Jeremy M Beaulieu

List of Publications by Year
in descending order

51 papers	6,393 citations	147566 31 h-index	182168 51 g-index
59 all docs	59 docs citations	59 times ranked	8670 citing authors

#	Article	IF	Citations
1	Linking mode of seed dispersal and climatic niche evolution in flowering plants. Journal of Biogeography, 2023, 50, 43-56.	1.4	17
2	Retiring â€œCradlesâ€•and â€œMuseumsâ€•of Biodiversity. American Naturalist, 2022, 199, 194-205.	1.0	22
3	A flexible method for estimating tip diversification rates across a range of speciation and extinction scenarios. Evolution; International Journal of Organic Evolution, 2022, 76, 1420-1433.	1.1	26
4	Synthesizing Existing Phylogenetic Data to Advance Phylogenetic Research in Orobanchaceae. Systematic Botany, 2022, 47, 533-544.	0.2	2
5	Generalized hidden Markov models for phylogenetic comparative datasets. Methods in Ecology and Evolution, 2021, 12, 468-478.	2.2	58
6	A Spatially Explicit Model of Stabilizing Selection for Improving Phylogenetic Inference. Molecular Biology and Evolution, 2021, 38, 1641-1652.	3.5	1
7	Geophytism in monocots leads to higher rates of diversification. New Phytologist, 2020, 225, 1023-1032.	3.5	22
8	Comparative Analyses of Phenotypic Sequences Using Phylogenetic Trees. American Naturalist, 2020, 195, E38-E50.	1.0	2
9	Diatoms diversify and turn over faster in freshwater than marine environments*. Evolution; International Journal of Organic Evolution, 2019, 73, 2497-2511.	1.1	65
10	The monocotyledonous underground: global climatic and phylogenetic patterns of geophyte diversity. American Journal of Botany, 2019, 106, 850-863.	0.8	44
11	Diversity and skepticism are vital for comparative biology: aÂresponse to Donoghue and Edwards (2019). American Journal of Botany, 2019, 106, 613-617.	0.8	15
12	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
13	Can we build it? Yes we can, but should we use it? AssessingÂthe quality and value of a very large phylogeny ofÂcampanulid angiosperms. American Journal of Botany, 2018, 105, 417-432.	0.8	45
14	Accelerated diversification is related to life history and locomotion in a hyperdiverse lineage of microbial eukaryotes (Diatoms, Bacillariophyta). New Phytologist, 2018, 219, 462-473.	3.5	104
15	Hidden state models improve state-dependent diversification approaches, including biogeographical models. Evolution; International Journal of Organic Evolution, 2018, 72, 2308-2324.	1.1	145
16	Adaptive evolution to novel predators facilitates the evolution of damselfly species range shifts. Evolution; International Journal of Organic Evolution, 2017, 71, 974-984.	1.1	9
17	Variation in seed size is structured by dispersal syndrome and cone morphology in conifers and other nonflowering seed plants. New Phytologist, 2017, 216, 429-437.	3.5	53
18	Past, future, and present of stateâ€dependent models of diversification. American Journal of Botany, 2016, 103, 792-795.	0.8	39

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19	Detecting Hidden Diversification Shifts in Models of Trait-Dependent Speciation and Extinction. Systematic Biology, 2016, 65, 583-601.	2.7	447
20	Zanne et al. reply. Nature, 2015, 521, E6-E7.	13.7	3
21	Extinction can be estimated from moderately sized molecular phylogenies. Evolution; International Journal of Organic Evolution, 2015, 69, 1036-1043.	1.1	92
22	Integration and macroevolutionary patterns in the pollination biology of conifers. Evolution; International Journal of Organic Evolution, 2015, 69, 1573-1583.	1.1	11
23	Heterogeneous Rates of Molecular Evolution and Diversification Could Explain the Triassic Age Estimate for Angiosperms. Systematic Biology, 2015, 64, 869-878.	2.7	108
24	Functional distinctiveness of major plant lineages. Journal of Ecology, 2014, 102, 345-356.	1.9	108
25	Cone size is related to branching architecture in conifers. New Phytologist, 2014, 203, 1119-1127.	3.5	21
26	Three keys to the radiation of angiosperms into freezing environments. Nature, 2014, 506, 89-92.	13.7	1,284
27	Modelling Stabilizing Selection: The Attraction of Ornsteinâ€“Uhlenbeck Models. , 2014, , 381-393.		16
28	Hidden Markov Models for Studying the Evolution of Binary Morphological Characters. , 2014, , 395-408.		17
29	FRUIT EVOLUTION AND DIVERSIFICATION IN CAMPANULID ANGIOSPERMS. Evolution; International Journal of Organic Evolution, 2013, 67, 3132-3144.	1.1	85
30	A Southern Hemisphere origin for campanulid angiosperms, with traces of the break-up of Gondwana. BMC Evolutionary Biology, 2013, 13, 80.	3.2	122
31	Explaining the distribution of breeding and dispersal syndromes in conifers. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131812.	1.2	29
32	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
33	Synthesizing phylogenetic knowledge for ecological research. Ecology, 2012, 93, S4-S13.	1.5	52
34	Megacycles of atmospheric carbon dioxide concentration correlate with fossil plant genome size. Philosophical Transactions of the Royal Society B: Biological Sciences, 2012, 367, 556-564.	1.8	39
35	Hemisphere-scale differences in conifer evolutionary dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16217-16221.	3.3	280
36	MODELING STABILIZING SELECTION: EXPANDING THE ORNSTEIN-UHLENBECK MODEL OF ADAPTIVE EVOLUTION. Evolution; International Journal of Organic Evolution, 2012, 66, 2369-2383.	1.1	537

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37	Understanding angiosperm diversification using small and large phylogenetic trees. American Journal of Botany, 2011, 98, 404-414.	0.8	161
38	Integrating Fossil Preservation Biases in the Selection of Calibrations for Molecular Divergence Time Estimation. Systematic Biology, 2011, 60, 519-527.	2.7	62
39	The right stuff: evidence for an â€˜optimalâ€™ genome size in a wild grass population. New Phytologist, 2010, 187, 883-885.	3.5	6
40	On the Relationship between Pollen Size and Genome Size. Journal of Botany, 2010, 2010, 1-7.	1.2	38
41	Genome Size Dynamics and Evolution in Monocots. Journal of Botany, 2010, 2010, 1-18.	1.2	66
42	On the Tempo of Genome Size Evolution in Angiosperms. Journal of Botany, 2010, 2010, 1-8.	1.2	24
43	An uncorrelated relaxed-clock analysis suggests an earlier origin for flowering plants. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5897-5902.	3.3	352
44	Life history influences rates of climatic niche evolution in flowering plants. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 4345-4352.	1.2	129
45	Mega-phylogeny approach for comparative biology: an alternative to supertree and supermatrix approaches. BMC Evolutionary Biology, 2009, 9, 37.	3.2	231
46	CORRELATED EVOLUTION OF GENOME SIZE AND CELL VOLUME IN DIATOMS (BACILLARIOPHYCEAE)¹. Journal of Phycology, 2008, 44, 124-131.	1.0	60
47	Genome size is a strong predictor of cell size and stomatal density in angiosperms. New Phytologist, 2008, 179, 975-986.	3.5	436
48	The Dynamic Ups and Downs of Genome Size Evolution in Brassicaceae. Molecular Biology and Evolution, 2008, 26, 85-98.	3.5	158
49	Genome Size Scaling through Phenotype Space. Annals of Botany, 2008, 101, 759-766.	1.4	138
50	Genome Size Evolution in Relation to Leaf Strategy and Metabolic Rates Revisited. Annals of Botany, 2007, 99, 495-505.	1.4	65
51	Correlated evolution of genome size and seed mass. New Phytologist, 2007, 173, 422-437.	3.5	189