

Brian C O'meara

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

7,334
citations

147566

31
h-index

143772

57
g-index

75
all docs

75
docs citations

75
times ranked

10193
citing authors

#	ARTICLE	IF	CITATIONS
1	Three keys to the radiation of angiosperms into freezing environments. <i>Nature</i> , 2014, 506, 89-92.	13.7	1,284
2	treePL: divergence time estimation using penalized likelihood for large phylogenies. <i>Bioinformatics</i> , 2012, 28, 2689-2690.	1.8	558
3	MODELING STABILIZING SELECTION: EXPANDING THE ORNSTEIN-UHLENBECK MODEL OF ADAPTIVE EVOLUTION. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2369-2383.	1.1	537
4	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922-933.	1.1	516
5	Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction. <i>Systematic Biology</i> , 2016, 65, 583-601.	2.7	447
6	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. <i>Frontiers in Plant Science</i> , 2011, 2, 34.	1.7	396
7	Identifying Hidden Rate Changes in the Evolution of a Binary Morphological Character: The Evolution of Plant Habit in Campanulid Angiosperms. <i>Systematic Biology</i> , 2013, 62, 725-737.	2.7	306
8	New Heuristic Methods for Joint Species Delimitation and Species Tree Inference. <i>Systematic Biology</i> , 2010, 59, 59-73.	2.7	241
9	Prospects for Building the Tree of Life from Large Sequence Databases. <i>Science</i> , 2004, 306, 1172-1174.	6.0	233
10	Evolutionary Inferences from Phylogenies: A Review of Methods. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2012, 43, 267-285.	3.8	200
11	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922.	1.1	183
12	Five <i>Drosophila</i> Genomes Reveal Nonneutral Evolution and the Signature of Host Specialization in the Chemoreceptor Superfamily. <i>Genetics</i> , 2007, 177, 1395-1416.	1.2	179
13	The evolution of a tropical biodiversity hotspot. <i>Science</i> , 2020, 370, 1343-1348.	6.0	179
14	Testing for different rates of continuous trait evolution using likelihood. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 922-33.	1.1	153
15	The ecological and genomic basis of explosive adaptive radiation. <i>Nature</i> , 2020, 586, 75-79.	13.7	146
16	Hidden state models improve state-dependent diversification approaches, including biogeographical models. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 2308-2324.	1.1	145
17	PISCIVORY LIMITS DIVERSIFICATION OF FEEDING MORPHOLOGY IN CENTRARCHID FISHES. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 1557-1573.	1.1	139
18	Species Delimitation with Gene Flow. <i>Systematic Biology</i> , 2017, 66, syw117.	2.7	118

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19	Functional distinctiveness of major plant lineages. <i>Journal of Ecology</i> , 2014, 102, 345-356.	1.9	108
20	Heterogeneous Rates of Molecular Evolution and Diversification Could Explain the Triassic Age Estimate for Angiosperms. <i>Systematic Biology</i> , 2015, 64, 869-878.	2.7	108
21	Phylogenetic relationships and character evolution analysis of Saxifragales using a supermatrix approach. <i>American Journal of Botany</i> , 2013, 100, 916-929.	0.8	92
22	Extinction can be estimated from moderately sized molecular phylogenies. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1036-1043.	1.1	92
23	Habitat use affects morphological diversification in dragon lizards. <i>Journal of Evolutionary Biology</i> , 2010, 23, 1033-1049.	0.8	79
24	Non-equilibrium dynamics and floral trait interactions shape extant angiosperm diversity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20152304.	1.2	79
25	Leaf reflectance spectra capture the evolutionary history of seed plants. <i>New Phytologist</i> , 2020, 228, 485-493.	3.5	72
26	PHRAPL: Phylogeographic Inference Using Approximate Likelihoods. <i>Systematic Biology</i> , 2017, 66, 1045-1053.	2.7	59
27	Repeated evolution of tricellular (and bicellular) pollen. <i>American Journal of Botany</i> , 2014, 101, 559-571.	0.8	53
28	Speciation with Gene Flow in North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2017, 66, syw100.	2.7	50
29	Can we build it? Yes we can, but should we use it? Assessing the quality and value of a very large phylogeny of <i>Campanulid</i> angiosperms. <i>American Journal of Botany</i> , 2018, 105, 417-432.	0.8	45
30	Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. <i>BMC Research Notes</i> , 2012, 5, 574.	0.6	42
31	Past, future, and present of state-dependent models of diversification. <i>American Journal of Botany</i> , 2016, 103, 792-795.	0.8	39
32	Developmental evolution of flowering plant pollen tube cell walls: callose synthase (CalS) gene expression patterns. <i>EvoDevo</i> , 2011, 2, 14.	1.3	38
33	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. <i>BMC Bioinformatics</i> , 2013, 14, 158.	1.2	33
34	A flexible method for estimating tip diversification rates across a range of speciation and extinction scenarios. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1420-1433.	1.1	26
35	Reef fish functional traits evolve fastest at trophic extremes. <i>Nature Ecology and Evolution</i> , 2019, 3, 191-199.	3.4	23
36	Retiring "Cradles" and "Museums" of Biodiversity. <i>American Naturalist</i> , 2022, 199, 194-205.	1.0	22

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37	<i>MonoPhy</i> : a simple R package to find and visualize monophyly issues. PeerJ Computer Science, 0, 2, e56.	2.7	22
38	Hidden Markov Models for Studying the Evolution of Binary Morphological Characters. , 2014, , 395-408.		17
39	Modelling Stabilizing Selection: The Attraction of Ornstein-Uhlenbeck Models. , 2014, , 381-393.		16
40	The <i>Xeromphalina campanella/kauffmanii</i> complex: species delineation and biogeographical patterns of speciation. Mycologia, 2015, 107, 1270-1284.	0.8	16
41	Mitochondrial genome primers for Lake Malawi cichlids. Molecular Ecology Resources, 2013, 13, 347-353.	2.2	15
42	Diversity and skepticism are vital for comparative biology: a response to Donoghue and Edwards (2019). American Journal of Botany, 2019, 106, 613-617.	0.8	15
43	Associations Between Eating Occasion Characteristics and Age, Gender, Presence of Children and BMI Among U.S. Adults. Journal of the American College of Nutrition, 2014, 33, 315-327.	1.1	14
44	Objective choice of phylogeographic models. Molecular Phylogenetics and Evolution, 2017, 116, 136-140.	1.2	13
45	<i>RBrownie</i> : an R package for testing hypotheses about rates of evolutionary change. Methods in Ecology and Evolution, 2011, 2, 660-662.	2.2	11
46	Population Genetics Based Phylogenetics Under Stabilizing Selection for an Optimal Amino Acid Sequence: A Nested Modeling Approach. Molecular Biology and Evolution, 2019, 36, 834-851.	3.5	11
47	Investigating the performance of AIC in selecting phylogenetic models. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 459-75.	0.2	10
48	Evolutionary models for the retention of adult social play in primates: The roles of diet and other factors associated with resource acquisition. Adaptive Behavior, 2015, 23, 381-391.	1.1	10
49	Gene expression of functionally-related genes coevolves across fungal species: detecting coevolution of gene expression using phylogenetic comparative methods. BMC Genomics, 2020, 21, 370.	1.2	10
50	The ontogeny of personality traits in the desert funnelweb spider, <i>Agelenopsis lisa</i> (Araneae: Tetragnathidae). <i>Journal of Herpetology</i> , 2019, 53, 107-115.	0.5	9
51	<i>AnnotationBustR</i> : an R package to extract subsequences from GenBank annotations. PeerJ, 2018, 6, e5179.	0.9	9
52	Reol: R interface to the Encyclopedia of Life. Ecology and Evolution, 2014, 4, 2577-2583.	0.8	5
53	Unlocking a signal of introgression from codons in <i>Lachancea kluyveri</i> using a mutation-selection model. BMC Evolutionary Biology, 2020, 20, 109.	3.2	5
54	Morphogenera, monophyly, and macroevolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, E97-8; author reply E99-100.	3.3	4

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55	Zanne et al. reply. Nature, 2015, 521, E6-E7.	13.7	3
56	On the Matrix Condition of Phylogenetic Tree. Evolutionary Bioinformatics, 2020, 16, 117693432090172.	0.6	3
57	Phylotastic: Improving Access to Tree-of-Life Knowledge With Flexible, on-the-Fly Delivery of Trees. Evolutionary Bioinformatics, 2020, 16, 117693431989938.	0.6	2
58	A Spatially Explicit Model of Stabilizing Selection for Improving Phylogenetic Inference. Molecular Biology and Evolution, 2021, 38, 1641-1652.	3.5	1