

Bryan C Carstens

List of Publications by Year in descending order

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106
papers

9,067
citations

70961

41
h-index

43802

91
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115
all docs

115
docs citations

115
times ranked

9375
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative and predictive phylogeography in the South American diagonal of open formations: Unravelling the biological and environmental influences on multitaxon demography. <i>Molecular Ecology</i> , 2022, 31, 331-342.	2.0	6
2	Assessing model adequacy leads to more robust phylogeographic inference. <i>Trends in Ecology and Evolution</i> , 2022, 37, 402-410.	4.2	7
3	Analysis of biodiversity data suggests that mammal species are hidden in predictable places. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2103400119.	3.3	13
4	Genomic evidence of an ancient inland temperate rainforest in the Pacific Northwest of North America. <i>Molecular Ecology</i> , 2022, , .	2.0	4
5	Identifying traits that enable lizard adaptation to different habitats. <i>Journal of Biogeography</i> , 2022, 49, 104-116.	1.4	2
6	<sc>phylogatR</sc>: Phylogeographic data aggregation and repurposing. <i>Molecular Ecology Resources</i> , 2022, 22, 2830-2842.	2.2	11
7	The role of multiple Pleistocene refugia in promoting diversification in the Pacific Northwest. <i>Molecular Ecology</i> , 2022, 31, 4402-4416.	2.0	4
8	Predicting amphibian intraspecific diversity with machine learning: Challenges and prospects for integrating traits, geography, and genetic data. <i>Molecular Ecology Resources</i> , 2021, 21, 2818-2831.	2.2	13
9	P2C2M.GMYC: An R package for assessing the utility of the Generalized Mixed Yule Coalescent model. <i>Methods in Ecology and Evolution</i> , 2021, 12, 487-493.	2.2	10
10	Genomic data from the Brazilian sibilator frog reveal contrasting pleistocene dynamics and regionalism in two South American dry biomes. <i>Journal of Biogeography</i> , 2021, 48, 1112-1123.	1.4	13
11	Predicting migration routes for three species of migratory bats using species distribution models. <i>PeerJ</i> , 2021, 9, e11177.	0.9	17
12	Comparative phylogeography of two Northern Rocky Mountain endemics: the widespread <i>Anguispira kochi occidentalis</i> and the narrow-range <i>Anguispira nimapuna</i> (Gastropoda: Discidae). <i>Biological Journal of the Linnean Society</i> , 2021, 133, 817-834.	0.7	2
13	Phylogeographic model selection using convolutional neural networks. <i>Molecular Ecology Resources</i> , 2021, 21, 2661-2675.	2.2	14
14	Comment on "Population genetics reveal <i>Myotis keenii</i> (Keen's myotis) and <i>Myotis evotis</i> (long-eared myotis) to be a single species" Canadian Journal of Zoology, 2021, 99, 415-422.	0.4	5
15	A role of asynchrony of seasons in explaining genetic differentiation in a Neotropical toad. <i>Heredity</i> , 2021, 127, 363-372.	1.2	7
16	The Phylogeographic Shortfall in Hexapods: A Lot of Leg Work Remaining. <i>Insect Systematics and Diversity</i> , 2021, 5, .	0.7	6
17	Genetic diversity of North American vertebrates in protected areas. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 388-399.	0.7	7
18	Process-based species delimitation leads to identification of more biologically relevant species*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 216-229.	1.1	63

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19	Does habitat stability structure intraspecific genetic diversity? It's complicated.... Frontiers of Biogeography, 2020, 12, .	0.8	10
20	Population genetic structure and demographic history of the lone star tick, <i>Amblyomma americanum</i> (Ixodida: Ixodidae): New evidence supporting old records. Molecular Ecology, 2020, 29, 2810-2823.	2.0	11
21	Using trace elements to identify the geographic origin of migratory bats. PeerJ, 2020, 8, e10082.	0.9	11
22	Identifying model violations under the multispecies coalescent model using P2C2M.SNAPP. PeerJ, 2020, 8, e8271.	0.9	6
23	Diversification rates have no effect on the convergent evolution of foraging strategies in the most speciose genus of bats, <i>Myotis</i> *. Evolution; International Journal of Organic Evolution, 2019, 73, 2263-2280.	1.1	40
24	Integrating life history traits into predictive phylogeography. Molecular Ecology, 2019, 28, 2062-2073.	2.0	11
25	Complex interplay of ancient vicariance and recent patterns of geographical speciation in north-western North American temperate rainforests explains the phylogeny of jumping slugs (<i>Hemphillia</i> spp.). Biological Journal of the Linnean Society, 2019, 127, 876-889.	0.7	10
26	The <i>Sarracenia alata</i> pitcher plant system and obligate arthropod inquilines should be considered an evolutionary community. Journal of Biogeography, 2019, 46, 485-496.	1.4	6
27	Evidence that <i>Myotis lucifugus</i> "Subspecies" are Five Nonsister Species, Despite Gene Flow. Systematic Biology, 2018, 67, 756-769.	2.7	37
28	Combining allele frequency and tree-based approaches improves phylogeographic inference from natural history collections. Molecular Ecology, 2018, 27, 1012-1024.	2.0	9
29	Geographical range size and latitude predict population genetic structure in a global survey. Biology Letters, 2018, 14, 20170566.	1.0	50
30	Predicting plant conservation priorities on a global scale. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 13027-13032.	3.3	92
31	A global analysis of bats using automated comparative phylogeography uncovers a surprising impact of Pleistocene glaciation. Journal of Biogeography, 2018, 45, 1795-1805.	1.4	26
32	Testing for the presence of cryptic diversity in tail-dropper slugs (<i>Prophysaon</i>) using molecular data. Biological Journal of the Linnean Society, 2018, 124, 518-532.	0.7	10
33	Evaluating the adaptive evolutionary convergence of carnivorous plant taxa through functional genomics. PeerJ, 2018, 6, e4322.	0.9	6
34	Species Delimitation with Gene Flow. Systematic Biology, 2017, 66, syw117.	2.7	118
35	Speciation with Gene Flow in North American <i>Myotis</i> Bats. Systematic Biology, 2017, 66, syw100.	2.7	50
36	PHRAPL: Phylogeographic Inference Using Approximate Likelihoods. Systematic Biology, 2017, 66, 1045-1053.	2.7	59

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37	Do ecological communities disperse across biogeographic barriers as a unit?. <i>Molecular Ecology</i> , 2017, 26, 3533-3545.	2.0	35
38	Objective choice of phylogeographic models. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 136-140.	1.2	13
39	Statistical hybrid detection and the inference of ancestral distribution areas in <i>Tolpis</i> (Asteraceae). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 133-149.	0.7	6
40	From inland to the coast: Spatial and environmental signatures on the genetic diversity in the colonization of the South Atlantic Coastal Plain. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2017, 28, 47-57.	1.1	18
41	Demographic model selection using random forests and the site frequency spectrum. <i>Molecular Ecology</i> , 2017, 26, 4562-4573.	2.0	49
42	Community trees: Identifying codiversification in the Páramo dipteran community. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1080-1093.	1.1	5
43	Recurrent connections between Amazon and Atlantic forests shaped diversity in Caatinga four-eyed frogs. <i>Journal of Biogeography</i> , 2016, 43, 1045-1056.	1.4	64
44	Phylogeographic concordance factors quantify phylogeographic congruence among co-distributed species in the <i>Sarracenia alata</i> pitcher plant system. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 1105-1119.	1.1	37
45	Posterior predictive checks of coalescent models: P2C2M, an R package. <i>Molecular Ecology Resources</i> , 2016, 16, 193-205.	2.2	21
46	Comparing range evolution in two western <i>Plethodon</i> salamanders: glacial refugia, competition, ecological niches, and spatial sorting. <i>Journal of Biogeography</i> , 2016, 43, 2237-2249.	1.4	16
47	Phylogeographic model selection leads to insight into the evolutionary history of four-eyed frogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8010-8017.	3.3	43
48	Identifying cryptic diversity with predictive phylogeography. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20161529.	1.2	45
49	Anonymous nuclear markers data supporting species tree phylogeny and divergence time estimates in a cactus species complex in South America. <i>Data in Brief</i> , 2016, 6, 456-460.	0.5	3
50	Anonymous nuclear markers reveal taxonomic incongruence and long-term disjunction in a cactus species complex with continental-island distribution in South America. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 11-19.	1.2	16
51	Biogeographic barriers drive co-diversification within associated eukaryotes of the <i>Sarracenia alata</i> pitcher plant system. <i>PeerJ</i> , 2016, 4, e1576.	0.9	11
52	Genetic diversity in migratory bats: Results from RADseq data for three tree bat species at an Ohio windfarm. <i>PeerJ</i> , 2016, 4, e1647.	0.9	33
53	Diversification of North American natricine snakes. <i>Biological Journal of the Linnean Society</i> , 2015, 116, 1-12.	0.7	23
54	Comparative Gut Microbiota of 59 Neotropical Bird Species. <i>Frontiers in Microbiology</i> , 2015, 6, 1403.	1.5	216

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55	The evolution of phylogeographic data sets. <i>Molecular Ecology</i> , 2015, 24, 1164-1171.	2.0	119
56	Historical Species Distribution Models Predict Species Limits in Western <i>Plethodon</i> Salamanders. <i>Systematic Biology</i> , 2015, 64, 909-925.	2.7	31
57	Using Next Generation RAD Sequencing to Isolate Multispecies Microsatellites for <i>Pilosocereus</i> (Cactaceae). <i>PLoS ONE</i> , 2015, 10, e0142602.	1.1	19
58	Sampling locality is more detectable than taxonomy or ecology in the gut microbiota of the brood-parasitic Brown-headed Cowbird (<i>Molothrus ater</i>). <i>PeerJ</i> , 2014, 2, e321.	0.9	126
59	Model choice for phylogeographic inference using a large set of models. <i>Molecular Ecology</i> , 2014, 23, 3028-3043.	2.0	55
60	Poor Fit to the Multispecies Coalescent is Widely Detectable in Empirical Data. <i>Systematic Biology</i> , 2014, 63, 322-333.	2.7	78
61	Comparative phylogeography of mutualists and the effect of the host on the genetic structure of its partners. <i>Biological Journal of the Linnean Society</i> , 2014, 113, 1021-1035.	0.7	23
62	Climate refugia: joint inference from fossil records, species distribution models and phylogeography. <i>New Phytologist</i> , 2014, 204, 37-54.	3.5	361
63	How to fail at species delimitation. <i>Molecular Ecology</i> , 2013, 22, 4369-4383.	2.0	896
64	The carnivorous plant described as <i>Sarracenia alata</i> contains two cryptic species. <i>Biological Journal of the Linnean Society</i> , 2013, 109, 737-746.	0.7	56
65	Model selection as a tool for phylogeographic inference: an example from the willow <i>Saxifraga alix melanopsis</i> . <i>Molecular Ecology</i> , 2013, 22, 4014-4028.	2.0	58
66	Testing monophyly without well-supported gene trees: Evidence from multi-locus nuclear data conflicts with existing taxonomy in the snake tribe <i>Thamnophiini</i> . <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 425-431.	1.2	15
67	Multilocus Species Delimitation in a Complex of Morphologically Conserved Trapdoor Spiders (Mygalomorphae, Antrodiaetidae, <i>Aliatypus</i>). <i>Systematic Biology</i> , 2013, 62, 805-823.	2.7	221
68	Applications of next-generation sequencing to phylogeography and phylogenetics. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 526-538.	1.2	531
69	Assessing model fit in phylogeographical investigations: an example from the <i>North American sandbar willow</i> <i>Saxifraga alix melanopsis</i> . <i>Journal of Biogeography</i> , 2013, 40, 131-141.	1.4	35
70	A road map for molecular ecology. <i>Molecular Ecology</i> , 2013, 22, 2605-2626.	2.0	100
71	The Promises and Pitfalls of Next-Generation Sequencing Data in Phylogeography. <i>Systematic Biology</i> , 2012, 61, 713-715.	2.7	36
72	Deep Phylogeographic Structure and Environmental Differentiation in the Carnivorous Plant <i>Sarracenia alata</i> . <i>Systematic Biology</i> , 2012, 61, 763-777.	2.7	69

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73	Phylogenetic estimation error can decrease the accuracy of species delimitation: a Bayesian implementation of the general mixed Yule-coalescent model. <i>BMC Evolutionary Biology</i> , 2012, 12, 196.	3.2	432
74	SpedeSTEM: a rapid and accurate method for species delimitation. <i>Molecular Ecology Resources</i> , 2011, 11, 473-480.	2.2	223
75	PRGmatic: an efficient pipeline for collating genome-enriched second-generation sequencing data using a "provisional" reference genome™. <i>Molecular Ecology Resources</i> , 2011, 11, 743-748. ^{2,2}		52
76	The Microbial Phylogeography of the Carnivorous Plant <i>Sarracenia alata</i> . <i>Microbial Ecology</i> , 2011, 61, 750-758.	1.4	34
77	Conservation genetic inferences in the carnivorous pitcher plant <i>Sarracenia alata</i> (Sarraceniaceae). <i>Conservation Genetics</i> , 2010, 11, 2027-2038.	0.8	32
78	Rapid and accurate species tree estimation for phylogeographic investigations using replicated subsampling. <i>Molecular Phylogenetics and Evolution</i> , 2010, 57, 888-898.	1.2	29
79	Navigating the unknown: model selection in phylogeography. <i>Molecular Ecology</i> , 2010, 19, 4581-4582.	2.0	8
80	Phylogeography's past, present, and future: 10 years after <i>Avice</i> , 2000. <i>Molecular Phylogenetics and Evolution</i> , 2010, 54, 291-301.	1.2	535
81	The Carnivorous Pale Pitcher Plant Harbors Diverse, Distinct, and Time-Dependent Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1851-1860.	1.4	56
82	Species Delimitation Using a Combined Coalescent and Information-Theoretic Approach: An Example from North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2010, 59, 400-414.	2.7	167
83	STEM: species tree estimation using maximum likelihood for gene trees under coalescence. <i>Bioinformatics</i> , 2009, 25, 971-973.	1.8	419
84	An information-theoretical approach to phylogeography. <i>Molecular Ecology</i> , 2009, 18, 4270-4282.	2.0	66
85	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 May 2009–31 July 2009. <i>Molecular Ecology Resources</i> , 2009, 9, 1460-1466.	2.2	128
86	X Chromosome Inactivation and Xist Evolution in a Rodent Lacking LINE-1 Activity. <i>PLoS ONE</i> , 2009, 4, e6252.	1.1	23
87	Does gene flow destroy phylogenetic signal? The performance of three methods for estimating species phylogenies in the presence of gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 832-842.	1.2	132
88	Insights into the Biogeography of the Pacific Northwest of North America: Evidence from the Phylogeography of <i>Salix melanopsis</i> . <i>Systematic Botany</i> , 2007, 32, 129-139.	0.2	44
89	Estimating Species Phylogeny from Gene-Tree Probabilities Despite Incomplete Lineage Sorting: An Example from <i>Melanoplus</i> Grasshoppers. <i>Systematic Biology</i> , 2007, 56, 400-411.	2.7	309
90	Delimiting Species without Monophyletic Gene Trees. <i>Systematic Biology</i> , 2007, 56, 887-895.	2.7	657

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91	Distribution modelling and statistical phylogeography: an integrative framework for generating and testing alternative biogeographical hypotheses. <i>Journal of Biogeography</i> , 2007, 34, 1833-1845.	1.4	245
92	ESTIMATING A GEOGRAPHICALLY EXPLICIT MODEL OF POPULATION DIVERGENCE. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 477-493.	1.1	92
93	INTEGRATING COALESCENT AND ECOLOGICAL NICHE MODELING IN COMPARATIVE PHYLOGEOGRAPHY. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1439-1454.	1.1	290
94	Coupling Genetic and Ecological-Niche Models to Examine How Past Population Distributions Contribute to Divergence. <i>Current Biology</i> , 2007, 17, 940-946.	1.8	148
95	Variable nuclear markers for <i>Melanoplus oregonensis</i> identified from the screening of a genomic library. <i>Molecular Ecology Notes</i> , 2006, 6, 683-685.	1.7	15
96	Shifting distributions and speciation: species divergence during rapid climate change. <i>Molecular Ecology</i> , 2006, 16, 619-627.	2.0	168
97	Testing hypotheses of speciation timing in <i>Dicamptodon copei</i> and <i>Dicamptodon aterrimus</i> (Caudata: Tj ETQq1 1 0.784314 48 BT / Over	1.2	48
98	Testing population genetic structure using parametric bootstrapping and MIGRATE-N. <i>Genetica</i> , 2005, 124, 71-75.	0.5	6
99	INVESTIGATING THE EVOLUTIONARY HISTORY OF THE PACIFIC NORTHWEST MESIC FOREST ECOSYSTEM: HYPOTHESIS TESTING WITHIN A COMPARATIVE PHYLOGEOGRAPHIC FRAMEWORK. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 1639.	1.1	170
100	Phylogeny of Leafhopper Subgenus <i>Errhomus</i> (<i>Erronus</i>) (Hemiptera: Cicadellidae) Based on Mitochondrial DNA Sequences. <i>Annals of the Entomological Society of America</i> , 2005, 98, 165-172.	1.3	3
101	Exploring population genetic structure in three species of Lesser Antillean bats. <i>Molecular Ecology</i> , 2004, 13, 2557-2566.	2.0	64
102	Accounting for coalescent stochasticity in testing phylogeographical hypotheses: modelling Pleistocene population structure in the Idaho giant salamander <i>Dicamptodon aterrimus</i> . <i>Molecular Ecology</i> , 2004, 14, 255-265.	2.0	89
103	Testing Nested Phylogenetic and Phylogeographic Hypotheses in the <i>Plethodon vandykei</i> Species Group. <i>Systematic Biology</i> , 2004, 53, 781-792.	2.7	85
104	Title is missing!. <i>Journal of Mammalian Evolution</i> , 2002, 9, 23-53.	1.0	38
105	Genomic Resources for the North American Water Vole (<i>Microtus richardsoni</i>) and the Montane Vole (<i>Microtus montanus</i>). <i>GigaByte</i> , 0, 2021, 1-13.	0.0	1
106	Giant tree frogs exemplify the promise of integrating multiple types of data in phylogeographic investigations. <i>Molecular Ecology</i> , 0, , .	2.0	1