

Brian C O'meara

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2556200/publications.pdf>

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	Retiring "Cradles" and "Museums" of Biodiversity. <i>American Naturalist</i> , 2022, 199, 194-205.	1.0	22
2	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
3	A Spatially Explicit Model of Stabilizing Selection for Improving Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2021, 38, 1641-1652.	3.5	1
4	The ecological and genomic basis of explosive adaptive radiation. <i>Nature</i> , 2020, 586, 75-79.	13.7	146
5	Unlocking a signal of introgression from codons in <i>Lachancea kluyveri</i> using a mutation-selection model. <i>BMC Evolutionary Biology</i> , 2020, 20, 109.	3.2	5
6	The evolution of a tropical biodiversity hotspot. <i>Science</i> , 2020, 370, 1343-1348.	6.0	179
7	Phylotastic: Improving Access to Tree-of-Life Knowledge With Flexible, on-the-Fly Delivery of Trees. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693431989938.	0.6	2
8	On the Matrix Condition of Phylogenetic Tree. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432090172.	0.6	3
9	Leaf reflectance spectra capture the evolutionary history of seed plants. <i>New Phytologist</i> , 2020, 228, 485-493.	3.5	72
10	Gene expression of functionally-related genes coevolves across fungal species: detecting coevolution of gene expression using phylogenetic comparative methods. <i>BMC Genomics</i> , 2020, 21, 370.	1.2	10
11	Diversity and skepticism are vital for comparative biology: a response to Donoghue and Edwards (2019). <i>American Journal of Botany</i> , 2019, 106, 613-617.	0.8	15
12	Reef fish functional traits evolve fastest at trophic extremes. <i>Nature Ecology and Evolution</i> , 2019, 3, 191-199.	3.4	23
13	Population Genetics Based Phylogenetics Under Stabilizing Selection for an Optimal Amino Acid Sequence: A Nested Modeling Approach. <i>Molecular Biology and Evolution</i> , 2019, 36, 834-851.	3.5	11
14	Can we build it? Yes we can, but should we use it? Assessing the quality and value of a very large phylogeny of Campanulid angiosperms. <i>American Journal of Botany</i> , 2018, 105, 417-432.	0.8	45
15	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
16	<i>AnnotationBustR</i> : an R package to extract subsequences from GenBank annotations. <i>PeerJ</i> , 2018, 6, e5179.	0.9	9
17	Species Delimitation with Gene Flow. <i>Systematic Biology</i> , 2017, 66, syw117.	2.7	118
18	Speciation with Gene Flow in North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2017, 66, syw100.	2.7	50

#	ARTICLE	IF	CITATIONS
19	PHRAPL: Phylogeographic Inference Using Approximate Likelihoods. <i>Systematic Biology</i> , 2017, 66, 1045-1053.	2.7	59
20	Objective choice of phylogeographic models. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 136-140.	1.2	13
21	The ontogeny of personality traits in the desert funnelweb spider, <i>Agelenopsis lisa</i> (Araneae). <i>Tj ETQq1 1 0.784314 ggBT /Over</i>	0.5	9
22	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
23	Past, future, and present of state-dependent models of diversification. <i>American Journal of Botany</i> , 2016, 103, 792-795.	0.8	39
24	Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction. <i>Systematic Biology</i> , 2016, 65, 583-601.	2.7	447
25	Zanne et al. reply. <i>Nature</i> , 2015, 521, E6-E7.	13.7	3
26	Extinction can be estimated from moderately sized molecular phylogenies. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1036-1043.	1.1	92
27	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
28	Evolutionary models for the retention of adult social play in primates: The roles of diet and other factors associated with resource acquisition. <i>Adaptive Behavior</i> , 2015, 23, 381-391.	1.1	10
29	The <i>Xeromphalina campanella/kauffmanii</i> complex: species delineation and biogeographical patterns of speciation. <i>Mycologia</i> , 2015, 107, 1270-1284.	0.8	16
30	Repeated evolution of tricellular (and bicellular) pollen. <i>American Journal of Botany</i> , 2014, 101, 559-571.	0.8	53
31	Functional distinctiveness of major plant lineages. <i>Journal of Ecology</i> , 2014, 102, 345-356.	1.9	108
32	Investigating the performance of AIC in selecting phylogenetic models. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 459-75.	0.2	10
33	Three keys to the radiation of angiosperms into freezing environments. <i>Nature</i> , 2014, 506, 89-92.	13.7	1,284
34	Reol: R interface to the Encyclopedia of Life. <i>Ecology and Evolution</i> , 2014, 4, 2577-2583.	0.8	5
35	Associations Between Eating Occasion Characteristics and Age, Gender, Presence of Children and BMI Among U.S. Adults. <i>Journal of the American College of Nutrition</i> , 2014, 33, 315-327.	1.1	14
36	Modelling Stabilizing Selection: The Attraction of Ornstein-Uhlenbeck Models. , 2014, , 381-393.		16

#	ARTICLE	IF	CITATIONS
37	Hidden Markov Models for Studying the Evolution of Binary Morphological Characters. , 2014, , 395-408.		17
38	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics, 2013, 14, 158.	1.2	33
39	Phylogenetic relationships and character evolution analysis of Saxifragales using a supermatrix approach. American Journal of Botany, 2013, 100, 916-929.	0.8	92
40	Identifying Hidden Rate Changes in the Evolution of a Binary Morphological Character: The Evolution of Plant Habit in Campanulid Angiosperms. Systematic Biology, 2013, 62, 725-737.	2.7	306
41	Mitochondrial genome primers for Lake Malawi cichlids. Molecular Ecology Resources, 2013, 13, 347-353.	2.2	15
42	treePL: divergence time estimation using penalized likelihood for large phylogenies. Bioinformatics, 2012, 28, 2689-2690.	1.8	558
43	Evolutionary Inferences from Phylogenies: A Review of Methods. Annual Review of Ecology, Evolution, and Systematics, 2012, 43, 267-285.	3.8	200
44	Sharing and re-use of phylogenetic trees (and associated data) to facilitate synthesis. BMC Research Notes, 2012, 5, 574.	0.6	42
45	MODELING STABILIZING SELECTION: EXPANDING THE ORNSTEIN-UHLENBECK MODEL OF ADAPTIVE EVOLUTION. Evolution; International Journal of Organic Evolution, 2012, 66, 2369-2383.	1.1	537
46	RBrownie: an R package for testing hypotheses about rates of evolutionary change. Methods in Ecology and Evolution, 2011, 2, 660-662.	2.2	11
47	The iPlant Collaborative: Cyberinfrastructure for Plant Biology. Frontiers in Plant Science, 2011, 2, 34.	1.7	396
48	Developmental evolution of flowering plant pollen tube cell walls: callose synthase (CaS) gene expression patterns. EvoDevo, 2011, 2, 14.	1.3	38
49	Habitat use affects morphological diversification in dragon lizards. Journal of Evolutionary Biology, 2010, 23, 1033-1049.	0.8	79
50	New Heuristic Methods for Joint Species Delimitation and Species Tree Inference. Systematic Biology, 2010, 59, 59-73.	2.7	241
51	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
52	PISCIVORY LIMITS DIVERSIFICATION OF FEEDING MORPHOLOGY IN CENTRARCHID FISHES. Evolution; International Journal of Organic Evolution, 2009, 63, 1557-1573.	1.1	139
53	Five Drosophila Genomes Reveal Nonneutral Evolution and the Signature of Host Specialization in the Chemoreceptor Superfamily. Genetics, 2007, 177, 1395-1416.	1.2	179
54	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. Evolution; International Journal of Organic Evolution, 2006, 60, 922.	1.1	183

#	ARTICLE	IF	CITATIONS
55	TESTING FOR DIFFERENT RATES OF CONTINUOUS TRAIT EVOLUTION USING LIKELIHOOD. Evolution; International Journal of Organic Evolution, 2006, 60, 922-933.	1.1	516
56	Testing for different rates of continuous trait evolution using likelihood. Evolution; International Journal of Organic Evolution, 2006, 60, 922-33.	1.1	153
57	Prospects for Building the Tree of Life from Large Sequence Databases. Science, 2004, 306, 1172-1174.	6.0	233
58	<i>MonoPhy</i> : a simple R package to find and visualize monophyly issues. PeerJ Computer Science, 0, 2, e56.	2.7	22