodontia puerulus</i> and <i>E. moreni</i> (Rodentia, Cricetidae,) Tj ETQq1 1 0.784314 rgBT /Overlock	0.8	4
1340	Multilocus coalescent species delimitation to evaluate traditionally defined morphotypes in <i>Hydrangea</i> sect. <i>Asperae</i> (Hydrangeaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 114, 415-425.	1.2	3
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1348	Exploring Evolutionary Relationships Across the Genome Using Topology Weighting. <i>Genetics</i> , 2017, 206, 429-438.	1.2	193
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#	ARTICLE	IF	CITATIONS
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1357	Phylogeographic and phylogenetic analysis for <i>Tripterygium</i> species delimitation. <i>Ecology and Evolution</i> , 2017, 7, 8612-8623.	0.8	16
1358	ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. <i>Lecture Notes in Computer Science</i> , 2017, , 53-75.	1.0	129
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1366	The evolutionary history of <i>Senna</i> ser. <i>Aphyllae</i> (Leguminosae "Caesalpinioideae), an endemic clade of southern South America. <i>Plant Systematics and Evolution</i> , 2017, 303, 1351-1366.	0.3	3
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#	ARTICLE	IF	CITATIONS
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1372	A biologist's guide to Bayesian phylogenetic analysis. <i>Nature Ecology and Evolution</i> , 2017, 1, 1446-1454.	3.4	154
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1377	Species trees from consensus single nucleotide polymorphism (SNP) data: Testing phylogenetic approaches with simulated and empirical data. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 192-201.	1.2	16
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1385	Inferring incomplete lineage sorting, duplications, transfers and losses with reconciliations. <i>Journal of Theoretical Biology</i> , 2017, 432, 1-13.	0.8	30
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#	ARTICLE	IF	CITATIONS
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1391	Widespread paleopolyploidy, gene tree conflict, and recalcitrant relationships among the carnivorous Caryophyllales. <i>American Journal of Botany</i> , 2017, 104, 858-867.	0.8	62
1392	Mechanical Transgressive Segregation and the Rapid Origin of Trophic Novelty. <i>Scientific Reports</i> , 2017, 7, 40306.	1.6	29
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1394	Reconciliation feasibility in the presence of gene duplication, loss, and coalescence with multiple individuals per species. <i>BMC Bioinformatics</i> , 2017, 18, 292.	1.2	7
1395	Integrative taxonomy by molecular species delimitation: multi-locus data corroborate a new species of Balkan Drusinae micro-endemics. <i>BMC Evolutionary Biology</i> , 2017, 17, 129.	3.2	53
1396	Hirudins and hirudin-like factors in Hirudinidae: implications for function and phylogenetic relationships. <i>Parasitology Research</i> , 2017, 116, 313-325.	0.6	33
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1402	Resolution of a concatenation/coalescence kerfuffle: partitioned coalescence support and a robust family-level tree for Mammalia. <i>Cladistics</i> , 2017, 33, 295-332.	1.5	70
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1405	Resolving incongruence: Species of hybrid origin in <i>Columnea</i> (Gesneriaceae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 228-240.	1.2	10
1406	Expected pairwise congruence among gene trees under the coalescent model. <i>Molecular Phylogenetics and Evolution</i> , 2017, 106, 144-150.	1.2	5
1407	Multi-rate Poisson tree processes for single-locus species delimitation under maximum likelihood and Markov chain Monte Carlo. <i>Bioinformatics</i> , 2017, 33, 1630-1638.	1.8	580

#	ARTICLE	IF	CITATIONS
1408	A phylogenetic circumscription of <i>Silene</i> sect. <i>Siphonomorpha</i> (Caryophyllaceae) in the Mediterranean Basin. <i>Taxon</i> , 2017, 66, 91-108.	0.4	26
1409	Distance-based species tree estimation under the coalescent: Information-theoretic trade-off between number of loci and sequence length. <i>Annals of Applied Probability</i> , 2017, 27, .	0.6	5
1410	Fungal Phylogeny in the Age of Genomics: Insights Into Phylogenetic Inference From Genome-Scale Datasets. <i>Advances in Genetics</i> , 2017, 100, 49-72.	0.8	16
1412	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
1413	Avian introgression in the genomic era. <i>Avian Research</i> , 2017, 8, .	0.5	58
1414	Molecular phylogeny of the genus <i>Themisto</i> (Guérin, 1925) (Amphipoda: Hyperiididae) in the Northern Hemisphere. <i>Journal of Crustacean Biology</i> , 2017, 37, 732-742.	0.3	8
1415	Comparing mitogenomic timetrees for two African savannah primate genera (<i>Chlorocebus</i> and <i>Papio</i>). <i>Zoological Journal of the Linnean Society</i> , 2017, 181, 471-483.	1.0	15
1416	Principal component analysis and the locus of the Fréchet mean in the space of phylogenetic trees. <i>Biometrika</i> , 2017, 104, 901-922.	1.3	23
1417	Probing planetary biodiversity with DNA barcodes: The Noctuoidea of North America. <i>PLoS ONE</i> , 2017, 12, e0178548.	1.1	49
1418	The influence of molecular markers and methods on inferring the phylogenetic relationships between the representatives of the Arini (parrots, Psittaciformes), determined on the basis of their complete mitochondrial genomes. <i>BMC Evolutionary Biology</i> , 2017, 17, 166.	3.2	15
1419	A history of hybrids? Genomic patterns of introgression in the True Geese. <i>BMC Evolutionary Biology</i> , 2017, 17, 201.	3.2	47
1420	Rooting phylogenetic trees under the coalescent model using site pattern probabilities. <i>BMC Evolutionary Biology</i> , 2017, 17, 263.	3.2	12
1421	Reconstructing the Evolutionary History of Powdery Mildew Lineages (<i>Blumeria graminis</i>) at Different Evolutionary Time Scales with NGS Data. <i>Genome Biology and Evolution</i> , 2017, 9, 446-456.	1.1	34
1422	Phylogenomic Insights into Mouse Evolution Using a Pseudoreference Approach. <i>Genome Biology and Evolution</i> , 2017, 9, 726-739.	1.1	47
1423	Mammalian Evolution: The Phylogenetics Story. , 2017, , 77-86.		1
1424	The Performance of Two Supertree Schemes Compared Using Synthetic and Real Data Quartet Input. <i>Journal of Molecular Evolution</i> , 2018, 86, 150-165.	0.8	5
1425	Inferring Phylogenetic Networks Using PhyloNet. <i>Systematic Biology</i> , 2018, 67, 735-740.	2.7	242
1426	Exploring species boundaries with multiple genetic loci using empirical data from nonbiting midges. <i>Zoologica Scripta</i> , 2018, 47, 325-341.	0.7	18

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1428	Can we build it? Yes we can, but should we use it? Assessing the quality and value of a very large phylogeny of <i>Ampanulid</i> angiosperms. <i>American Journal of Botany</i> , 2018, 105, 417-432.	0.8	45
1429	Phylogenetic Comparative Methods on Phylogenetic Networks with Reticulations. <i>Systematic Biology</i> , 2018, 67, 800-820.	2.7	88
1430	Molecular evolution of key metabolic genes during transitions to C_4 and <i>CAM</i> photosynthesis. <i>American Journal of Botany</i> , 2018, 105, 602-613.	0.8	24
1431	Gene tree discordance and coalescent methods support ancient intergeneric hybridisation between <i>Dasymaschalon</i> and <i>Friesodielsia</i> (Annonaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 14-29.	1.2	19
1432	Phylogenomic analyses reveal a deep history of hybridization and polyploidy in the Neotropical genus <i>Lachemilla</i> (Rosaceae). <i>New Phytologist</i> , 2018, 218, 1668-1684.	3.5	141
1433	Hybridization could be a common phenomenon within the highly diverse lizard genus <i>Liolaemus</i> . <i>Journal of Evolutionary Biology</i> , 2018, 31, 893-903.	0.8	24
1434	Phylogenetic relationships within a patagonian clade of reptiles (Liolaemidae: Phymaturus) based on DNA sequences and morphology. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2018, 56, 549-569.	0.6	7
1435	Comparison of taxon-specific versus general locus sets for targeted sequence capture in plant phylogenomics. <i>Applications in Plant Sciences</i> , 2018, 6, e1032.	0.8	55
1436	Relative Optimality Conditions and Algorithms for Treespace Fractal Means. <i>SIAM Journal on Optimization</i> , 2018, 28, 959-988.	1.2	3
1437	Mitochondrial genome diversity and population structure of two western honey bee subspecies in the Republic of South Africa. <i>Scientific Reports</i> , 2018, 8, 1333.	1.6	23
1438	Bayesian selection of misspecified models is overconfident and may cause spurious posterior probabilities for phylogenetic trees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1854-1859.	3.3	61
1439	Genetic and morphological support for possible sympatric origin of fish from subterranean habitats. <i>Scientific Reports</i> , 2018, 8, 2909.	1.6	16
1440	Phylogenetics and systematics of <i>Eria</i> and related genera (Orchidaceae: Podochileae). <i>Botanical Journal of the Linnean Society</i> , 2018, 186, 179-201.	0.8	16
1441	Bayesian Divergence-Time Estimation with Genome-Wide Single-Nucleotide Polymorphism Data of Sea Catfishes (Ariidae) Supports Miocene Closure of the Panamanian Isthmus. <i>Systematic Biology</i> , 2018, 67, 681-699.	2.7	137
1442	Genomics-informed species delimitation to support morphological identification of anglewing butterflies (Lepidoptera: Nymphalidae: Polytonia). <i>Zoological Journal of the Linnean Society</i> , 2018, 183, 372-389.	1.0	1
1443	DiscoVista: Interpretable visualizations of gene tree discordance. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 110-115.	1.2	106
1444	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413

#	ARTICLE	IF	CITATIONS
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1446	Phylogenomics. <i>Methods in Molecular Biology</i> , 2018, 1704, 103-187.	0.4	15
1447	Fungal species and their boundaries matter – Definitions, mechanisms and practical implications. <i>Fungal Biology Reviews</i> , 2018, 32, 104-116.	1.9	51
1448	An In Silico Comparison of Protocols for Dated Phylogenomics. <i>Systematic Biology</i> , 2018, 67, 633-650.	2.7	24
1449	Improved Maximum Parsimony Models for Phylogenetic Networks. <i>Systematic Biology</i> , 2018, 67, 518-542.	2.7	10
1450	<sc>GPS</sc>it: An automated method for evolutionary analysis of nonculturable ciliated microeukaryotes. <i>Molecular Ecology Resources</i> , 2018, 18, 700-713.	2.2	36
1451	Gene flow analysis method, the D-statistic, is robust in a wide parameter space. <i>BMC Bioinformatics</i> , 2018, 19, 10.	1.2	68
1452	OCTAL: Optimal Completion of gene trees in polynomial time. <i>Algorithms for Molecular Biology</i> , 2018, 13, 6.	0.3	12
1453	Integrative taxonomy and the operationalization of evolutionary independence. <i>European Journal for Philosophy of Science</i> , 2018, 8, 587-603.	0.6	19
1454	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
1455	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
1456	Multilocus Phylogenetics of New World Milkweed Vines (Apocynaceae, Asclepiadoideae, Gonolobinae). <i>Systematic Botany</i> , 2018, 43, 77-96.	0.2	13
1457	Multi-locus phylogenetics, lineage sorting, and reticulation in <i>Pinus</i> subsection <i>Australes</i> . <i>American Journal of Botany</i> , 2018, 105, 711-725.	0.8	51
1458	A matter of phylogenetic scale: Distinguishing incomplete lineage sorting from lateral gene transfer as the cause of gene tree discord in recent versus deep diversification histories. <i>American Journal of Botany</i> , 2018, 105, 376-384.	0.8	45
1459	Gene transfers can date the tree of life. <i>Nature Ecology and Evolution</i> , 2018, 2, 904-909.	3.4	52
1460	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
1461	Phylogenomic Analysis of the Explosive Adaptive Radiation of the Espeletia Complex (Asteraceae) in the Tropical Andes. <i>Systematic Biology</i> , 2018, 67, 1041-1060.	2.7	118
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#	ARTICLE	IF	CITATIONS
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1464	Missing data, clade support and "reticulation" the molecular systematics of <i>Heliconius</i> and related genera (Lepidoptera: Nymphalidae) re-examined. <i>Cladistics</i> , 2018, 34, 151-166.	1.5	11
1465	Optimal data partitioning, multispecies coalescent and Bayesian concordance analyses resolve early divergences of the grape family (Vitaceae). <i>Cladistics</i> , 2018, 34, 57-77.	1.5	44
1466	Efficient Quartet Representations of Trees and Applications to Supertree and Summary Methods. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1010-1015.	1.9	5
1467	Phylogeny and historical biogeography of silky lacewings (Insecta: Neuroptera: Chrysomelidae). <i>Systematic Biology</i> , 2018, 67, 158-169.	1.7	5
1468	An Evaluation of Different Partitioning Strategies for Bayesian Estimation of Species Divergence Times. <i>Systematic Biology</i> , 2018, 67, 61-77.	2.7	32
1469	Phylogeny of the manta and devilrays (Chondrichthyes: mobulidae), with an updated taxonomic arrangement for the family. <i>Zoological Journal of the Linnean Society</i> , 2018, 182, 50-75.	1.0	113
1470	Detecting hybridization by likelihood calculation of gene tree extra lineages given explicit models. <i>Methods in Ecology and Evolution</i> , 2018, 9, 121-133.	2.2	8
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1472	Signal, Uncertainty, and Conflict in Phylogenomic Data for a Diverse Lineage of Microbial Eukaryotes (Diatoms, Bacillariophyta). <i>Molecular Biology and Evolution</i> , 2018, 35, 80-93.	3.5	43
1473	Issues and Perspectives in Species Delimitation using Phenotypic Data: Atlantean Evolution in Darwin's Finches. <i>Systematic Biology</i> , 2018, 67, 181-194.	2.7	48
1474	Impact of Model Violations on the Inference of Species Boundaries Under the Multispecies Coalescent. <i>Systematic Biology</i> , 2018, 67, 269-284.	2.7	76
1475	To Include or Not to Include: The Impact of Gene Filtering on Species Tree Estimation Methods. <i>Systematic Biology</i> , 2018, 67, 285-303.	2.7	189
1476	Exon-based phylogenomics strengthens the phylogeny of Neotropical cichlids and identifies remaining conflicting clades (Cichliformes: Cichlidae: Cichlinae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 232-243.	1.2	44
1477	Uncertainty in Phylogenetic Tree Estimates. <i>Journal of Computational and Graphical Statistics</i> , 2018, 27, 542-552.	0.9	15
1478	Transcriptome mining for phylogenetic markers in a recently radiated genus of tropical plants (<i>Renealmia</i> L.f., Zingiberaceae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 119, 13-24.	1.2	13
1479	Genomic data resolve gene tree discordance in spiderhunters (Nectariniidae, Arachnothera). <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 151-157.	1.2	7
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#	ARTICLE	IF	CITATIONS
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1482	Bayesian molecular dating: opening up the black box. <i>Biological Reviews</i> , 2018, 93, 1165-1191.	4.7	128
1483	Cryptic diversity in <i>Rhampholeon boulengeri</i> (Sauria: Chamaeleonidae), a pygmy chameleon from the Albertine Rift biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2018, 122, 125-141.	1.2	17
1484	Alternative methods of phylogenetic inference for the Patagonian lizard group <i>Liolaemus elongatus-kriegi</i> (Iguania: Liolaemini) based on mitochondrial and nuclear markers. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 158-169.	1.2	10
1485	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
1486	Plastid capture and resultant fitness costs of hybridization in the Hirta clade of southern African <i>Oxalis</i> . <i>South African Journal of Botany</i> , 2018, 118, 329-341.	1.2	4
1487	HomBlocks: A multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. <i>Genomics</i> , 2018, 110, 18-22.	1.3	183
1488	Reconstruction of real and simulated phylogenies based on quartet plurality inference. <i>BMC Genomics</i> , 2018, 19, 570.	1.2	1
1489	Species identification and connectivity of marine amphipods in Canada's three oceans. <i>PLoS ONE</i> , 2018, 13, e0197174.	1.1	22
1490	Biological Research, 2018,		
1491	Integrative Taxonomy of Birds: The Nature and Delimitation of Species. <i>Fascinating Life Sciences</i> , 2018, , 9-37.	0.5	34
1492	Towards an accurate and efficient heuristic for species/gene tree co-estimation. <i>Bioinformatics</i> , 2018, 34, i697-i705.	1.8	10
1493	Integrative taxonomy reveals hidden species within a common fungal parasite of ladybirds. <i>Scientific Reports</i> , 2018, 8, 15966.	1.6	52
1494	Phylogenetic Consensus for Exact Median Trees. , 2018, , .		2
1495	Quantifying the risk of hemiplasy in phylogenetic inference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12787-12792.	3.3	49
1496	NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees. <i>Lecture Notes in Computer Science</i> , 2018, , 260-276.	1.0	11
1497	Towards integrative taxonomy in Neotropical botany: disentangling the <i>Pagamea guianensis</i> species complex (Rubiaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 188, 213-231.	0.8	41
1498	Minimizing the deep coalescence cost. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840021.	0.3	1

#	ARTICLE	IF	CITATIONS
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1501	Mitochondrial introgression and interspecies recombination in the <i>Fusarium fujikuroi</i> species complex. <i>IMA Fungus</i> , 2018, 9, 37-48.	1.7	28
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1503	Genetic diversity and biogeography of <i>T. officinale</i> inferred from multi locus sequence typing approach. <i>PLoS ONE</i> , 2018, 13, e0203275.	1.1	3
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1505	On the Variance of Internode Distance Under the Multispecies Coalescent. <i>Lecture Notes in Computer Science</i> , 2018, , 196-206.	1.0	1
1506	Three new genome assemblies support a rapid radiation in <i>Musa acuminata</i> (wild banana). <i>Genome Biology and Evolution</i> , 2018, 10, 3129-3140.	1.1	29
1507	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. <i>Communications Biology</i> , 2018, 1, 169.	2.0	84
1508	Universal common ancestry, LUCA, and the Tree of Life: three distinct hypotheses about the evolution of life. <i>Biology and Philosophy</i> , 2018, 33, 1.	0.7	32
1509	Speciation genes are more likely to have discordant gene trees. <i>Evolution Letters</i> , 2018, 2, 281-296.	1.6	10
1510	Evidence of body size and shape stasis driven by selection in Patagonian lizards of the <i>Phymaturus patagonicus</i> clade (Squamata: Liolaemini). <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 226-241.	1.2	11
1511	Pleistocene diversification in an ancient lineage: a role for glacial cycles in the evolutionary history of <i>Dioon</i> Lindl. (Zamiaceae). <i>American Journal of Botany</i> , 2018, 105, 1512-1530.	0.8	18
1512	Demographic inference in barn swallows using whole-genome data shows signal for bottleneck and subspecies differentiation during the Holocene. <i>Molecular Ecology</i> , 2018, 27, 4200-4212.	2.0	29
1513	Rapid diversification and hybridization have shaped the dynamic history of the genus <i>Elaenia</i> . <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 522-533.	1.2	9
1514	A tangle of forms and phylogeny: Extensive morphological homoplasy and molecular clock heterogeneity in <i>Bonnetina</i> and related tarantulas. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 55-73.	1.2	25
1515	Revisiting the Darwinian shortfall in biodiversity conservation. <i>Biodiversity and Conservation</i> , 2018, 27, 2859-2875.	1.2	37
1516	Molecular phylogenetic species in <i>Alternaria</i> pathogens infecting pistachio and wild relatives. <i>3 Biotech</i> , 2018, 8, 250.	1.1	6

#	ARTICLE	IF	CITATIONS
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1518	An evolutionary model motivated by physicochemical properties of amino acids reveals variation among proteins. <i>Bioinformatics</i> , 2018, 34, i350-i356.	1.8	12
1519	Which Model(s) Explain Biodiversity?. , 2018, , 39-61.		0
1520	Consistency and convergence rate of phylogenetic inference via regularization. <i>Annals of Statistics</i> , 2018, 46, 1481-1512.	1.4	5
1521	An integrative species delimitation approach reveals fine-scale endemism and substantial unrecognized avian diversity in the Philippine Archipelago. <i>Conservation Genetics</i> , 2018, 19, 1153-1168.	0.8	16
1522	Dissecting the basis of novel trait evolution in a radiation with widespread phylogenetic discordance. <i>Molecular Ecology</i> , 2018, 27, 3301-3316.	2.0	59
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1524	Resolving the rapid plant radiation of early diverging lineages in the tropical Zingiberales: Pushing the limits of genomic data. <i>Molecular Phylogenetics and Evolution</i> , 2018, 128, 55-68.	1.2	53
1525	Are species-pairs diverging lineages? A nine-locus analysis uncovers speciation among species-pairs of the <i>Lobaria meridionalis</i> -group (Ascomycota). <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 48-59.	1.2	5
1526	Species Tree Inference with BPP Using Genomic Sequences and the Multispecies Coalescent. <i>Molecular Biology and Evolution</i> , 2018, 35, 2585-2593.	3.5	265
1527	Reconciliation Feasibility of Non-binary Gene Trees Under a Duplication-Loss-Coalescence Model. <i>Lecture Notes in Computer Science</i> , 2018, , 11-23.	1.0	0
1529	Delimiting Coalescence Genes (C-Genes) in Phylogenomic Data Sets. <i>Genes</i> , 2018, 9, 123.	1.0	30
1530	Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. <i>Genes</i> , 2018, 9, 132.	1.0	107
1531	Taxonomic changes and description of two new species for the <i>Phyllodactylus lanei</i> complex (Gekkota: Phyllodactylidae) in Mexico. <i>Zootaxa</i> , 2018, 4407, 151-190.	0.2	11
1532	Detecting introgression despite phylogenetic uncertainty: The case of the South American siskins. <i>Molecular Ecology</i> , 2018, 27, 4350-4367.	2.0	18
1533	Correlated Selection on Amino Acid Deletion and Replacement in Mammalian Protein Sequences. <i>Journal of Molecular Evolution</i> , 2018, 86, 365-378.	0.8	1
1534	Evaluating Model Performance in Evolutionary Biology. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2018, 49, 95-114.	3.8	39
1535	Inferring Ancient Relationships with Genomic Data: A Commentary on Current Practices. <i>Integrative and Comparative Biology</i> , 2018, 58, 623-639.	0.9	14

#	ARTICLE	IF	CITATIONS
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1537	Anchored hybrid enrichment generated nuclear, plastid and mitochondrial markers resolve the <i>Lepanthes horrida</i> (Orchidaceae: Pleurothallidinae) species complex. <i>Molecular Phylogenetics and Evolution</i> , 2018, 129, 27-47.	1.2	42
1538	The performance of coalescent-based species tree estimation methods under models of missing data. <i>BMC Genomics</i> , 2018, 19, 286.	1.2	60
1539	SIESTA: enhancing searches for optimal supertrees and species trees. <i>BMC Genomics</i> , 2018, 19, 252.	1.2	4
1540	Allele phasing is critical to revealing a shared allopolyploid origin of <i>Medicago arborea</i> and <i>M. strasseri</i> (Fabaceae). <i>BMC Evolutionary Biology</i> , 2018, 18, 9.	3.2	34
1541	Phylogenomics of a rapid radiation: the Australian rainbow skinks. <i>BMC Evolutionary Biology</i> , 2018, 18, 15.	3.2	26
1542	Gene tree parsimony for incomplete gene trees: addressing true biological loss. <i>Algorithms for Molecular Biology</i> , 2018, 13, 1.	0.3	30
1543	ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. <i>BMC Bioinformatics</i> , 2018, 19, 153.	1.2	1,451
1544	Integrative identification of incipient lineages in <i>Heuchera longiflora</i> (Saxifragaceae). <i>Botanical Journal of the Linnean Society</i> , 2018, 187, 327-345.	0.8	6
1545	From cacti to carnivores: Improved phylotranscriptomic sampling and hierarchical homology inference provide further insight into the evolution of Caryophyllales. <i>American Journal of Botany</i> , 2018, 105, 446-462.	0.8	87
1546	Phylogeny Estimation by Integration over Isolation with Migration Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2805-2818.	3.5	89
1547	Is population genetic structure of vascular plants shaped more by ecological or geographic factors? A study case on the Mediterranean endemic <i>Centaurea filiformis</i> (Asteraceae). <i>Plant Biology</i> , 2018, 20, 936-947.	1.8	6
1548	Harnessing the power of phylogenomics to disentangle the directionality and signatures of interkingdom host jumping in the parasitic fungal genus <i>Tolyposcladium</i> . <i>Mycologia</i> , 2018, 110, 104-117.	0.8	12
1549	Distinguishing Phylogenetic Networks. <i>SIAM Journal on Applied Algebra and Geometry</i> , 2018, 2, 72-93.	0.9	18
1550	Worldwide phylogeny of three-spined sticklebacks. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 613-625.	1.2	50
1551	Molecular phylogenetic analysis and generic delimitations in tribe Chiococceae (Cinchonoideae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i>	0.8	12
1552	Cryptic speciation associated with geographic and ecological divergence in two Amazonian <i>Heliconius</i> butterflies. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 233-249.	1.0	15
1553	Identifiability and Reconstructibility of Species Phylogenies Under a Modified Coalescent. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 408-430.	0.9	17

#	ARTICLE	IF	CITATIONS
1554	The Spectre of Too Many Species. <i>Systematic Biology</i> , 2019, 68, 168-181.	2.7	189
1555	Gondwanan vicariance or trans-Atlantic dispersal of cichlid fishes: a review of the molecular evidence. <i>Hydrobiologia</i> , 2019, 832, 9-37.	1.0	23
1556	A transcriptome-based resolution for a key taxonomic controversy in Cupressaceae. <i>Annals of Botany</i> , 2019, 123, 153-167.	1.4	18
1557	Enumeration of compact coalescent histories for matching gene trees and species trees. <i>Journal of Mathematical Biology</i> , 2019, 78, 155-188.	0.8	8
1558	Ongoing hybridization obscures phylogenetic relationships in the <i>Drosophila subquinaria</i> species complex. <i>Journal of Evolutionary Biology</i> , 2019, 32, 1093-1105.	0.8	9
1559	Evidence for sympatric speciation in a Wallacean ancient lake. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1898-1915.	1.1	23
1560	Identification and assessment of variable single-copy orthologous (SCO) nuclear loci for low-level phylogenomics: a case study in the genus <i>Rosa</i> (Rosaceae). <i>BMC Evolutionary Biology</i> , 2019, 19, 152.	3.2	16
1561	Population genomic evidence for radiative divergence of four <i>Orychophragmus</i> (Brassicaceae) species in eastern Asia. <i>Botanical Journal of the Linnean Society</i> , 2019, 191, 18-29.	0.8	8
1563	Phylogenomic Reconstruction of the Neotropical Poison Frogs (Dendrobatidae) and Their Conservation. <i>Diversity</i> , 2019, 11, 126.	0.7	23
1564	The Unconstrained Diameters of the Duplication-Loss Cost and the Loss Cost. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 18, 1-1.	1.9	0
1565	Speciation, gene flow, and seasonal migration in <i>Catharus</i> thrushes (Aves:Turdidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106564.	1.2	21
1566	TreeMerge: a new method for improving the scalability of species tree estimation methods. <i>Bioinformatics</i> , 2019, 35, i417-i426.	1.8	15
1567	Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model. <i>Methods in Molecular Biology</i> , 2019, 1910, 211-239.	0.4	30
1568	A customized nuclear target enrichment approach for developing a phylogenomic baseline for <i>Dioscorea</i> yams (Dioscoreaceae). <i>Applications in Plant Sciences</i> , 2019, 7, e11254.	0.8	49
1569	Comparative Phylogenomics, a Stepping Stone for Bird Biodiversity Studies. <i>Diversity</i> , 2019, 11, 115.	0.7	26
1570	Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge. <i>Algorithms for Molecular Biology</i> , 2019, 14, 14.	0.3	16
1571	A multigene phylogeny to infer the evolutionary history of Chaetocerotaceae (Bacillariophyta). <i>Molecular Phylogenetics and Evolution</i> , 2019, 140, 106575.	1.2	16
1572	Chance and predictability in evolution: The genomic basis of convergent dietary specializations in an adaptive radiation. <i>Molecular Ecology</i> , 2019, 28, 4028-4045.	2.0	21

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1574	What does mitogenomics tell us about the evolutionary history of the <i>Drosophila buzzatii</i> cluster (repleta group)?. PLoS ONE, 2019, 14, e0220676.	1.1	12
1575	Measuring evolutionary independence: A pragmatic approach to species classification. Biology and Philosophy, 2019, 34, 1.	0.7	5
1576	<i>Chloris circumfontinalis</i> (Poaceae): a recently discovered species from the saline scalds surrounding artesian springs in north-eastern Australia. Australian Systematic Botany, 2019, , .	0.3	0
1577	Consensus of all Solutions for Intractable Phylogenetic Tree Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	1.9	3
1578	Evaluating methodologies for species delimitation: the mismatch between phenotypes and genotypes in lichenized fungi (<i>Bryoria</i> sect. <i>Implexae</i>, <i>Parmeliaceae</i>). Persoonia: Molecular Phylogeny and Evolution of Fungi, 2019, 42, 75-100.	1.6	44
1579	Mitochondrial genomes of the bird genus <i>Piranga</i>: rates of sequence evolution, and discordance between mitochondrial and nuclear markers. Mitochondrial DNA Part B: Resources, 2019, 4, 2566-2569.	0.2	7
1580	What Is a Lineage?. Philosophy of Science, 2019, 86, 1099-1110.	0.5	7
1581	Accurate Inference of Tree Topologies from Multiple Sequence Alignments Using Deep Learning. Systematic Biology, 2020, 69, 221-233.	2.7	53
1582	Generation of Binary Tree-Child phylogenetic networks. PLoS Computational Biology, 2019, 15, e1007347.	1.5	7
1583	Phylogenomics resolves major relationships and reveals significant diversification rate shifts in the evolution of silk moths and relatives. BMC Evolutionary Biology, 2019, 19, 182.	3.2	49
1584	Conservation of Atypical Allostery in <i>C. elegans</i> UDP-Glucose Dehydrogenase. ACS Omega, 2019, 4, 16318-16329.	1.6	5
1585	Quartet-based inference of cell differentiation trees from ChIP-Seq histone modification data. PLoS ONE, 2019, 14, e0221270.	1.1	3
1586	Resolving Phylogenetic Relationships within Passeriformes Based on Mitochondrial Genes and Inferring the Evolution of Their Mitogenomes in Terms of Duplications. Genome Biology and Evolution, 2019, 11, 2824-2849.	1.1	32
1587	Taxonomic revision of the dolphin genus <i>Lagenorhynchus</i>. Marine Mammal Science, 2019, 35, 957-1057.	0.9	22
1588	New Divide-and-Conquer Techniques for Large-Scale Phylogenetic Estimation. Lecture Notes in Computer Science, 2019, , 3-21.	1.0	0
1589	Bioinformatics Research and Applications. Lecture Notes in Computer Science, 2019, , .	1.0	1
1590	Using INC Within Divide-and-Conquer Phylogeny Estimation. Lecture Notes in Computer Science, 2019, , 167-178.	1.0	5

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1592	Multiple historical processes obscure phylogenetic relationships in a taxonomically difficult group (Lobariaceae, Ascomycota). <i>Scientific Reports</i> , 2019, 9, 8968.	1.6	32
1593	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
1594	An invariants-based method for efficient identification of hybrid species from large-scale genomic data. <i>BMC Evolutionary Biology</i> , 2019, 19, 112.	3.2	55
1595	A next generation approach to species delimitation reveals the role of hybridization in a cryptic species complex of corals. <i>BMC Evolutionary Biology</i> , 2019, 19, 116.	3.2	75
1596	Multi-locus phylogenetic reconstructions reveal ample reticulate relationships among genera in Anthemideae subtribe Handeliinae (Compositae). <i>Plant Systematics and Evolution</i> , 2019, 305, 487-502.	0.3	3
1597	Phylogenomic analyses reveal intractable evolutionary history of a temperate bamboo genus (Poaceae: Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 30	1.8	14
1598	Intertidal or subtidal/circalittoral species: which appeared first? A phylogenetic approach to the evolution of non-planktotrophic species in Atlantic Archipelagos. <i>Marine Biology</i> , 2019, 166, 1.	0.7	7
1599	Computing a Consensus Phylogeny via Leaf Removal. <i>Lecture Notes in Computer Science</i> , 2019, , 3-15.	1.0	0
1600	Unifying Gene Duplication, Loss, and Coalescence on Phylogenetic Networks. <i>Lecture Notes in Computer Science</i> , 2019, , 40-51.	1.0	8
1601	Using nuclear loci and allelic variation to disentangle the phylogeny of Phyllostachys (Poaceae,) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 30	1.2	18
1602	A fossil-calibrated phylogenomic analysis of Daphnia and the Daphniidae. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 250-262.	1.2	43
1603	Coalescent-based species delimitation in the sand lizards of the Liolaemus wiegmannii complex (Squamata: Liolaemidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 89-101.	1.2	16
1604	PhyloToL: A Taxon/Gene-Rich Phylogenomic Pipeline to Explore Genome Evolution of Diverse Eukaryotes. <i>Molecular Biology and Evolution</i> , 2019, 36, 1831-1842.	3.5	23
1605	Dual colonization of European high-altitude areas from Asia by Callianthemum (Ranunculaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 431-443.	0.3	8
1607	Low-copy nuclear sequence data confirm complex patterns of farina evolution in notholaenid ferns (Pteridaceae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 138, 139-155.	1.2	14
1608	Complete plastome sequences of <i>Picea asperata</i> and <i>P. crassifolia</i> and comparative analyses with <i>P. abies</i> and <i>P. morrisonicola</i> . <i>Genome</i> , 2019, 62, 317-328.	0.9	5
1609	The Coral of Life. <i>Evolutionary Biology</i> , 2019, 46, 123-144.	0.5	7

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1611	Divide-and-Conquer Tree Estimation: Opportunities and Challenges. <i>Computational Biology</i> , 2019, , 121-150.	0.1	11
1612	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
1613	COI-based species delimitation in Indochinese <i>Tetraserica</i> chafers reveal hybridisation despite strong divergence in male copulation organs. <i>Organisms Diversity and Evolution</i> , 2019, 19, 277-286.	0.7	7
1614	Reconciling multiple genes trees via segmental duplications and losses. <i>Algorithms for Molecular Biology</i> , 2019, 14, 7.	0.3	15
1615	Reticulate evolution in nuclear Middle America causes discordance in the phylogeny of palmá€pitvipers (Viperidae: <i>Bothriechis</i>). <i>Journal of Biogeography</i> , 2019, 46, 833-844.	1.4	24
1616	The phylogenomic revolution and its conceptual innovations: a text mining approach. <i>Organisms Diversity and Evolution</i> , 2019, 19, 99-103.	0.7	8
1617	ASTRAL-MP: scaling ASTRAL to very large datasets using randomization and parallelization. <i>Bioinformatics</i> , 2019, 35, 3961-3969.	1.8	57
1618	Living on the edge: Exploring the role of coastal refugia in the Alexander Archipelago of Alaska. <i>Ecology and Evolution</i> , 2019, 9, 1777-1797.	0.8	16
1619	Unraveling patterns and processes of diversification in the South Andean-Patagonian <i>Nassauvia</i> subgenus <i>Strongyloma</i> (Asteraceae, Nassauvieae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 164-182.	1.2	12
1620	Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. <i>Molecular Biology and Evolution</i> , 2019, 36, 1294-1301.	3.5	27
1621	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
1622	Morphometric, phylogenetic and biogeographic analyses of <i>Pyrularia</i> (Santalales), a parasitic disjunct lineage between eastern Asia and eastern North America. <i>Taxon</i> , 2019, 68, 47-71.	0.4	9
1623	Saffron (<i>Crocus sativus</i>) is an autotriploid that evolved in Attica (Greece) from wild <i>Crocus cartwrightianus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 14-20.	1.2	62
1624	Gene Family Evolutionâ€”An Algorithmic Framework. <i>Computational Biology</i> , 2019, , 87-119.	0.1	9
1625	The nested Kingman coalescent: Speed of coming down from infinity. <i>Annals of Applied Probability</i> , 2019, 29, .	0.6	5
1626	Character Evolution and Recircumscription of the Northern Andean <i>Begonia</i> Section <i>Casparya</i> (Begoniaceae). <i>Systematic Botany</i> , 2019, 44, 52-65.	0.2	4
1627	Historical Biogeography and Temporal Diversification in <i>Symphoricarpos</i> (Caprifoliaceae.) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 T</i>	0.2	4

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1629	Multilocus phylogeny and a new classification for African, Asian and Indian supple and writhing skinks (Scincidae: Lygosominae). <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 1067-1096.	1.0	15
1630	Large ancestral effective population size explains the difficult phylogenetic placement of owl monkeys. <i>American Journal of Primatology</i> , 2019, 81, e22955.	0.8	18
1631	Target sequence capture in the Brazil nut family (Lecythidaceae): Marker selection and in silico capture from genome skimming data. <i>Molecular Phylogenetics and Evolution</i> , 2019, 135, 98-104.	1.2	25
1632	Deconstructing an infamous extinction crisis: Survival of <i>Partula</i> species on Moorea and Tahiti. <i>Evolutionary Applications</i> , 2019, 12, 1017-1033.	1.5	8
1633	Assessing Combinability of Phylogenomic Data Using Bayes Factors. <i>Systematic Biology</i> , 2019, 68, 744-754.	2.7	6
1634	Genetic diversity and origin of the rare, narrow endemic <i>Asperula crassifolia</i> (Rubiaceae). <i>Plant Systematics and Evolution</i> , 2019, 305, 181-192.	0.3	2
1635	A Critical Appraisal of the Placement of <i>Xiphosura</i> (Chelicerata) with Account of Known Sources of Phylogenetic Error. <i>Systematic Biology</i> , 2019, 68, 896-917.	2.7	138
1636	Parameterized Algorithms in Bioinformatics: An Overview. <i>Algorithms</i> , 2019, 12, 256.	1.2	14
1637	Target Capture Sequencing Unravels <i>Rubus</i> Evolution. <i>Frontiers in Plant Science</i> , 2019, 10, 1615.	1.7	73
1638	Taxonomy and Phylo Genetic Systematics. , 2019, , 17-52.		0
1639	Phylogenetics of <i>Pinus</i> Subsection <i>Cembroides</i> Engelm. (Pinaceae) Inferred from Low-Copy Nuclear Gene Sequences. <i>Systematic Botany</i> , 2019, 44, 501-518.	0.2	14
1640	Integrated speciesâ€“phenon trees: visualizing infraspecific diversity within lineages. <i>Scientific Reports</i> , 2019, 9, 18968.	1.6	0
1641	Development of a multi-locus sequence typing system helps reveal the evolution of <i>Cardinium hertigii</i> , a reproductive manipulator symbiont of insects. <i>BMC Microbiology</i> , 2019, 19, 266.	1.3	12
1642	Speciation of North American pygmy shrews (Eulipotyphla: Soricidae) supports spatial but not temporal congruence of diversification among boreal species. <i>Biological Journal of the Linnean Society</i> , 0, , .	0.7	2
1643	Representations of Partial Leaf Sets in Phylogenetic Tree Space. <i>SIAM Journal on Applied Algebra and Geometry</i> , 2019, 3, 691-720.	0.9	3
1644	Inferring Pareto-optimal reconciliations across multiple event costs under the duplication-loss-coalescence model. <i>BMC Bioinformatics</i> , 2019, 20, 639.	1.2	7
1645	PhySpeTree: an automated pipeline for reconstructing phylogenetic species trees. <i>BMC Evolutionary Biology</i> , 2019, 19, 219.	3.2	3

#	ARTICLE	IF	CITATIONS
1646	New Insights on Liliaceae Phylogeny Based on a Comparative Phylogenomic Study Using Complete Plastome Sequences. <i>Plants</i> , 2019, 8, 547.	1.6	13
1647	Lichen chemistry is concordant with multilocus gene genealogy in the genus <i>Cetrelia</i> (Parmeliaceae). <i>Trends in Ecology and Evolution</i> , 2019, 30, 107-114.	1.1	10
1648	Exploring gene tree incongruence at the origin of ants and bees (Hymenoptera). <i>Zoologica Scripta</i> , 2019, 48, 215-225.	0.7	3
1649	The diversification of neopasiphaeine bees during the Cenozoic (Hymenoptera: Colletidae). <i>Zoologica Scripta</i> , 2019, 48, 226-242.	0.7	27
1650	A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-Medoids Clustering. <i>Systematic Biology</i> , 2019, 68, 594-606.	2.7	371
1651	Cryptic diversity in the Mexican highlands: Thousands of UCE loci help illuminate phylogenetic relationships, species limits and divergence times of montane rattlesnakes (Viperidae: <i>Crotalus</i>). <i>Molecular Ecology Resources</i> , 2019, 19, 349-365.	2.2	37
1652	Phylogenomic Signatures of Ancient Introgression in a Rogue Lineage of Darters (Teleostei: Percidae). <i>Systematic Biology</i> , 2019, 68, 329-346.	2.7	42
1653	A New Quartet-Based Statistical Method for Comparing Sets of Gene Trees Is Developed Using a Generalized Hoeffding Inequality. <i>Journal of Computational Biology</i> , 2019, 26, 27-37.	0.8	1
1654	Cophenetic Median Trees. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1459-1470.	1.9	0
1655	The Species Problem from the Modeler's Point of View. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 878-898.	0.9	2
1656	Evaluating Statistical Multiple Sequence Alignment in Comparison to Other Alignment Methods on Protein Data Sets. <i>Systematic Biology</i> , 2019, 68, 396-411.	2.7	23
1657	Phylotranscriptomic Insights into the Diversification of Endothermic <i>Thunnus</i> Tunas. <i>Molecular Biology and Evolution</i> , 2019, 36, 84-96.	3.5	15
1658	Multi-allele species reconstruction using ASTRAL. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 286-296.	1.2	106
1659	Gene-wise resampling outperforms site-wise resampling in phylogenetic coalescence analyses. <i>Molecular Phylogenetics and Evolution</i> , 2019, 131, 80-92.	1.2	33
1660	Resolving Deep Nodes in an Ancient Radiation of Neotropical Fishes in the Presence of Conflicting Signals from Incomplete Lineage Sorting. <i>Systematic Biology</i> , 2019, 68, 573-593.	2.7	54
1661	imPhy: Imputing Phylogenetic Trees with Missing Information using Mathematical Programming. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	1.9	1
1662	Species delimitation in Neotropical fishes of the genus <i>Characidium</i> (Teleostei, Characiformes). <i>Zoologica Scripta</i> , 2019, 48, 69-80.	0.7	22
1663	What are the roles of taxon sampling and model fit in tests of cyto-nuclear discordance using avian mitogenomic data?. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 132-142.	1.2	30

#	ARTICLE	IF	CITATIONS
1664	Long-Branch Attraction in Species Tree Estimation: Inconsistency of Partitioned Likelihood and Topology-Based Summary Methods. <i>Systematic Biology</i> , 2019, 68, 281-297.	2.7	77
1665	Enumeration of lonely pairs of gene trees and species trees by means of antipodal cherries. <i>Advances in Applied Mathematics</i> , 2019, 102, 1-17.	0.4	7
1666	Calculating the Unrooted Subtree Prune-and-Regraft Distance. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 898-911.	1.9	11
1667	Multilocus phylogenetic analysis with gene tree clustering. <i>Annals of Operations Research</i> , 2019, 276, 293-313.	2.6	13
1668	CURatio: Genome-Wide Phylogenomic Analysis Method Using Ratios of Total Branch Lengths. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 981-989.	1.9	2
1669	Faster Exact Computation of rSPR Distance via Better Approximation. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020, 17, 916-929.	1.9	2
1670	Probabilistic Species Tree Distances: Implementing the Multispecies Coalescent to Compare Species Trees Within the Same Model-Based Framework Used to Estimate Them. <i>Systematic Biology</i> , 2020, 69, 194-207.	2.7	2
1671	Phylogenomics Uncovers Confidence and Conflict in the Rapid Radiation of Australo-Papuan Rodents. <i>Systematic Biology</i> , 2020, 69, 431-444.	2.7	44
1672	The Multispecies Coalescent Over-Splits Species in the Case of Geographically Widespread Taxa. <i>Systematic Biology</i> , 2020, 69, 184-193.	2.7	99
1673	Unraveling Deep Branches of the Sigmodontinae Tree (Rodentia: Cricetidae) in Eastern South America. <i>Journal of Mammalian Evolution</i> , 2020, 27, 139-160.	1.0	24
1674	Evolutionary history of mountain voles of the subgenus <i>Aschizomys</i> (Cricetidae, Rodentia), inferred from mitochondrial and nuclear markers. <i>Integrative Zoology</i> , 2020, 15, 187-201.	1.3	3
1675	Phylogenetic Trees and Networks Can Serve as Powerful and Complementary Approaches for Analysis of Genomic Data. <i>Systematic Biology</i> , 2020, 69, 593-601.	2.7	72
1676	INSTRAL: Discordance-Aware Phylogenetic Placement Using Quartet Scores. <i>Systematic Biology</i> , 2020, 69, 384-391.	2.7	14
1677	DNA barcoding approach fails to discriminate Central European bladderworts (<i>Utricularia</i>). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf</i> 326-336.	0.8	7
1678	Different filtering strategies of genotyping-by-sequencing data provide complementary resolutions of species boundaries and relationships in a clade of sexually deceptive orchids. <i>Journal of Systematics and Evolution</i> , 2020, 58, 133-144.	1.6	12
1679	Quartet-Based Computations of Internode Certainty Provide Robust Measures of Phylogenetic Incongruence. <i>Systematic Biology</i> , 2020, 69, 308-324.	2.7	38
1680	Roadblocked monotonic paths and the enumeration of coalescent histories for non-matching caterpillar gene trees and species trees. <i>Advances in Applied Mathematics</i> , 2020, 113, 101939.	0.4	4
1681	Dur3 and nrt2 genes in the bloom-forming dinoflagellate <i>Prorocentrum minimum</i> : Transcriptional responses to available nitrogen sources. <i>Chemosphere</i> , 2020, 241, 125083.	4.2	9

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1683	Optimizing Phylogenomics with Rapidly Evolving Long Exons: Comparison with Anchored Hybrid Enrichment and Ultraconserved Elements. <i>Molecular Biology and Evolution</i> , 2020, 37, 904-922.	3.5	39
1684	Asymmetric Distribution of Gene Trees Can Arise under Purifying Selection If Differences in Population Size Exist. <i>Molecular Biology and Evolution</i> , 2020, 37, 881-892.	3.5	12
1685	Non-parametric correction of estimated gene trees using TRACTION. <i>Algorithms for Molecular Biology</i> , 2020, 15, 1.	0.3	11
1686	Disentangling Population History and Character Evolution among Hybridizing Lineages. <i>Molecular Biology and Evolution</i> , 2020, 37, 1295-1305.	3.5	5
1687	The roles of vicariance and dispersal in the differentiation of two species of the <i>Rhinella marina</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106723.	1.2	12
1688	Morphological Variation in North American <i>Tilia</i> and Its Value in Species Delineation. <i>International Journal of Plant Sciences</i> , 2020, 181, 175-195.	0.6	8
1689	Phylogenomic analysis of the beetle suborder Adephaga with comparison of tailored and generalized ultraconserved element probe performance. <i>Systematic Entomology</i> , 2020, 45, 552-570.	1.7	35
1690	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. <i>Annual Review of Plant Biology</i> , 2020, 71, 741-765.	8.6	41
1691	Computing a Consensus Phylogeny via Leaf Removal. <i>Journal of Computational Biology</i> , 2020, 27, 175-188.	0.8	0
1692	Phylogenetic Conflicts, Combinability, and Deep Phylogenomics in Plants. <i>Systematic Biology</i> , 2020, 69, 579-592.	2.7	53
1693	Taming the Red Bastards: Hybridisation and species delimitation in the <i>Rhodanthemum arundanum</i> -group (Compositae, Anthemideae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106702.	1.2	14
1694	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
1695	Genome-wide sequence information reveals recurrent hybridization among diploid wheat wild relatives. <i>Plant Journal</i> , 2020, 102, 493-506.	2.8	40
1696	Comparison of colonial volvocine algae based on phylotranscriptomic analysis of gene family evolution and natural selection. <i>European Journal of Phycology</i> , 2020, 55, 100-112.	0.9	10
1697	Evolutionary history of a relict conifer, <i>Pseudotaxus chienii</i> (Taxaceae), in south-east China during the late Neogene: old lineage, young populations. <i>Annals of Botany</i> , 2020, 125, 105-117.	1.4	27
1698	ASTRAL-Pro: Quartet-Based Species-Tree Inference despite Paralogy. <i>Molecular Biology and Evolution</i> , 2020, 37, 3292-3307.	3.5	116
1699	Comparing mitogenomic timetrees for two African savannah primate genera (<i>Chlorocebus</i> and <i>Papio</i>). <i>Zoological Journal of the Linnean Society</i> , 2020, 190, 1071-1073.	1.0	1

#	ARTICLE	IF	CITATIONS
1700	Unraveling the Spiraling Radiation: A Phylogenomic Analysis of Neotropical <i>Costus</i> L. <i>Frontiers in Plant Science</i> , 2020, 11, 1195.	1.7	10
1701	AllCoPol: inferring allele co-ancestry in polyploids. <i>BMC Bioinformatics</i> , 2020, 21, 441.	1.2	14
1702	Machine learning based imputation techniques for estimating phylogenetic trees from incomplete distance matrices. <i>BMC Genomics</i> , 2020, 21, 497.	1.2	15
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1705	Testing for population decline using maximal linkage disequilibrium blocks. <i>Theoretical Population Biology</i> , 2020, 134, 171-181.	0.5	7
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1707	The genomic view of diversification. <i>Journal of Evolutionary Biology</i> , 2020, 33, 1387-1404.	0.8	5
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1713	SEQUENCE-FREE PHYLOGENETICS WITH MASS SPECTROMETRY. <i>Mass Spectrometry Reviews</i> , 2020, 41, 3-14.	2.8	12
1714	The Multilocus Multispecies Coalescent: A Flexible New Model of Gene Family Evolution. <i>Systematic Biology</i> , 2021, 70, 822-837.	2.7	9
1715	Phylogenomics and species delimitation for effective conservation of manta and devil rays. <i>Molecular Ecology</i> , 2020, 29, 4783-4796.	2.0	45
1716	Evolutionary Phycology: Toward a Macroalgal Species Conceptual Framework. <i>Journal of Phycology</i> , 2020, 56, 1404-1413.	1.0	4
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#	ARTICLE	IF	CITATIONS
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1720	Comparing rates of introgression in parasitic feather lice with differing dispersal capabilities. <i>Communications Biology</i> , 2020, 3, 610.	2.0	6
1721	Evolutionary History of Alzheimer Disease-Causing Protein Family Presenilins with Pathological Implications. <i>Journal of Molecular Evolution</i> , 2020, 88, 674-688.	0.8	29
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1728	Evolutionary history of species of the firefly subgenus <i>Hotaria</i> (Coleoptera, Lampyridae, Luciolinae). <i>Tj ETQqO 0 0 rgBT /Overlock 10 Tf 5</i>	0.2	7
1729	Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020, 21, 428-444.	7.7	226
1730	Phylogeography of the Cranâ€™s bully <i>Gobiomorphus basalis</i> (Gobiiformes: Eleotridae) and an analysis of species boundaries within the New Zealand radiation of <i>Gobiomorphus</i> . <i>Biological Journal of the Linnean Society</i> , 2020, 130, 365-381.	0.7	3
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1734	Integrative taxonomy of extant maras supports the recognition of the genera <i>Pediolagus</i> and <i>Dolichotis</i> within the Dolichotinae (Rodentia, Caviidae). <i>Journal of Mammalogy</i> , 2020, 101, 817-834.	0.6	4
1735	Cryptic speciation in gentoo penguins is driven by geographic isolation and regional marine conditions: Unforeseen vulnerabilities to global change. <i>Diversity and Distributions</i> , 2020, 26, 958-975.	1.9	17
1736	The potential of genome-wide RAD sequences for resolving rapid radiations: a case study in Cactaceae. <i>Molecular Phylogenetics and Evolution</i> , 2020, 151, 106896.	1.2	16
1737	Phylogenetic relationships based on nuclear and plastid DNA sequences reveal recent diversification and discordant patterns of morphological evolution of the Chilean genera of Gilliesieae (Amaryllidaceae: Alliioideae). <i>Botanical Journal of the Linnean Society</i> , 2020, 194, 84-99.	0.8	6

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1739	Whole genome phylogeny of <i>Gallus</i> : introgression and data-type effects. <i>Avian Research</i> , 2020, 11, .	0.5	17
1740	Complex patterns of reticulate evolution in opportunistic weeds (<i>Potentilla</i> L., Rosaceae), as revealed by low-copy nuclear markers. <i>BMC Evolutionary Biology</i> , 2020, 20, 38.	3.2	9
1741	Regulators of an ancient polyphenism evolved through episodic protein divergence and parallel gene radiations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20192595.	1.2	7
1742	Towards rectifying limitations on species delineation in dusky salamanders (<i>Desmognathus</i>): Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 T 2020, 4734, zootaxa.4734.1.1.	0.2	15
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1744	Pleistocene range disruption and postglacial expansion with secondary contacts explain the genetic and cytotype structure in the western Balkan endemic <i>Alyssum austrodalmaticum</i> (Brassicaceae). <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	10
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1748	Broccoli: Combining Phylogenetic and Network Analyses for Orthology Assignment. <i>Molecular Biology and Evolution</i> , 2020, 37, 3389-3396.	3.5	65
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1750	Mammalian Evolution: The Phylogenetics Story. , 2020, , 321-331.		1
1751	Integrative taxonomy and species delimitation of <i>Rhipicephalus turanicus</i> (Acari: Ixodida: Ixodidae). <i>International Journal for Parasitology</i> , 2020, 50, 577-594.	1.3	34
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1755	Utility of targeted sequence capture for phylogenomics in rapid, recent angiosperm radiations: Neotropical <i>Burmeistera</i> bellflowers as a case study. <i>Molecular Phylogenetics and Evolution</i> , 2020, 152, 106769.	1.2	34

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1758	Phylogenomic analysis of trichomycterid catfishes (Teleostei: Siluriformes) inferred from ultraconserved elements. <i>Scientific Reports</i> , 2020, 10, 2697.	1.6	45
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1761	The Impact of Cross-Species Gene Flow on Species Tree Estimation. <i>Systematic Biology</i> , 2020, 69, 830-847.	2.7	37
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1770	A Project-Based Guide to Undergraduate Research in Mathematics. <i>Foundations for Undergraduate Research in Mathematics</i> , 2020, , .	0.0	2
1771	Research in Computational Molecular Biology. <i>Lecture Notes in Computer Science</i> , 2020, , .	1.0	0
1772	The complex phylogenetic relationships of a 4mC/6mA DNA methyltransferase in prokaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2020, 149, 106837.	1.2	8
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#	ARTICLE	IF	CITATIONS
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#	ARTICLE	IF	CITATIONS
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1793	Phylogeny, taxonomics, and ovipositor length variation of the <i>Pteromalus albipennis</i> species group (Hymenoptera: Chalcidoidea: Pteromalidae: Pteromalinae). <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 349-358.	0.6	2
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1803	Molecular epidemiology of foodborne pathogens. , 2021, , 47-62.		2
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1807	Comparative Performance of Popular Methods for Hybrid Detection using Genomic Data. <i>Systematic Biology</i> , 2021, 70, 891-907.	2.7	29
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1813	Genetic and endosymbiotic diversity of Greek populations of <i>Philaenus spumarius</i> , <i>Philaenus signatus</i> and <i>Neophilaenus campestris</i> , vectors of <i>Xylella fastidiosa</i> . <i>Scientific Reports</i> , 2021, 11, 3752.	1.6	12
1815	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
1816	Dissecting Incongruence between Concatenation- and Quartet-Based Approaches in Phylogenomic Data. <i>Systematic Biology</i> , 2021, 70, 997-1014.	2.7	28
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1825	Phylogeny, evolution and ecological speciation analyses of <i>Imperata</i> (Poaceae: Andropogoneae) in the Neotropics. <i>Systematics and Biodiversity</i> , 2021, 19, 526-543.	0.5	3
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#	ARTICLE	IF	CITATIONS
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1833	Molecular evidence for hybridization in the aquatic plant <i>Limosella</i> on sub-Antarctic Marion Island. <i>Antarctic Science</i> , 2021, 33, 243-251.	0.5	2
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1835	Molecular phylogeny and character evolution of <i>Flemingia</i> (Leguminosae, Papilionoideae, Phaseoleae). <i>Trends in Plant Science</i> , 2021, 16, 307, 1.	0.3	6
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1847	Using Robinson-Foulds supertrees in divide-and-conquer phylogeny estimation. <i>Algorithms for Molecular Biology</i> , 2021, 16, 12.	0.3	0
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1852	Timber identification of <i>Autranella</i> , <i>Baillonella</i> and <i>Tieghemella</i> in the taxonomically challenging Sapotaceae family. <i>Plant Methods</i> , 2021, 17, 64.	1.9	5
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1866	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales. <i>Systematic Biology</i> , 2021, 71, 208-220.	2.7	9
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1932

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2041	Ancient Mitochondrial Capture as Factor Promoting Mitonuclear Discordance in Freshwater Fishes: A Case Study in the Genus <i>Squalius</i> (Actinopterygii, Cyprinidae) in Greece. <i>PLoS ONE</i> , 2016, 11, e0166292.	1.1	43
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