

Matthew David MacManes

List of Publications by Year in descending order

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43
papers

9,080
citations

430874

18
h-index

254184

43
g-index

73
all docs

73
docs citations

73
times ranked

16421
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome size affects sequence divergence between species through the interplay of recombination and selection. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 782-798.	2.3	11
2	Lord of the Diptera (and Moths and a Spider): Molecular Diet Analyses and Foraging Ecology of Indiana Bats in Illinois. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	15
3	Limited Evidence for Parallel Evolution Among Desert-Adapted <i>Peromyscus</i> Deer Mice. <i>Journal of Heredity</i> , 2021, 112, 286-302.	2.4	14
4	Signal, bias, and the role of transcriptome assembly quality in phylogenomic inference. <i>Bmc Ecology and Evolution</i> , 2021, 21, 43.	1.6	8
5	Feather Gene Expression Elucidates the Developmental Basis of Plumage Iridescence in African Starlings. <i>Journal of Heredity</i> , 2021, 112, 417-429.	2.4	15
6	Isolating the Role of Corticosterone in the Hypothalamic-Pituitary-Gonadal Transcriptomic Stress Response. <i>Frontiers in Endocrinology</i> , 2021, 12, 632060.	3.5	11
7	The genomics of mimicry: Gene expression throughout development provides insights into convergent and divergent phenotypes in a Müllerian mimicry system. <i>Molecular Ecology</i> , 2021, 30, 4039-4061.	3.9	20
8	Disentangling environmental drivers of circadian metabolism in desert-adapted mice. <i>Journal of Experimental Biology</i> , 2021, 224, .	1.7	5
9	The Genome of the Softshell Clam <i>Mya arenaria</i> and the Evolution of Apoptosis. <i>Genome Biology and Evolution</i> , 2020, 12, 1681-1693.	2.5	7
10	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , 2020, 10, 9721-9739.	1.9	40
11	A linked-read approach to museomics: Higher quality de novo genome assemblies from degraded tissues. <i>Molecular Ecology Resources</i> , 2020, 20, 856-870.	4.8	15
12	Comparative and population genomics approaches reveal the basis of adaptation to deserts in a small rodent. <i>Molecular Ecology</i> , 2020, 29, 1300-1314.	3.9	39
13	De novo assembly and functional annotation of the heart hemolymph transcriptome in the Caribbean spiny lobster <i>Panulirus argus</i> . <i>Marine Genomics</i> , 2020, 54, 100783.	1.1	6
14	Variation in pigmentation gene expression is associated with distinct aposematic color morphs in the poison frog <i>Dendrobates auratus</i> . <i>BMC Evolutionary Biology</i> , 2019, 19, 85.	3.2	25
15	Dynamic pigmentary and structural coloration within cephalopod chromatophore organs. <i>Nature Communications</i> , 2019, 10, 1004.	12.8	105
16	Divergent selection and drift shape the genomes of two avian sister species spanning a saline-freshwater ecotone. <i>Ecology and Evolution</i> , 2019, 9, 13477-13494.	1.9	15
17	Sex-biased transcriptomic response of the reproductive axis to stress. <i>Hormones and Behavior</i> , 2018, 100, 56-68.	2.1	25
18	The Oyster River Protocol: a multi-assembler and kmer approach for de novo transcriptome assembly. <i>PeerJ</i> , 2018, 6, e5428.	2.0	85

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19	Severe acute dehydration in a desert rodent elicits a transcriptional response that effectively prevents kidney injury. <i>American Journal of Physiology - Renal Physiology</i> , 2017, 313, F262-F272.	2.7	37
20	Widespread patterns of sexually dimorphic gene expression in an avian hypothalamicâ€“pituitaryâ€“gonadal (HPG) axis. <i>Scientific Reports</i> , 2017, 7, 45125.	3.3	45
21	Physiological and biochemical changes associated with acute experimental dehydration in the desert adapted mouse, <i>Peromyscus eremicus</i> . <i>Physiological Reports</i> , 2017, 5, e13218.	1.7	19
22	Comparative Genomics of Color Morphs In the Coral <i>Montastraea cavernosa</i> . <i>Scientific Reports</i> , 2017, 7, 16039.	3.3	16
23	Characterizing the reproductive transcriptomic correlates of acute dehydration in males in the desert-adapted rodent, <i>Peromyscus eremicus</i> . <i>BMC Genomics</i> , 2017, 18, 473.	2.8	10
24	Comparative Genomics of Pathogenic and Nonpathogenic Beetle-Vectored Fungi in the Genus <i>Geosmithia</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 3312-3327.	2.5	18
25	Brain Transcriptional Profiles of Male Alternative Reproductive Tactics and Females in Bluegill Sunfish. <i>PLoS ONE</i> , 2016, 11, e0167509.	2.5	25
26	Transcriptomic Resources for the Rocky Intertidal Blue Mussel <i>Mytilus edulis</i> from the Gulf of Maine. <i>Journal of Shellfish Research</i> , 2016, 35, 435-465.	0.9	6
27	Comparative genomics explains the evolutionary success of reef-forming corals. <i>ELife</i> , 2016, 5, .	6.0	169
28	<i>De novo</i> genome assembly of <i>Geosmithia morbida</i> , the causal agent of thousand cankers disease. <i>PeerJ</i> , 2016, 4, e1952.	2.0	9
29	Characterizing the adult and larval transcriptome of the multicolored Asian lady beetle, <i>Harmonia axyridis</i> . <i>PeerJ</i> , 2016, 4, e2098.	2.0	6
30	Characterization of a male reproductive transcriptome for <i>Peromyscus eremicus</i> (Cactus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	2.0	11
31	RNAseq-ing a more integrative understanding of animal behavior. <i>Current Opinion in Behavioral Sciences</i> , 2015, 6, 65-68.	3.9	14
32	Genomic takeover by transposable elements in the Strawberry poison frog. <i>Molecular Biology and Evolution</i> , 2014, 35, 2913-2927.	8.9	45
33	On the optimal trimming of high-throughput mRNA sequence data. <i>Frontiers in Genetics</i> , 2014, 5, 13.	2.3	205
34	Characterization of the transcriptome, nucleotide sequence polymorphism, and natural selection in the desert adapted mouse <i>Peromyscus eremicus</i> . <i>PeerJ</i> , 2014, 2, e642.	2.0	34
35	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
36	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582

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37	Improving transcriptome assembly through error correction of high-throughput sequence reads. PeerJ, 2013, 1, e113.	2.0	38
38	Is Promiscuity Associated with Enhanced Selection on MHC-DQ β in Mice (genus <i>Peromyscus</i>)?. PLoS ONE, 2012, 7, e37562.	2.5	12
39	The Social Brain: Transcriptome Assembly and Characterization of the Hippocampus from a Social Subterranean Rodent, the Colonial Tuco-Tuco (<i>Ctenomys sociabilis</i>). PLoS ONE, 2012, 7, e45524.	2.5	21
40	Museum genomics: low-cost and high-accuracy genetic data from historical specimens. Molecular Ecology Resources, 2011, 11, 1082-1092.	4.8	122
41	Promiscuity in mice is associated with increased vaginal bacterial diversity. Die Naturwissenschaften, 2011, 98, 951-960.	1.6	20
42	When non-coding is non-neutral: the role of CHD1 gene polymorphism in sexing, in phylogenetics and as a correlate of fitness in birds. Ibis, 2010, 152, 223-225.	1.9	4
43	Isolation and characterization of polymorphic microsatellite loci from <i>Octodon degus</i> . Molecular Ecology Resources, 2009, 9, 999-1001.	4.8	24