

Julian M Catchen

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

12,240
citations

172457
29
h-index

197818
49
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59
all docs

59
docs citations

59
times ranked

14019
citing authors

#	ARTICLE	IF	CITATIONS
1	Leafy and weedy seadragon genomes connect genic and repetitive DNA features to the extravagant biology of syngnathid fishes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	8
2	The genomic basis of the plant island syndrome in Darwin's giant daisies. <i>Nature Communications</i> , 2022, 13, .	12.8	6
3	Simulation with RADinitio improves RADseq experimental design and sheds light on sources of missing data. <i>Molecular Ecology Resources</i> , 2021, 21, 363-378.	4.8	29
4	The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. <i>Current Biology</i> , 2021, 31, 911-922.e4.	3.9	24
5	Incomplete lineage sorting and ancient admixture, and speciation without morphological change in ghost-worm cryptic species. <i>PeerJ</i> , 2021, 9, e10896.	2.0	15
6	Removing the bad apples: A simple bioinformatic method to improve loci recovery in de novo RADseq data for non-model organisms. <i>Methods in Ecology and Evolution</i> , 2021, 12, 805-817.	5.2	25
7	Sequence Analysis and Ontogenetic Expression Patterns of Cone Opsin Genes in the Bluefin Killifish (<i>Lucania goodei</i>). <i>Journal of Heredity</i> , 2021, 112, 357-366.	2.4	11
8	Genomic Resources for Darters (Percidae: Etheostominae) Provide Insight into Postzygotic Barriers Implicated in Speciation. <i>Molecular Biology and Evolution</i> , 2020, 37, 711-729.	8.9	22
9	Chromonomer: A Tool Set for Repairing and Enhancing Assembled Genomes Through Integration of Genetic Maps and Conserved Synteny. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4115-4128.	1.8	44
10	Parallel selection on thermal physiology facilitates repeated adaptation of city lizards to urban heat islands. <i>Nature Ecology and Evolution</i> , 2020, 4, 652-658.	7.8	102
11	Stacks 2: Analytical methods for paired-end sequencing improve RADseq-based population genomics. <i>Molecular Ecology</i> , 2019, 28, 4737-4754.	3.9	648
12	Selection, Linkage, and Population Structure Interact To Shape Genetic Variation Among Threespine Stickleback Genomes. <i>Genetics</i> , 2019, 212, 1367-1382.	2.9	6
13	Antarctic blackfin icefish genome reveals adaptations to extreme environments. <i>Nature Ecology and Evolution</i> , 2019, 3, 469-478.	7.8	115
14	Hybridization and postzygotic isolation promote reinforcement of male mating preferences in a diverse group of fishes with traditional sex roles. <i>Ecology and Evolution</i> , 2018, 8, 9282-9294.	1.9	12
15	Repeated Selection of Alternatively Adapted Haplotypes Creates Sweeping Genomic Remodeling in Stickleback. <i>Genetics</i> , 2018, 209, 921-939.	2.9	64
16	Genomic diversity is similar between Atlantic Forest restorations and natural remnants for the native tree <i>Casearia sylvestris</i> Sw.. <i>PLoS ONE</i> , 2018, 13, e0192165.	2.5	10
17	Lost in parameter space: a road map for <sc>stacks</sc>. <i>Methods in Ecology and Evolution</i> , 2017, 8, 1360-1373.	5.2	466
18	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 362-365.	4.8	156

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19	Ancient three-spined stickleback (<i>Gasterosteus aculeatus</i>) mtDNA lineages are not associated with phenotypic or nuclear genetic variation. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 579-588.	1.6	4
20	Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. <i>Science</i> , 2017, 357, 495-498.	12.6	204
21	Male and female contributions to behavioral isolation in darters as a function of genetic distance and color distance. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2428-2444.	2.3	36
22	The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , 2017, 9, 3260-3264.	2.5	33
23	When structure leads to sex: Untangling signals in population genetic data sets. <i>Molecular Ecology</i> , 2017, 26, 6763-6766.	3.9	3
24	Deriving genotypes from RAD-seq short-read data using Stacks. <i>Nature Protocols</i> , 2017, 12, 2640-2659.	12.0	335
25	<scp>RAD</scp>cap: sequence capture of dualâ€digest <scp>RAD</scp>seq libraries with identifiable duplicates and reduced missing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1264-1278.	4.8	117
26	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. <i>Nature Genetics</i> , 2016, 48, 427-437.	21.4	545
27	Evolution of stickleback in 50 years on earthquake-uplifted islands. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E7204-12.	7.1	156
28	A RAD-Tag Genetic Map for the Platyfish (<i>Xiphophorus maculatus</i>) Reveals Mechanisms of Karyotype Evolution Among Teleost Fish. <i>Genetics</i> , 2014, 197, 625-641.	2.9	80
29	Stacks: an analysis tool set for population genomics. <i>Molecular Ecology</i> , 2013, 22, 3124-3140.	3.9	3,077
30	The population structure and recent colonization history of <scp>O</scp>regon threespine stickleback determined using restrictionâ€site associated <scp>DNA</scp>â€sequencing. <i>Molecular Ecology</i> , 2013, 22, 2864-2883.	3.9	119
31	The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. <i>Nature Genetics</i> , 2013, 45, 567-572.	21.4	251
32	Comparative Oncogenomic Analysis of Copy Number Alterations in Human and Zebrafish Tumors Enables Cancer Driver Discovery. <i>PLoS Genetics</i> , 2013, 9, e1003734.	3.5	30
33	Replicate Phylogenies and Post-Glacial Range Expansion of the Pitcher-Plant Mosquito, <i>Wyeomyia smithii</i> , in North America. <i>PLoS ONE</i> , 2013, 8, e72262.	2.5	15
34	Retinoic Acid Metabolic Genes, Meiosis, and Gonadal Sex Differentiation in Zebrafish. <i>PLoS ONE</i> , 2013, 8, e73951.	2.5	83
35	Footprints in time: comparative quantitative trait loci mapping of the pitcher-plant mosquito, <i>Wyeomyia smithii</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 4551-4558.	2.6	18
36	Population Genomic Analysis of Model and Nonmodel Organisms Using Sequenced RAD Tags. <i>Methods in Molecular Biology</i> , 2012, 888, 235-260.	0.9	56

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37	Conserved Synteny and the Zebrafish Genome. <i>Methods in Cell Biology</i> , 2011, 104, 259-285.	1.1	41
38	Genome-wide genetic marker discovery and genotyping using next-generation sequencing. <i>Nature Reviews Genetics</i> , 2011, 12, 499-510.	16.3	2,198
39	Genome Evolution and Meiotic Maps by Massively Parallel DNA Sequencing: Spotted Gar, an Outgroup for the Teleost Genome Duplication. <i>Genetics</i> , 2011, 188, 799-808.	2.9	333
40	<i>Stacks</i> : Building and Genotyping Loci <i>De Novo</i> From Short-Read Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 171-182.	1.8	1,643
41	Resolving postglacial phylogeography using high-throughput sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16196-16200.	7.1	412
42	UDP xylose synthase 1 is required for morphogenesis and histogenesis of the craniofacial skeleton. <i>Developmental Biology</i> , 2010, 341, 400-415.	2.0	51
43	Automated identification of conserved synteny after whole-genome duplication. <i>Genome Research</i> , 2009, 19, 1497-1505.	5.5	205
44	Expression profiling of zebrafish <i>sox9</i> mutants reveals that <i>Sox9</i> is required for retinal differentiation. <i>Developmental Biology</i> , 2009, 329, 1-15.	2.0	46
45	The Gene History of Zebrafish <i>tlr4a</i> and <i>tlr4b</i> Is Predictive of Their Divergent Functions. <i>Journal of Immunology</i> , 2009, 183, 5896-5908.	0.8	160
46	Consequences of Lineage-Specific Gene Loss on Functional Evolution of Surviving Paralogs: <i>ALDH1A</i> and Retinoic Acid Signaling in Vertebrate Genomes. <i>PLoS Genetics</i> , 2009, 5, e1000496.	3.5	69
47	Evolution of a New Function by Degenerative Mutation in Cephalochordate Steroid Receptors. <i>PLoS Genetics</i> , 2008, 4, e1000191.	3.5	104
48	Inferring Ancestral Gene Order. <i>Methods in Molecular Biology</i> , 2008, 452, 365-383.	0.9	9
49	Rule-based workflow management for bioinformatics. <i>VLDB Journal</i> , 2005, 14, 318-329.	4.1	14
50	Evaluating the genome-wide impacts of species translocations: the greater prairie-chicken as a case study. <i>Conservation Genetics</i> , 0, , 1.	1.5	2