

Susan Bassham

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

5,078
citations

933447

10
h-index

888059

17
g-index

21
all docs

21
docs citations

21
times ranked

7515
citing authors

#	ARTICLE	IF	CITATIONS
1	Stacks: an analysis tool set for population genomics. <i>Molecular Ecology</i> , 2013, 22, 3124-3140.	3.9	3,077
2	Population Genomics of Parallel Adaptation in Threespine Stickleback using Sequenced RAD Tags. <i>PLoS Genetics</i> , 2010, 6, e1000862.	3.5	1,219
3	Local De Novo Assembly of RAD Paired-End Contigs Using Short Sequencing Reads. <i>PLoS ONE</i> , 2011, 6, e18561.	2.5	187
4	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.	3.9	119
5	Development of the central nervous system in the larvacean <i>Oikopleura dioica</i> and the evolution of the chordate brain. <i>Developmental Biology</i> , 2005, 285, 298-315.	2.0	107
6	Effects of Crossovers Between Homeologs on Inheritance and Population Genomics in Polyploid-Derived Salmonid Fishes. <i>Journal of Heredity</i> , 2015, 106, 217-227.	2.4	97
7	Repeated Selection of Alternatively Adapted Haplotypes Creates Sweeping Genomic Remodeling in Stickleback. <i>Genetics</i> , 2018, 209, 921-939.	2.9	64
8	Brachyury (T) Expression in Embryos of a Larvacean Urochordate, <i>Oikopleura dioica</i> , and the Ancestral Role of T. <i>Developmental Biology</i> , 2000, 220, 322-332.	2.0	63
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	Host Genotype and Microbiota Contribute Asymmetrically to Transcriptional Variation in the Threespine Stickleback Gut. <i>Genome Biology and Evolution</i> , 2017, 9, 504-520.	2.5	40
11	Genome-wide single nucleotide polymorphism markers reveal population structure and dispersal direction of an expanding nuisance algal bloom species. <i>Molecular Ecology</i> , 2021, 30, 912-925.	3.9	13
12	Remembering James Alan Bassham (1922–2012). <i>Photosynthesis Research</i> , 2016, 128, 3-13.	2.9	10
13	Single-cell Iso-Sequencing enables rapid genome annotation for scRNAseq analysis. <i>Genetics</i> , 2022, 220, .	2.9	10
14	Highly Reproducible 16S Sequencing Facilitates Measurement of Host Genetic Influences on the Stickleback Gut Microbiome. <i>MSystems</i> , 2019, 4, .	3.8	8
15	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
16	Developmental timing differences underlie armor loss across threespine stickleback populations. <i>Evolution & Development</i> , 2017, 19, 231-243.	2.0	7
17	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
18	Response to May and Delany: We Never Said Wright was Wrong. <i>Journal of Heredity</i> , 2015, 106, esv072.	2.4	0