

Michael J Hickerson

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,732
citations

394421

19
h-index

454955

30
g-index

33
all docs

33
docs citations

33
times ranked

3971
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic scale data shows that <i>Parastacus nicoleti</i> encompasses more than one species of burrowing continental crayfishes and that lineage divergence occurred with and without gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107443.	2.7	3
2	Riverscape genomics of cichlid fishes in the lower Congo: Uncovering mechanisms of diversification in an extreme hydrological regime. <i>Molecular Ecology</i> , 2022, 31, 3516-3532.	3.9	2
3	Rugged relief and climate promote isolation and divergence between two neotropical cold-associated birds. <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 2371-2387.	2.3	7
4	Asymmetrical gene flow in five co-distributed syngnathids explained by ocean currents and rafting propensity. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200657.	2.6	27
5	Quaternary climate changes as speciation drivers in the Amazon floodplains. <i>Science Advances</i> , 2020, 6, eaax4718.	10.3	55
6	Unifying macroecology and macroevolution to answer fundamental questions about biodiversity. <i>Global Ecology and Biogeography</i> , 2019, 28, 1925-1936.	5.8	44
7	A topoclimate model for Quaternary insular speciation. <i>Journal of Biogeography</i> , 2019, 46, 2769-2786.	3.0	8
8	An integrated model of population genetics and community ecology. <i>Journal of Biogeography</i> , 2019, 46, 816-829.	3.0	37
9	Phenotypic and Genetic Structure Support Gene Flow Generating Gene Tree Discordances in an Amazonian Floodplain Endemic Species. <i>Systematic Biology</i> , 2018, 67, 700-718.	5.6	60
10	Testing Hypotheses of Diversification in Panamanian Frogs and Freshwater Fishes Using Hierarchical Approximate Bayesian Computation with Model Averaging. <i>Diversity</i> , 2018, 10, 120.	1.7	9
11	ABLE: blockwise site frequency spectra for inferring complex population histories and recombination. <i>Genome Biology</i> , 2018, 19, 145.	8.8	16
12	Comment on Rieux and Balloux: calibration from tip-dating can compromise topological accuracy and evolutionary inference. <i>Molecular Ecology</i> , 2017, 26, 2623-2624.	3.9	1
13	Asynchronous diversification of snakes in the North American warm deserts. <i>Journal of Biogeography</i> , 2017, 44, 461-474.	3.0	40
14	Strategies for improving approximate Bayesian computation tests for synchronous diversification. <i>BMC Evolutionary Biology</i> , 2017, 17, 203.	3.2	10
15	Inferring responses to climate dynamics from historical demography in neotropical forest lizards. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7978-7985.	7.1	91
16	Spatially explicit summary statistics for historical population genetic inference. <i>Methods in Ecology and Evolution</i> , 2016, 7, 418-427.	5.2	21
17	Predicting the genetic consequences of future climate change: The power of coupling spatial demography, the coalescent, and historical landscape changes. <i>American Journal of Botany</i> , 2016, 103, 153-163.	1.7	43
18	The aggregate site frequency spectrum for comparative population genomic inference. <i>Molecular Ecology</i> , 2015, 24, 6223-6240.	3.9	49

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19	Model misspecification confounds the estimation of rates and exaggerates their time dependency. <i>Molecular Ecology</i> , 2015, 24, 6013-6020.	3.9	7
20	Comparative Population Genomics of African Montane Forest Mammals Support Population Persistence across a Climatic Gradient and Quaternary Climatic Cycles. <i>PLoS ONE</i> , 2015, 10, e0131800.	2.5	28
21	Population Genomics Reveals Seahorses (<i>Hippocampus erectus</i>) of the Western Mid-Atlantic Coast to Be Residents Rather than Vagrants. <i>PLoS ONE</i> , 2015, 10, e0116219.	2.5	45
22	Sampling strategies for frequency spectrum-based population genomic inference. <i>BMC Evolutionary Biology</i> , 2014, 14, 254.	3.2	69
23	RECOMMENDATIONS FOR USING MSBAYES TO INCORPORATE UNCERTAINTY IN SELECTING AN ABC MODEL PRIOR: A RESPONSE TO OAKS ET AL.. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 284-294.	2.3	29
24	Uncovering cryptic diversity and refugial persistence among small mammal lineages across the Eastern Afrotropical biodiversity hotspot. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 41-54.	2.7	80
25	The drivers of tropical speciation. <i>Nature</i> , 2014, 515, 406-409.	27.8	452
26	All models are wrong. <i>Molecular Ecology</i> , 2014, 23, 2887-2889.	3.9	7
27	Stability Predicts Genetic Diversity in the Brazilian Atlantic Forest Hotspot. <i>Science</i> , 2009, 323, 785-789.	12.6	922
28	DNA Barcoding Will Often Fail to Discover New Animal Species over Broad Parameter Space. <i>Systematic Biology</i> , 2006, 55, 729-739.	5.6	369
29	TEST FOR SIMULTANEOUS DIVERGENCE USING APPROXIMATE BAYESIAN COMPUTATION. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 2435-2453.	2.3	145
30	Test for simultaneous divergence using approximate Bayesian computation. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 2435-53.	2.3	48