

Julian M Catchen

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

12,240
citations

172207

29
h-index

197535

49
g-index

59
all docs

59
docs citations

59
times ranked

14019
citing authors

#	ARTICLE	IF	CITATIONS
1	Stacks: an analysis tool set for population genomics. <i>Molecular Ecology</i> , 2013, 22, 3124-3140.	2.0	3,077
2	Genome-wide genetic marker discovery and genotyping using next-generation sequencing. <i>Nature Reviews Genetics</i> , 2011, 12, 499-510.	7.7	2,198
3	<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.	0.8	1,643
4	Stacks 2: Analytical methods for paired-end sequencing improve RADseq-based population genomics. <i>Molecular Ecology</i> , 2019, 28, 4737-4754.	2.0	648
5	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. <i>Nature Genetics</i> , 2016, 48, 427-437.	9.4	545
6	Lost in parameter space: a road map for <code>stacks</code> . <i>Methods in Ecology and Evolution</i> , 2017, 8, 1360-1373.	2.2	466
7	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.	3.3	412
8	Deriving genotypes from RAD-seq short-read data using Stacks. <i>Nature Protocols</i> , 2017, 12, 2640-2659.	5.5	335
9	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.	1.2	333
10	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.	9.4	251
11	Automated identification of conserved synteny after whole-genome duplication. <i>Genome Research</i> , 2009, 19, 1497-1505.	2.4	205
12	Winter storms drive rapid phenotypic, regulatory, and genomic shifts in the green anole lizard. <i>Science</i> , 2017, 357, 495-498.	6.0	204
13	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.	0.4	160
14	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.	3.3	156
15	Unbroken: RADseq remains a powerful tool for understanding the genetics of adaptation in natural populations. <i>Molecular Ecology Resources</i> , 2017, 17, 362-365.	2.2	156
16	The population structure and recent colonization history of Oregon threespine stickleback determined using restriction-site associated DNA sequencing. <i>Molecular Ecology</i> , 2013, 22, 2864-2883.	2.0	119
17	<code>RADcap</code> : sequence capture of dual-digest <code>RADseq</code> libraries with identifiable duplicates and reduced missing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1264-1278.	2.2	117
18	Antarctic blackfin icefish genome reveals adaptations to extreme environments. <i>Nature Ecology and Evolution</i> , 2019, 3, 469-478.	3.4	115

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19	Evolution of a New Function by Degenerative Mutation in Cephalochordate Steroid Receptors. <i>PLoS Genetics</i> , 2008, 4, e1000191.	1.5	104
20	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.	3.4	102
21	Retinoic Acid Metabolic Genes, Meiosis, and Gonadal Sex Differentiation in Zebrafish. <i>PLoS ONE</i> , 2013, 8, e73951.	1.1	83
22	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.	1.2	80
23	Consequences of Lineage-Specific Gene Loss on Functional Evolution of Surviving Paralogs: ALDH1A and Retinoic Acid Signaling in Vertebrate Genomes. <i>PLoS Genetics</i> , 2009, 5, e1000496.	1.5	69
24	Repeated Selection of Alternatively Adapted Haplotypes Creates Sweeping Genomic Remodeling in Stickleback. <i>Genetics</i> , 2018, 209, 921-939.	1.2	64
25	Population Genomic Analysis of Model and Nonmodel Organisms Using Sequenced RAD Tags. <i>Methods in Molecular Biology</i> , 2012, 888, 235-260.	0.4	56
26	UDP xylose synthase 1 is required for morphogenesis and histogenesis of the craniofacial skeleton. <i>Developmental Biology</i> , 2010, 341, 400-415.	0.9	51
27	Expression profiling of zebrafish sox9 mutants reveals that Sox9 is required for retinal differentiation. <i>Developmental Biology</i> , 2009, 329, 1-15.	0.9	46
28	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.	0.8	44
29	Conserved Synteny and the Zebrafish Genome. <i>Methods in Cell Biology</i> , 2011, 104, 259-285.	0.5	41
30	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.	1.1	36
31	The Novel Evolution of the Sperm Whale Genome. <i>Genome Biology and Evolution</i> , 2017, 9, 3260-3264.	1.1	33
32	Comparative Oncogenomic Analysis of Copy Number Alterations in Human and Zebrafish Tumors Enables Cancer Driver Discovery. <i>PLoS Genetics</i> , 2013, 9, e1003734.	1.5	30
33	Simulation with RADinitio improves RADseq experimental design and sheds light on sources of missing data. <i>Molecular Ecology Resources</i> , 2021, 21, 363-378.	2.2	29
34	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.	2.2	25
35	The Developmental and Genetic Architecture of the Sexually Selected Male Ornament of Swordtails. <i>Current Biology</i> , 2021, 31, 911-922.e4.	1.8	24
36	Genomic Resources for Darters (Percidae: Etheostominae) Provide Insight into Postzygotic Barriers Implicated in Speciation. <i>Molecular Biology and Evolution</i> , 2020, 37, 711-729.	3.5	22

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37	Footprints in time: comparative quantitative trait loci mapping of the pitcher-plant mosquito, <i>Wyeomyia smithii</i> . Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 4551-4558.	1.2	18
38	Replicate Phylogenies and Post-Glacial Range Expansion of the Pitcher-Plant Mosquito, <i>Wyeomyia smithii</i> , in North America. PLoS ONE, 2013, 8, e72262.	1.1	15
39	Incomplete lineage sorting and ancient admixture, and speciation without morphological change in ghost-worm cryptic species. PeerJ, 2021, 9, e10896.	0.9	15
40	Rule-based workflow management for bioinformatics. VLDB Journal, 2005, 14, 318-329.	2.7	14
41	Hybridization and postzygotic isolation promote reinforcement of male mating preferences in a diverse group of fishes with traditional sex roles. Ecology and Evolution, 2018, 8, 9282-9294.	0.8	12
42	Sequence Analysis and Ontogenetic Expression Patterns of Cone Opsin Genes in the Bluefin Killifish (<i>Lucania goodei</i>). Journal of Heredity, 2021, 112, 357-366.	1.0	11
43	Genomic diversity is similar between Atlantic Forest restorations and natural remnants for the native tree <i>Casearia sylvestris</i> Sw.. PLoS ONE, 2018, 13, e0192165.	1.1	10
44	Inferring Ancestral Gene Order. Methods in Molecular Biology, 2008, 452, 365-383.	0.4	9
45	Leafy and weedy seadragon genomes connect genic and repetitive DNA features to the extravagant biology of syngnathid fishes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	8
46	Selection, Linkage, and Population Structure Interact To Shape Genetic Variation Among Threespine Stickleback Genomes. Genetics, 2019, 212, 1367-1382.	1.2	6
47	The genomic basis of the plant island syndrome in Darwin's giant daisies. Nature Communications, 2022, 13, .	5.8	6
48	Ancient three-spined stickleback (<i>Gasterosteus aculeatus</i>) mtDNA lineages are not associated with phenotypic or nuclear genetic variation. Biological Journal of the Linnean Society, 2017, 122, 579-588.	0.7	4
49	When structure leads to sex: Untangling signals in population genetic data sets. Molecular Ecology, 2017, 26, 6763-6766.	2.0	3
50	Evaluating the genome-wide impacts of species translocations: the greater prairie-chicken as a case study. Conservation Genetics, 0, , 1.	0.8	2