Brant C Faircloth

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3325965/publications.pdf

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		44042	30894
104	20,804	48	102
papers	citations	h-index	g-index

127	127	127	27788
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Primer3â€"new capabilities and interfaces. Nucleic Acids Research, 2012, 40, e115-e115.	6.5	7,501
2	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
3	Ultraconserved Elements Anchor Thousands of Genetic Markers Spanning Multiple Evolutionary Timescales. Systematic Biology, 2012, 61, 717-726.	2.7	983
4	msatcommander: detection of microsatellite repeat arrays and automated, locus-specific primer design. Molecular Ecology Resources, 2008, 8, 92-94.	2.2	853
5	PHYLUCE is a software package for the analysis of conserved genomic loci. Bioinformatics, 2016, 32, 786-788.	1.8	609
6	The drivers of tropical speciation. Nature, 2014, 515, 406-409.	13.7	452
7	Ultraconserved elements are novel phylogenomic markers that resolve placental mammal phylogeny when combined with species-tree analysis. Genome Research, 2012, 22, 746-754.	2.4	349
8	More than 1000 ultraconserved elements provide evidence that turtles are the sister group of archosaurs. Biology Letters, 2012, 8, 783-786.	1.0	331
9	Phylogenomic Insights into the Evolution of Stinging Wasps and the Origins of Ants and Bees. Current Biology, 2017, 27, 1019-1025.	1.8	329
10	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. Molecular Phylogenetics and Evolution, 2016, 94, 447-462.	1.2	321
11	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	6.0	300
12	A Phylogeny of Birds Based on Over 1,500 Loci Collected by Target Enrichment and High-Throughput Sequencing. PLoS ONE, 2013, 8, e54848.	1.1	287
13	Target Capture and Massively Parallel Sequencing of Ultraconserved Elements for Comparative Studies at Shallow Evolutionary Time Scales. Systematic Biology, 2014, 63, 83-95.	2.7	286
14	Not All Sequence Tags Are Created Equal: Designing and Validating Sequence Identification Tags Robust to Indels. PLoS ONE, 2012, 7, e42543.	1.1	267
15	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	13.7	251
16	A Phylogenomic Perspective on the Radiation of Ray-Finned Fishes Based upon Targeted Sequencing of Ultraconserved Elements (UCEs). PLoS ONE, 2013, 8, e65923.	1.1	247
17	Target enrichment of ultraconserved elements from arthropods provides a genomic perspective on relationships among <scp>H</scp>ymenoptera. Molecular Ecology Resources, 2015, 15, 489-501.	2.2	244
18	A phylogenomic analysis of turtles. Molecular Phylogenetics and Evolution, 2015, 83, 250-257.	1.2	244

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19	Adapterama I: universal stubs and primers for 384 unique dual-indexed or 147,456 combinatorially-indexed Illumina libraries (iTru & iNext). PeerJ, 2019, 7, e7755.	0.9	243
20	Earth history and the passerine superradiation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7916-7925.	3.3	238
21	Sequence Capture versus Restriction Site Associated DNA Sequencing for Shallow Systematics. Systematic Biology, 2016, 65, 910-924.	2.7	220
22	Avoiding Missing Data Biases in Phylogenomic Inference: An Empirical Study in the Landfowl (Aves:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.5	208
23	Sequence capture of ultraconserved elements from bird museum specimens. Molecular Ecology Resources, 2016, 16, 1189-1203.	2.2	206
24	Enriching the ant tree of life: enhanced UCE bait set for genomeâ€scale phylogenetics of ants and other Hymenoptera. Methods in Ecology and Evolution, 2017, 8, 768-776.	2.2	190
25	Relating belowground microbial composition to the taxonomic, phylogenetic, and functional trait distributions of trees in a tropical forest. Ecology Letters, 2015, 18, 1397-1405.	3.0	183
26	Tectonic collision and uplift of Wallacea triggered the global songbird radiation. Nature Communications, 2016, 7, 12709.	5.8	183
27	The evolution of a tropical biodiversity hotspot. Science, 2020, 370, 1343-1348.	6.0	179
28	Explosive diversification of marine fishes at the Cretaceousâ€“Palaeogene boundary. Nature Ecology and Evolution, 2018, 2, 688-696.	3.4	156
29	Analysis of a Rapid Evolutionary Radiation Using Ultraconserved Elements: Evidence for a Bias in Some Multispecies Coalescent Methods. Systematic Biology, 2016, 65, 612-627.	2.7	137
30	Identifying conserved genomic elements and designing universal bait sets to enrich them. Methods in Ecology and Evolution, 2017, 8, 1103-1112.	2.2	133
31	Dry habitats were crucibles of domestication in the evolution of agriculture in ants. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170095.	1.2	130
32	Cultivation and genomics of the first freshwater SAR11 (LD12) isolate. ISME Journal, 2018, 12, 1846-1860.	4.4	123
33	<scp>RAD</scp>cap: sequence capture of dualâ€digest <scp>RAD</scp>seq libraries with identifiable duplicates and reduced missing data. Molecular Ecology Resources, 2016, 16, 1264-1278.	2.2	117
34	Universal targetâ€enrichment baits for anthozoan (Cnidaria) phylogenomics: New approaches to longâ€standing problems. Molecular Ecology Resources, 2018, 18, 281-295.	2.2	114
35	Investigating Difficult Nodes in the Placental Mammal Tree with Expanded Taxon Sampling and Thousands of Ultraconserved Elements. Genome Biology and Evolution, 2017, 9, 2308-2321.	1.1	102
36	High phylogenetic utility of an ultraconserved element probe set designed for Arachnida. Molecular Ecology Resources, 2017, 17, 812-823.	2.2	99

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37	Adapterama III: Quadruple-indexed, double/triple-enzyme RADseq libraries (2RAD/3RAD). PeerJ, 2019, 7, e7724.	0.9	96
38	A Phylogenomic Supertree of Birds. Diversity, 2019, 11, 109.	0.7	93
39	Palaeoclimate ocean conditions shaped the evolution of corals and their skeletons through deep time. Nature Ecology and Evolution, 2020, 4, 1531-1538.	3.4	90
40	Phylogenomic analysis of carangimorph fishes reveals flatfish asymmetry arose in a blink of the evolutionary eye. BMC Evolutionary Biology, 2016, 16, 224.	3.2	79
41	Incongruence among different mitochondrial regions: A case study using complete mitogenomes. Molecular Phylogenetics and Evolution, 2014, 78, 314-323.	1.2	75
42	Phylogenomic Systematics of Ostariophysan Fishes: Ultraconserved Elements Support the Surprising Non-Monophyly of Characiformes. Systematic Biology, 2017, 66, 881-895.	2.7	74
43	Allele Phasing Greatly Improves the Phylogenetic Utility of Ultraconserved Elements. Systematic Biology, 2019, 68, 32-46.	2.7	74
44	Phylogenomic analyses data of the avian phylogenomics project. GigaScience, 2015, 4, 4.	3.3	72
45	Genome-wide ultraconserved elements exhibit higher phylogenetic informativeness than traditional gene markers in percomorph fishes. Molecular Phylogenetics and Evolution, 2015, 92, 140-146.	1.2	68
46	Hidden histories of gene flow in highland birds revealed with genomic markers. Molecular Ecology, 2016, 25, 5144-5157.	2.0	64
47	Conflicting Evolutionary Histories of the Mitochondrial and Nuclear Genomes in New World Myotis Bats. Systematic Biology, 2018, 67, 236-249.	2.7	56
48	Resolving Deep Nodes in an Ancient Radiation of Neotropical Fishes in the Presence of Conflicting Signals from Incomplete Lineage Sorting. Systematic Biology, 2019, 68, 573-593.	2.7	54
49	Ultraconserved elements (UCEs) resolve the phylogeny of Australasian smurf-weevils. PLoS ONE, 2017, 12, e0188044.	1.1	51
50	Insight from an ultraconserved element bait set designed for hemipteran phylogenetics integrated with genomic resources. Molecular Phylogenetics and Evolution, 2019, 130, 297-303.	1.2	51
51	Replicated divergence in cichlid radiations mirrors a major vertebrate innovation. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20151413.	1.2	50
52	Phylogenomic analysis of a rapid radiation of misfit fishes (Syngnathiformes) using ultraconserved elements. Molecular Phylogenetics and Evolution, 2017, 113, 33-48.	1.2	49
53	Speciation in Western Scrub-Jays, Haldaneâ€™s rule, and genetic clines in secondary contact. BMC Evolutionary Biology, 2014, 14, 135.	3.2	48
54	The evolution of peafowl and other taxa with ocelli (eyespots): a phylogenomic approach. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140823.	1.2	47

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55	Adapterama II: universal amplicon sequencing on Illumina platforms (TaggiMatrix). PeerJ, 2019, 7, e7786.	0.9	47
56	Tetranucleotide microsatellites from the loggerhead sea turtle (Caretta caretta). Molecular Ecology Notes, 2007, 7, 784-787.	1.7	42
57	Accelerated Diversification Explains the Exceptional Species Richness of Tropical Characoid Fishes. Systematic Biology, 2021, 71, 78-92.	2.7	42
58	The critical importance of vouchers in genomics. ELife, 2021, 10, .	2.8	39
59	Prolonged morphological expansion of spiny-rayed fishes following the end-Cretaceous. Nature Ecology and Evolution, 2022, 6, 1211-1220.	3.4	39
60	Translocation to a fragmented landscape: survival, movement, and site fidelity of Northern Bobwhites. Ecological Applications, 2010, 20, 1040-1052.	1.8	37
61	Tetranucleotide markers from the loggerhead sea turtle (Caretta caretta) and their cross-amplification in other marine turtle species. Conservation Genetics, 2009, 10, 577-580.	0.8	34
62	Genomeâ€wide signals of drift and local adaptation during rapid lineage divergence in a songbird. Molecular Ecology, 2018, 27, 5137-5153.	2.0	33
63	Use of sonic tomography to detect and quantify wood decay in living trees. Applications in Plant Sciences, 2016, 4, 1600060.	0.8	32
64	A phylogenomic framework for pelagiarian fishes (Acanthomorpha: Percomorpha) highlights mosaic radiation in the open ocean. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191502.	1.2	31
65	Extensive paraphyly in the typical owl family (Strigidae). Auk, 2020, 137, .	0.7	31
66	Ultraconserved elements (UCEs) illuminate the population genomics of a recent, high-latitude avian speciation event. PeerJ, 2018, 6, e5735.	0.9	31
67	Nextâ€generation phylogenetics takes root. Molecular Ecology, 2013, 22, 19-21.	2.0	30
68	What are the roles of taxon sampling and model fit in tests of cyto-nuclear discordance using avian mitogenomic data?. Molecular Phylogenetics and Evolution, 2019, 130, 132-142.	1.2	30
69	Post-hatching brood amalgamation in Northern Bobwhites. Journal of Field Ornithology, 2005, 76, 175-182.	0.3	27
70	Significant variance in genetic diversity among populations of Schistosoma haematobium detected using microsatellite DNA loci from a genome-wide database. Parasites and Vectors, 2013, 6, 300.	1.0	26
71	gmconvert: file conversion for genemapper output files. Molecular Ecology Notes, 2006, 6, 968-970.	1.7	24
72	Developing a community-based genetic nomenclature for anole lizards. BMC Genomics, 2011, 12, 554.	1.2	23

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73	Capturing Darwin's dream. Molecular Ecology Resources, 2016, 16, 1051-1058.	2.2	22
74	A Target Enrichment Bait Set for Studying Relationships among Ostariophysan Fishes. Copeia, 2020, 108, 47.	1.4	20
75	Interactive effects of male and female age on extra-pair paternity in a socially monogamous seabird. Behavioral Ecology and Sociobiology, 2014, 68, 1603-1609.	0.6	19
76	Habitat structure and colony structure constrain extrapair paternity inÂa colonial bird. Animal Behaviour, 2014, 95, 121-127.	0.8	18
77	Divergence, gene flow, and speciation in eight lineages of transâ€Beringian birds. Molecular Ecology, 2020, 29, 3526-3542.	2.0	18
78	Displaced clines in an avian hybrid zone (Thamnophilidae:Rhegmatorhina) within an Amazonian interfluve[*]. Evolution; International Journal of Organic Evolution, 2022, 76, 455-475.	1.1	18
79	Tetranucleotide, trinucleotide, and dinucleotide loci from the bobcat (Lynx rufus). Molecular Ecology Notes, 2005, 5, 387-389.	1.7	17
80	Target enrichment of thousands of ultraconserved elements sheds new light on early relationships within New World sparrows (Aves: Passerellidae). Auk, 2016, 133, 451-458.	0.7	17
81	Phylogenomic species delimitation in microendemic frogs of the Brazilian Atlantic Forest. Molecular Phylogenetics and Evolution, 2019, 141, 106627.	1.2	16
82	Using ultraconserved elements to track the influence of seaâ€level change on leafy seadragon populations. Molecular Ecology, 2021, 30, 1364-1380.	2.0	16
83	Tetranucleotide microsatellite loci from the black bear (Ursus americanus). Molecular Ecology Resources, 2009, 9, 288-291.	2.2	14
84	Phylogenomic analysis of Lake Malawi cichlid fishes: Further evidence that the three-stage model of diversification does not fit. Molecular Phylogenetics and Evolution, 2017, 114, 40-48.	1.2	14
85	Tetranucleotide and dinucleotide microsatellite loci from the northern bobwhite (Colinus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf	1.7	13
86	Ten microsatellite loci from Northern Bobwhite (Colinus virginianus). Conservation Genetics, 2009, 10, 535-538.	0.8	13
87	A Highly Contiguous Reference Genome for Northern Bobwhite (Colinus virginianus). G3: Genes, Genomes, Genetics, 2019, 9, 3929-3932.	0.8	10
88	Historical specimens and the limits of subspecies phylogenomics in the New World quails (Odontophoridae). Molecular Phylogenetics and Evolution, 2022, 175, 107559.	1.2	10
89	Targeted DNA Region Re-sequencing. , 2016, , 43-68.		9
90	Isolation and characterization of microsatellite loci from blue-footed boobies (Sula nebouxii). Conservation Genetics Resources, 2009, 1, 159-162.	0.4	8

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91	Speciation despite gene flow in two owls (Aegolius ssp.): Evidence from 2,517 ultraconserved element loci. Auk, 2019, 136, .	0.7	8
92	Tetranucleotide microsatellite loci from eastern bluebirds Sialia sialis. Molecular Ecology Notes, 2006, 6, 646-649.	1.7	7
93	Phylogenomics of montane frogs of the Brazilian Atlantic Forest is consistent with isolation in sky islands followed by climatic stability. Biological Journal of the Linnean Society, 0, , .	0.7	7
94	Eighteen microsatellite loci developed from western burrowing owls (Athene cunicularia hypugaea). Conservation Genetics Resources, 2010, 2, 167-171.	0.4	6
95	Microsatellite markers for eastern hemlock (Tsuga canadensis). Molecular Ecology Resources, 2008, 8, 1354-1356.	2.2	5
96	Comparison of ultraconserved elements (UCEs) to microsatellite markers for the study of avian hybrid zones: a test in Aphelocoma jays. BMC Research Notes, 2019, 12, 456.	0.6	5
97	Biogeography of a neotropical songbird radiation reveals similar diversification dynamics between montane and lowland clades. Journal of Biogeography, 2022, 49, 1260-1273.	1.4	5
98	Systematics of Lepidothrix manakins (Aves: Passeriformes: Pipridae) using RADcap markers. Molecular Phylogenetics and Evolution, 2022, 173, 107525.	1.2	5
99	The mitochondrial genome of Brachycephalus brunneus (Anura: Brachycephalidae), with comments on the phylogenetic position of Brachycephalidae. Biochemical Systematics and Ecology, 2017, 71, 26-31.	0.6	3
100	Phylogenetic relationships of diurnal, phytotelm-breeding Melanophryniscus (Anura: Bufonidae) based on mitogenomic data. Gene, 2017, 628, 194-199.	1.0	3
101	Genome assemblies for two Neotropical trees: Jacaranda copaia and Handroanthus guayacan. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
102	Multiple species and deep genomic divergences despite little phenotypic differentiation in an ancient Neotropical songbird, Tunchiornis ochraceiceps (Sclater, 1860) (Aves: Vireonidae). Molecular Phylogenetics and Evolution, 2021, 162, 107206.	1.2	3
103	A reference genome for the nectar-robbing Black-throated Flowerpiercer (Diglossa) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 2	0.8	2
104	Effects of Tissue Collection Methods on Morphometrics and Survival of Captive Neonatal Northern Bobwhite. Journal of Wildlife Management, 2009, 73, 1241-1244.	0.7	1