

Thomas L Schmidt

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

527
citations

840585

11
h-index

940416

16
g-index

28
all docs

28
docs citations

28
times ranked

371
citing authors

#	ARTICLE	IF	CITATIONS
1	Estimating dispersal using close kin dyads: The <code>kindisperse</code> R package. <i>Molecular Ecology Resources</i> , 2022, 22, 1200-1212.	2.2	14
2	A decade of stability for wMel Wolbachia in natural <i>Aedes aegypti</i> populations. <i>PLoS Pathogens</i> , 2022, 18, e1010256.	2.1	40
3	Sex-specific distribution and classification of Wolbachia infections and mitochondrial DNA haplogroups in <i>Aedes albopictus</i> from the Indo-Pacific. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010139.	1.3	6
4	Migration trajectories of the diamondback moth <i>Plutella xylostella</i> in China inferred from population genomic variation. <i>Pest Management Science</i> , 2021, 77, 1683-1693.	1.7	18
5	Anthropogenic and natural barriers affect genetic connectivity in an Alpine butterfly. <i>Molecular Ecology</i> , 2021, 30, 114-130.	2.0	19
6	Spatial population genomics of a recent mosquito invasion. <i>Molecular Ecology</i> , 2021, 30, 1174-1189.	2.0	31
7	Unbiased population heterozygosity estimates from genome-wide sequence data. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1888-1898.	2.2	55
8	Improving mosquito control strategies with population genomics. <i>Trends in Parasitology</i> , 2021, 37, 907-921.	1.5	11
9	Genetic stability of <i>Aedes aegypti</i> populations following invasion by wMel Wolbachia. <i>BMC Genomics</i> , 2021, 22, 894.	1.2	11
10	Population genomics of two invasive mosquitoes (<i>Aedes aegypti</i> and <i>Aedes albopictus</i>) from the Indo-Pacific. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008463.	1.3	30
11	Heterogeneous genetic invasions of three insecticide resistance mutations in Indo-Pacific populations of <i>Aedes aegypti</i> (L.). <i>Molecular Ecology</i> , 2020, 29, 1628-1641.	2.0	34
12	Incursion pathways of the Asian tiger mosquito (<i>Aedes albopictus</i>) into Australia contrast sharply with those of the yellow fever mosquito (<i>Aedes</i> Tj ETQq0 0 0 rgBT1/0verlock210 Tf 50 2		
13	A genomic approach to inferring kinship reveals limited intergenerational dispersal in the yellow fever mosquito. <i>Molecular Ecology Resources</i> , 2019, 19, 1254-1264.	2.2	53
14	Tracking genetic invasions: Genome-wide single nucleotide polymorphisms reveal the source of pyrethroid-resistant <i>Aedes aegypti</i> (yellow fever mosquito) incursions at international ports. <i>Evolutionary Applications</i> , 2019, 12, 1136-1146.	1.5	40
15	Fine-scale landscape genomics helps explain the slow spatial spread of Wolbachia through the <i>Aedes aegypti</i> population in Cairns, Australia. <i>Heredity</i> , 2018, 120, 386-395.	1.2	86
16	Genome-wide SNPs reveal the drivers of gene flow in an urban population of the Asian Tiger Mosquito, <i>Aedes albopictus</i> . <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0006009.	1.3	40