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List of Publications by Year
in descending order

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40 papers	2,127 citations	394286 19 h-index	289141 40 g-index
53 all docs	53 docs citations	53 times ranked	2793 citing authors

#	Article	IF	Citations
1	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	13.7	426
2	Local introduction and heterogeneous spatial spread of dengue-suppressing Wolbachia through an urban population of Aedes aegypti. PLoS Biology, 2017, 15, e2001894.	2.6	202
3	<i>Wolbachia</i> strains for disease control: ecological and evolutionary considerations. Evolutionary Applications, 2015, 8, 751-768.	1.5	168
4	Genome-wide SNPs lead to strong signals of geographic structure and relatedness patterns in the major arbovirus vector, Aedes aegypti. BMC Genomics, 2014, 15, 275.	1.2	157
5	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 May 2009â€“31 July 2009. Molecular Ecology Resources, 2009, 9, 1460-1466.	2.2	128
6	Matching the genetics of released and local Aedes aegypti populations is critical to assure Wolbachia invasion. PLoS Neglected Tropical Diseases, 2019, 13, e0007023.	1.3	125
7	Fine-scale landscape genomics helps explain the slow spatial spread of Wolbachia through the Aedes aegypti population in Cairns, Australia. Heredity, 2018, 120, 386-395.	1.2	86
8	Mapping the virome in wild-caught Aedes aegypti from Cairns and Bangkok. Scientific Reports, 2018, 8, 4690.	1.6	84
9	Releasing incompatible males drives strong suppression across populations of wild and <i>Wolbachia</i> -carrying <i>Aedes aegypti</i> in Australia. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	71
10	Core commitments for field trials of gene drive organisms. Science, 2020, 370, 1417-1419.	6.0	67
11	Enhanced Zika virus susceptibility of globally invasive <i>Aedes aegypti</i> populations. Science, 2020, 370, 991-996.	6.0	61
12	Extensive Genetic Differentiation between Homomorphic Sex Chromosomes in the Mosquito Vector, Aedes aegypti. Genome Biology and Evolution, 2017, 9, 2322-2335.	1.1	45
13	Using <i>Wolbachia</i>â€based release for suppression of <i>Aedes</i> mosquitoes: insights from genetic data and population simulations. Ecological Applications, 2014, 24, 1226-1234.	1.8	41
14	Genome-wide SNPs reveal the drivers of gene flow in an urban population of the Asian Tiger Mosquito, Aedes albopictus. PLoS Neglected Tropical Diseases, 2017, 11, e0006009.	1.3	40
15	Aedes aegypti has spatially structured and seasonally stable populations in Yogyakarta, Indonesia. Parasites and Vectors, 2015, 8, 610.	1.0	39
16	Contrasting genetic structure between mitochondrial and nuclear markers in the dengue fever mosquito from Rio de Janeiro: implications for vector control. Evolutionary Applications, 2015, 8, 901-915.	1.5	36
17	Mitochondrial DNA variants help monitor the dynamics of Wolbachia invasion into host populations. Heredity, 2016, 116, 265-276.	1.2	30
18	Contrasting patterns of population connectivity between regions in a commercially important mollusc <i>Haliotis rubra</i>: integrating population genetics, genomics and marine LiDAR data. Molecular Ecology, 2016, 25, 3845-3864.	2.0	29

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19	Modeling confinement and reversibility of threshold-dependent gene drive systems in spatially-explicit Aedes aegypti populations. BMC Biology, 2020, 18, 50.	1.7	27
20	Evidence of cryptic genetic lineages within Aedes notoscriptus (Skuse). Infection, Genetics and Evolution, 2013, 18, 191-201.	1.0	20
21	Origin of resistance to pyrethroids in the redlegged earth mite (<i>Halotydeus destructor</i>) in Australia: repeated local evolution and migration. Pest Management Science, 2020, 76, 509-519.	1.7	20
22	Identifying the fitness costs of a pyrethroid-resistant genotype in the major arboviral vector Aedes aegypti. Parasites and Vectors, 2020, 13, 358.	1.0	20
23	The queenslandensis and the type Form of the Dengue Fever Mosquito (Aedes aegypti L.) Are Genomically Indistinguishable. PLoS Neglected Tropical Diseases, 2016, 10, e0005096.	1.3	19
24	Characterization of microsatellite loci for the western cherry fruit fly, <i>Rhagoletis indifferens</i> (Diptera: Tephritidae). Molecular Ecology Resources, 2009, 9, 1025-1028.	2.2	18
25	Using spatial genetics to quantify mosquito dispersal for control programs. BMC Biology, 2020, 18, 104.	1.7	18
26	Complete genome sequence of Oryctes rhinoceros nudivirus isolated from the coconut rhinoceros beetle in Solomon Islands. Virus Research, 2020, 278, 197864.	1.1	18
27	Monitoring of the genetic structure of natural populations: change of the effective population size and inversion polymorphism in Drosophila subobscura. Genetica, 2008, 133, 57-63.	0.5	15
28	From broadscale patterns to fineâ€scale processes: habitat structure influences genetic differentiation in the pitcher plant midge across multiple spatial scales. Molecular Ecology, 2012, 21, 223-236.	2.0	15
29	The complete mitochondrial genome sequence of <i>Oryctes rhinoceros</i> (Coleoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.9	12
30	The presence of knockdown resistance mutations reduces male mating competitiveness in the major arbovirus vector, Aedes aegypti. PLoS Neglected Tropical Diseases, 2021, 15, e0009121.	1.3	12
31	Monitoring Needs for Gene Drive Mosquito Projects: Lessons From Vector Control Field Trials and Invasive Species. Frontiers in Genetics, 2021, 12, 780327.	1.1	11
32	The effect of lead on fitness components and developmental stability in<i>Drosophila subobscura</i>. Acta Biologica Hungarica, 2008, 59, 47-56.	0.7	10
33	The Pitcher Plant Flesh Fly Exhibits a Mixture of Patchy and Metapopulation Attributes. Journal of Heredity, 2012, 103, 703-710.	1.0	6
34	Genetic and morphological analyses indicate that the Australian endemic scorpion<i>Urodacus yaschenkoi</i>(Scorpiones: Urodacidae) is a species complex. PeerJ, 2017, 5, e2759.	0.9	6
35	A high-quality de novo genome assembly based on nanopore sequencing of a wild-caught coconut rhinoceros beetle (Oryctes rhinoceros). BMC Genomics, 2022, 23, .	1.2	6
36	Characterization of microsatellite loci for the pitcher plant midge, <i>Metriocnemus knabi</i> Coq. (Diptera: Chironomidae). Molecular Ecology Resources, 2009, 9, 1388-1391.	2.2	5

#	Article	IF	Citations
37	The study of chromosomal inversion polymorphism of Drosophila subobscura over years in two different habitats from mountain Goc. Genetika, 2007, 39, 155-167.	0.1	4
38	Inbreeding reveals interpopulation differences in inversion polymorphism of Drosophila subobscura. Journal of Zoological Systematics and Evolutionary Research, 2007, 46, 070907105857004-???.	0.6	2
39	Effect of Microhabitat Variability on Body Size in Drosophila subobscura. Folia Biologica, 2008, 56, 51-56.	0.1	1
40	Does inbreeding affects developmental stability in Drosophila subobscura populations?. Genetika, 2011, 43, 639-654.	0.1	1