

Joseph W Brown

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

5,321
citations

236612

25
h-index

414034

32
g-index

51
all docs

51
docs citations

51
times ranked

7853
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic Conflicts, Combinability, and Deep Phylogenomics in Plants. <i>Systematic Biology</i> , 2020, 69, 579-592.	2.7	53
2	Verbalizing phylogenomic conflict: Representation of node congruence across competing reconstructions of the neoavian explosion. <i>PLoS Computational Biology</i> , 2019, 15, e1006493.	1.5	2
3	Evolution of Portulacineae Marked by Gene Tree Conflict and Gene Family Expansion Associated with Adaptation to Harsh Environments. <i>Molecular Biology and Evolution</i> , 2019, 36, 112-126.	3.5	55
4	The choice of tree prior and molecular clock does not substantially affect phylogenetic inferences of diversification rates. <i>PeerJ</i> , 2019, 7, e6334.	0.9	30
5	Constructing a broadly inclusive seed plant phylogeny. <i>American Journal of Botany</i> , 2018, 105, 302-314.	0.8	647
6	Quartet Sampling distinguishes lack of support from conflicting support in the green plant tree of life. <i>American Journal of Botany</i> , 2018, 105, 385-403.	0.8	194
7	The Past Sure is Tense: On Interpreting Phylogenetic Divergence Time Estimates. <i>Systematic Biology</i> , 2018, 67, 340-353.	2.7	67
8	Disparity, diversity, and duplications in the Caryophyllales. <i>New Phytologist</i> , 2018, 217, 836-854.	3.5	51
9	So many genes, so little time: A practical approach to divergence-time estimation in the genomic era. <i>PLoS ONE</i> , 2018, 13, e0197433.	1.1	167
10	Analyzing Contentious Relationships and Outlier Genes in Phylogenomics. <i>Systematic Biology</i> , 2018, 67, 916-924.	2.7	69
11	Phyx: phylogenetic tools for unix. <i>Bioinformatics</i> , 2017, 33, 1886-1888.	1.8	210
12	Bayesian and likelihood phylogenetic reconstructions of morphological traits are not discordant when taking uncertainty into consideration: a comment on Puttick <i>et al.</i> .. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170986.	1.2	30
13	The development of scientific consensus: Analyzing conflict and concordance among avian phylogenies. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 69-77.	1.2	21
14	Multi-locus phylogenetic inference among New World Vultures (Aves: Cathartidae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 193-199.	1.2	33
15	rotl: an R package to interact with the Open Tree of Life data. <i>Methods in Ecology and Evolution</i> , 2016, 7, 1476-1481.	2.2	288
16	Phylesystem: a git-based data store for community-curated phylogenetic estimates. <i>Bioinformatics</i> , 2015, 31, 2794-2800.	1.8	34
17	Nested radiations and the pulse of angiosperm diversification: increased diversification rates often follow whole genome duplications. <i>New Phytologist</i> , 2015, 207, 454-467.	3.5	315
18	A molecular genetic time scale demonstrates Cretaceous origins and multiple diversification rate shifts within the order Galliformes (Aves). <i>Molecular Phylogenetics and Evolution</i> , 2015, 92, 155-164.	1.2	42

#	ARTICLE	IF	CITATIONS
19	Analysis of phylogenomic datasets reveals conflict, concordance, and gene duplications with examples from animals and plants. <i>BMC Evolutionary Biology</i> , 2015, 15, 150.	3.2	350
20	<scp>BAMM</scp> tools: an R package for the analysis of evolutionary dynamics on phylogenetic trees. <i>Methods in Ecology and Evolution</i> , 2014, 5, 701-707.	2.2	751
21	Beyond aridification: multiple explanations for the elevated diversification of cacti in the New World Succulent Biome. <i>New Phytologist</i> , 2014, 202, 1382-1397.	3.5	176
22	geiger v2.0: an expanded suite of methods for fitting macroevolutionary models to phylogenetic trees. <i>Bioinformatics</i> , 2014, 30, 2216-2218.	1.8	722
23	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. <i>BMC Bioinformatics</i> , 2013, 14, 158.	1.2	33
24	Analyzing and Synthesizing Phylogenies Using Tree Alignment Graphs. <i>PLoS Computational Biology</i> , 2013, 9, e1003223.	1.5	30
25	Ancient divergence and biogeography of <i>Raukua</i> (Araliaceae) and close relatives in the southern hemisphere. <i>Australian Systematic Botany</i> , 2012, 25, 432.	0.3	27
26	Goldilocks Meets Santa Rosalia: An Ephemeral Speciation Model Explains Patterns of Diversification Across Time Scales. <i>Evolutionary Biology</i> , 2012, 39, 255-261.	0.5	195
27	Angiosperm phylogeny inferred from sequences of four mitochondrial genes. <i>Journal of Systematics and Evolution</i> , 2010, 48, 391-425.	1.6	173
28	The Use of Genetics for the Management of a Recovering Population: Temporal Assessment of Migratory Peregrine Falcons in North America. <i>PLoS ONE</i> , 2010, 5, e14042.	1.1	23
29	A Molecular Genetic Timescale for the Diversification of Autotrophic Stramenopiles (Ochrophyta): Substantive Underestimation of Putative Fossil Ages. <i>PLoS ONE</i> , 2010, 5, e12759.	1.1	116
30	Directional gene flow patterns in disjunct populations of the black ratsnake (<i>Pantheropsis obsoletus</i>) and the Blanding's turtle (<i>Emydoidea blandingii</i>). <i>Conservation Genetics</i> , 2009, 10, 407-417.	0.8	23
31	Strong mitochondrial DNA support for a Cretaceous origin of modern avian lineages. <i>BMC Biology</i> , 2008, 6, 6.	1.7	208
32	Nuclear DNA does not reconcile "rocks" and "clocks" in Neoaves: a comment on Ericson et al .. <i>Biology Letters</i> , 2007, 3, 257-260.	1.0	67
33	Appraisal of the consequences of the DDT-induced bottleneck on the level and geographic distribution of neutral genetic variation in Canadian peregrine falcons, <i>Falco peregrinus</i> . <i>Molecular Ecology</i> , 2007, 16, 327-343.	2.0	60