

Gordana RaÅ;iÄ

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

2,127
citations

394286

19
h-index

289141

40
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53
all docs

53
docs citations

53
times ranked

2793
citing authors

#	ARTICLE	IF	CITATIONS
1	A high-quality de novo genome assembly based on nanopore sequencing of a wild-caught coconut rhinoceros beetle (<i>Oryctes rhinoceros</i>). BMC Genomics, 2022, 23, .	1.2	6
2	The complete mitochondrial genome sequence of <i>Oryctes rhinoceros</i> (Coleoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td 0.9	0.9	12
3	The presence of knockdown resistance mutations reduces male mating competitiveness in the major arbovirus vector, <i>Aedes aegypti</i> . PLoS Neglected Tropical Diseases, 2021, 15, e0009121.	1.3	12
4	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
5	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
6	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
7	Identifying the fitness costs of a pyrethroid-resistant genotype in the major arboviral vector <i>Aedes aegypti</i> . Parasites and Vectors, 2020, 13, 358.	1.0	20
8	Enhanced Zika virus susceptibility of globally invasive <i>Aedes aegypti</i> populations. Science, 2020, 370, 991-996.	6.0	61
9	Using spatial genetics to quantify mosquito dispersal for control programs. BMC Biology, 2020, 18, 104.	1.7	18
10	Core commitments for field trials of gene drive organisms. Science, 2020, 370, 1417-1419.	6.0	67
11	Modeling confinement and reversibility of threshold-dependent gene drive systems in spatially-explicit <i>Aedes aegypti</i> populations. BMC Biology, 2020, 18, 50.	1.7	27
12	Complete genome sequence of <i>Oryctes rhinoceros nudivirus</i> isolated from the coconut rhinoceros beetle in Solomon Islands. Virus Research, 2020, 278, 197864.	1.1	18
13	Matching the genetics of released and local <i>Aedes aegypti</i> populations is critical to assure <i>Wolbachia</i> invasion. PLoS Neglected Tropical Diseases, 2019, 13, e0007023.	1.3	125
14	Mapping the virome in wild-caught <i>Aedes aegypti</i> from Cairns and Bangkok. Scientific Reports, 2018, 8, 4690.	1.6	84
15	Fine-scale landscape genomics helps explain the slow spatial spread of <i>Wolbachia</i> through the <i>Aedes aegypti</i> population in Cairns, Australia. Heredity, 2018, 120, 386-395.	1.2	86
16	Improved reference genome of <i>Aedes aegypti</i> informs arbovirus vector control. Nature, 2018, 563, 501-507.	13.7	426
17	Extensive Genetic Differentiation between Homomorphic Sex Chromosomes in the Mosquito Vector, <i>Aedes aegypti</i> . Genome Biology and Evolution, 2017, 9, 2322-2335.	1.1	45
18	Genome-wide SNPs reveal the drivers of gene flow in an urban population of the Asian Tiger Mosquito, <i>Aedes albopictus</i> . PLoS Neglected Tropical Diseases, 2017, 11, e0006009.	1.3	40

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19	Local introduction and heterogeneous spatial spread of dengue-suppressing <i>Wolbachia</i> through an urban population of <i>Aedes aegypti</i> . <i>PLoS Biology</i> , 2017, 15, e2001894.	2.6	202
20	Genetic and morphological analyses indicate that the Australian endemic scorpion <i>Urodacus yaschenkoi</i> (Scorpiones: Urodacidae) is a species complex. <i>PeerJ</i> , 2017, 5, e2759.	0.9	6
21	The queenslandensis and the type Form of the Dengue Fever Mosquito (<i>Aedes aegypti</i> L.) Are Genomically Indistinguishable. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005096.	1.3	19
22	Contrasting patterns of population connectivity between regions in a commercially important mollusc <i>Haliotis rubra</i> : integrating population genetics, genomics and marine LiDAR data. <i>Molecular Ecology</i> , 2016, 25, 3845-3864.	2.0	29
23	Mitochondrial DNA variants help monitor the dynamics of <i>Wolbachia</i> invasion into host populations. <i>Heredity</i> , 2016, 116, 265-276.	1.2	30
24	<i>Wolbachia</i> strains for disease control: ecological and evolutionary considerations. <i>Evolutionary Applications</i> , 2015, 8, 751-768.	1.5	168
25	Contrasting genetic structure between mitochondrial and nuclear markers in the dengue fever mosquito from Rio de Janeiro: implications for vector control. <i>Evolutionary Applications</i> , 2015, 8, 901-915.	1.5	36
26	<i>Aedes aegypti</i> has spatially structured and seasonally stable populations in Yogyakarta, Indonesia. <i>Parasites and Vectors</i> , 2015, 8, 610.	1.0	39
27	Genome-wide SNPs lead to strong signals of geographic structure and relatedness patterns in the major arbovirus vector, <i>Aedes aegypti</i> . <i>BMC Genomics</i> , 2014, 15, 275.	1.2	157
28	Using <i>Wolbachia</i> -based release for suppression of <i>Aedes</i> mosquitoes: insights from genetic data and population simulations. <i>Ecological Applications</i> , 2014, 24, 1226-1234.	1.8	41
29	Evidence of cryptic genetic lineages within <i>Aedes notoscriptus</i> (Skuse). <i>Infection, Genetics and Evolution</i> , 2013, 18, 191-201.	1.0	20
30	The Pitcher Plant Flesh Fly Exhibits a Mixture of Patchy and Metapopulation Attributes. <i>Journal of Heredity</i> , 2012, 103, 703-710.	1.0	6
31	From broadscale patterns to fine-scale processes: habitat structure influences genetic differentiation in the pitcher plant midge across multiple spatial scales. <i>Molecular Ecology</i> , 2012, 21, 223-236.	2.0	15
32	Does inbreeding affects developmental stability in <i>Drosophila subobscura</i> populations?. <i>Genetika</i> , 2011, 43, 639-654.	0.1	1
33	Characterization of microsatellite loci for the western cherry fruit fly, <i>Rhagoletis indifferens</i> (Diptera: Tephritidae). <i>Molecular Ecology Resources</i> , 2009, 9, 1025-1028.	2.2	18
34	Characterization of microsatellite loci for the pitcher plant midge, <i>Metricnemus knabi</i> Coq. (Diptera: Chironomidae). <i>Molecular Ecology Resources</i> , 2009, 9, 1388-1391.	2.2	5
35	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 May 2009–31 July 2009. <i>Molecular Ecology Resources</i> , 2009, 9, 1460-1466.	2.2	128
36	Monitoring of the genetic structure of natural populations: change of the effective population size and inversion polymorphism in <i>Drosophila subobscura</i> . <i>Genetica</i> , 2008, 133, 57-63.	0.5	15

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37	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
38	Effect of Microhabitat Variability on Body Size in <i>Drosophila subobscura</i> . Folia Biologica, 2008, 56, 51-56.	0.1	1
39	Inbreeding reveals interpopulation differences in inversion polymorphism of <i>Drosophila subobscura</i> . Journal of Zoological Systematics and Evolutionary Research, 2007, 46, 070907105857004-???	0.6	2
40	The study of chromosomal inversion polymorphism of <i>Drosophila subobscura</i> over years in two different habitats from mountain Goc. Genetika, 2007, 39, 155-167.	0.1	4