Mariangela Bonnizoni

List of Publications by Year
in descending order

73 papers	4,069 citations	126708 33 h-index	133063 59 g-index
82 all docs	82 docs citations	82 times ranked	4477 citing authors

#	Article	IF	Citations
1	Endogenous viral elements in mosquito genomes: current knowledge and outstanding questions. Current Opinion in Insect Science, 2022, 49, 22-30.	2.2	11
2	Thermal biology of invasive Aedes mosquitoes in the context of climate change. Current Opinion in Insect Science, 2022, 51, 100920.	2.2	14
3	Exploring Changes in the Microbiota of Aedes albopictus: Comparison Among Breeding Site Water, Larvae, and Adults. Frontiers in Microbiology, 2021, 12, 624170.	1.5	24
4	Population genomics in the arboviral vector Aedes aegypti reveals the genomic architecture and evolution of endogenous viral elements. Molecular Ecology, 2021, 30, 1594-1611.	2.0	37
5	ViR: a tool to solve intrasample variability in the prediction of viral integration sites using whole genome sequencing data. BMC Bioinformatics, 2021, 22, 45.	1.2	8
6	Profile of Small RNAs, vDNA Forms and Viral Integrations in Late Chikungunya Virus Infection of Aedes albopictus Mosquitoes. Viruses, 2021, 13, 553.	1.5	13
7	Cross Talk between Viruses and Insect Cells Cytoskeleton. Viruses, 2021, 13, 1658.	1.5	11
8	Improved reference genome of the arboviral vector Aedes albopictus. Genome Biology, 2020, 21, 215.	3.8	65
9	Genomic Variant Analyses in Pyrethroid Resistant and Susceptible Malaria Vector, Anopheles sinensis. G3: Genes, Genomes, Genetics, 2020, 10, 2185-2193.	0.8	4
10	Tracing temporal and geographic distribution of resistance to pyrethroids in the arboviral vector Aedes albopictus. PLoS Neglected Tropical Diseases, 2020, 14, e0008350.	1.3	13
11	Leaning Into the Bite: The piRNA Pathway as an Exemplar for the Genetic Engineering Need in Mosquitoes. Frontiers in Cellular and Infection Microbiology, 2020, 10, 614342.	1.8	2
12	The Widespread Occurrence and Potential Biological Roles of Endogenous Viral Elements in Insect Genomes. Current Issues in Molecular Biology, 2020, 34, 13-30.	1.0	40
13	Aedes spp. and Their Microbiota: A Review. Frontiers in Microbiology, 2019, 10, 2036.	1.5	90
14	Evolution and biological significance of flaviviral elements in the genome of the arboviral vector Aedes albopictus. Emerging Microbes and Infections, 2019, 8, 1265-1279.	3.0	7
15	Influence of blood meal and age of mosquitoes on susceptibility to pyrethroids in Anopheles gambiae from Western Kenya. Malaria Journal, 2019, 18, 112.	0.8	29
16	Insights Into an Unexplored Component of the Mosquito Repeatome: Distribution and Variability of Viral Sequences Integrated Into the Genome of the Arboviral Vector Aedes albopictus. Frontiers in Genetics, 2019, 10, 93.	1.1	21
17	Endogenous non-retroviral elements in genomes of Aedes mosquitoes and vector competence. Emerging Microbes and Infections, 2019, 8, 542-555.	3.0	34
18	Polymorphism analyses and protein modelling inform on functional specialization of PiwiÂclade genes in the arboviral vector Aedes albopictus. PLoS Neglected Tropical Diseases, 2019, 13, e0007919.	1.3	16

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19	Aedes aegypti vector competence studies: A review. Infection, Genetics and Evolution, 2019, 67, 191-209.	1.0	251
20	The piRNA pathway in host-pathogen interaction: Aedes albopictus and arboviruses. Access Microbiology, 2019, 1, .	0.2	0
21	Comparative transcriptome analysis and RNA interference reveal CYP6A8 and SNPs related to pyrethroid resistance in Aedes albopictus. PLoS Neglected Tropical Diseases, 2018, 12, e0006828.	1.3	20
22	Selection and Utility of Single Nucleotide Polymorphism Markers to Reveal Fine-Scale Population Structure in Human Malaria Parasite Plasmodium falciparum. Frontiers in Ecology and Evolution, 2018, 6, .	1.1	5
23	Nonretroviral integrated RNA viruses in arthropod vectors: an occasional event or something more?. Current Opinion in Insect Science, 2017, 22, 45-53.	2.2	45
24	Editorial overview: Vectors and medical and veterinary entomology: Becoming vectors or victims, the intriguing interplay between insects and viruses. Current Opinion in Insect Science, 2017, 22, v-vii.	2.2	0
25	Comparative genomics shows that viral integrations are abundant and express piRNAs in the arboviral vectors Aedes aegypti and Aedes albopictus. BMC Genomics, 2017, 18, 512.	1.2	138
26	Genetic evidence for a worldwide chaotic dispersion pattern of the arbovirus vector, Aedes albopictus. PLoS Neglected Tropical Diseases, 2017, 11, e0005332.	1.3	93
27	Multi-country Survey Revealed Prevalent and Novel F1534S Mutation in Voltage-Gated Sodium Channel (VGSC) Gene in Aedes albopictus. PLoS Neglected Tropical Diseases, 2016, 10, e0004696.	1.3	72
28	Landscape genetic structure and evolutionary genetics of insecticide resistance gene mutations in Anopheles sinensis. Parasites and Vectors, 2016, 9, 228.	1.0	40
29	A Multipurpose, High-Throughput Single-Nucleotide Polymorphism Chip for the Dengue and Yellow Fever Mosquito, Aedes aegypti. G3: Genes, Genomes, Genetics, 2015, 5, 711-718.	0.8	56
30	Genome sequence of the Asian Tiger mosquito, Aedes albopictus , reveals insights into its biology, genetics, and evolution. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5907-15.	3.3	251
31	RNA-seq analyses of changes in the Anopheles gambiae transcriptome associated with resistance to pyrethroids in Kenya: identification of candidate-resistance genes and candidate-resistance SNPs. Parasites and Vectors, 2015, 8, 474.	1.0	35
32	Relevant genetic differentiation among Brazilian populations of Anastrepha fraterculus (Diptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	0.5	23
33	<scp>piRNA</scp> pathway gene expression in the malaria vector mosquito <scp>A</scp>nopheles stephensi. Insect Molecular Biology, 2014, 23, 579-586.	1.0	18
34	The invasive mosquito species Aedes albopictus: current knowledge and future perspectives. Trends in Parasitology, 2013, 29, 460-468.	1.5	478
35	Probing functional polymorphisms in the dengue vector, Aedes aegypti. BMC Genomics, 2013, 14, 739.	1.2	12
36	Relationship between Knockdown Resistance, Metabolic Detoxification and Organismal Resistance to Pyrethroids in Anopheles sinensis. PLoS ONE, 2013, 8, e55475.	1.1	61

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37	Genetic Analysis of Invasive Aedes albopictus Populations in Los Angeles County, California and Its Potential Public Health Impact. PLoS ONE, 2013, 8, e68586.	1.1	84
38	Strain Variation in the Transcriptome of the Dengue Fever Vector,Aedes aegypti. G3: Genes, Genomes, Genetics, 2012, 2, 103-114.	0.8	36
39	A Low-Cost Microfluidic Chip for Rapid Genotyping of Malaria-Transmitting Mosquitoes. PLoS ONE, 2012, 7, e42222.	1.1	43
40	Comparative Transcriptome Analyses of Deltamethrin-Resistant and -Susceptible Anopheles gambiae Mosquitoes from Kenya by RNA-Seq. PLoS ONE, 2012, 7, e44607.	1.1	79
41	Complex Modulation of the Aedes aegypti Transcriptome in Response to Dengue Virus Infection. PLoS ONE, 2012, 7, e50512.	1.1	138
42	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 April 2011-31 May 2011. Molecular Ecology Resources, 2011, 11, 935-936.	2.2	8
43	RNA-seq analyses of blood-induced changes in gene expression in the mosquito vector species, Aedes aegypti. BMC Genomics, 2011, 12, 82.	1.2	133
44	Genetic diversity of Plasmodium vivax malaria in China and Myanmar. Infection, Genetics and Evolution, 2011, 11, 1419-1425.	1.0	28
45	Sperm storage and use in polyandrous females of the globally invasive fruitfly, Ceratitis capitata. Journal of Insect Physiology, 2010, 56, 1542-1551.	0.9	30
46	A cohort study of Plasmodium falciparum infection dynamics in Western Kenya Highlands. BMC Infectious Diseases, 2010, 10, 283.	1.3	16
47	Comparative fitness assessment of Anopheles stephensi transgenic lines receptive to siteâ€specific integration. Insect Molecular Biology, 2010, 19, 263-269.	1.0	47
48	Genetic structure of Plasmodium vivax and Plasmodium falciparum in the Bannu district of Pakistan. Malaria Journal, 2010, 9, 112.	0.8	36
49	Loop-Mediated Isothermal Amplification (LAMP) for Rapid Identification of Anopheles gambiae and Anopheles arabiensis Mosquitoes. American Journal of Tropical Medicine and Hygiene, 2009, 81, 1030-1034.	0.6	29
50	High Prevalence of AsymptomaticPlasmodium falciparumInfections in a Highland Area of Western Kenya: A Cohort Study. Journal of Infectious Diseases, 2009, 200, 66-74.	1.9	92
51	Genetic structure of Plasmodium falciparum populations between lowland and highland sites and antimalarial drug resistance in Western Kenya. Infection, Genetics and Evolution, 2009, 9, 806-812.	1.0	47
52	Prevalence of Antimalarial Drug Resistance Mutations in Plasmodium vivax and P. falciparum from a Malaria-Endemic Area of Pakistan. American Journal of Tropical Medicine and Hygiene, 2009, 81, 525-528.	0.6	50
53	Prevalence of antimalarial drug resistance mutations in Plasmodium vivax and P. falciparum from a malaria-endemic area of Pakistan. American Journal of Tropical Medicine and Hygiene, 2009, 81, 525-8.	0.6	36
54	Highly similar piggyBac transposaseâ€like sequences from various Bactrocera (Diptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.0	19

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55	Inferences on the population structure and colonization process of the invasive oriental fruit fly, Bactrocera dorsalis (Hendel). Molecular Ecology, 2007, 16, 3522-3532.	2.0	88
56	Globalization and fruitfly invasion and expansion: the medfly paradigm. Genetica, 2007, 131, 1-9.	0.5	225
57	Seventeen novel microsatellite markers from an enriched library of the pest species Bactrocera dorsalis sensu stricto. Molecular Ecology Notes, 2006, 6, 1138-1140.	1.7	25
58	Is Polyandry a Common Event Among Wild Populations of the Pest Ceratitis capitata?. Journal of Economic Entomology, 2006, 99, 1420-1429.	0.8	28
59	Is Polyandry a Common Event Among Wild Populations of the Pest <I>Ceratitis capitata</I>?. Journal of Economic Entomology, 2006, 99, 1420-1429.	0.8	21
60	Cchobo, a hobo-related sequence in Ceratitis capitata. Genetica, 2005, 123, 313-325.	0.5	12
61	Genetic Structure of Asian Populations of Bombus ignitus (Hymenoptera: Apidae). , 2004, 95, 46-52.		47
62	On the origins of medfly invasion and expansion in Australia. Molecular Ecology, 2004, 13, 3845-3855.	2.0	77
63	Origin of Toll-Like Receptor-Mediated Innate Immunity. Journal of Molecular Evolution, 2004, 58, 442-448.	0.8	46
64	Population genetics of the potentially invasive African fruit fly species, Ceratitis rosa and Ceratitis fasciventris (Diptera: Tephritidae). Molecular Ecology, 2004, 13, 683-695.	2.0	47
65	Medfly transposable elements: diversity, evolution, genomic impact and possible applications. Insect Biochemistry and Molecular Biology, 2004, 34, 139-148.	1.2	15
66	Comparative analysis of microsatellite loci in four fruit fly species of the genusCeratitis(Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	0.5	26
67	Microsatellite analysis reveals remating by wild Mediterranean fruit fly females, Ceratitis capitata. Molecular Ecology, 2002, 11, 1915-1921.	2.0	62
68	Genetic differentiation, gene flow and the origin of infestations of the medfly, Ceratitis capitata. Genetica, 2002, 116, 125-135.	0.5	92
69	A New Basal Subfamily of mariner Elements in Ceratitis rosa and Other Tephritid Flies. Journal of Molecular Evolution, 2001, 53, 597-606.	0.8	39
70	Microsatellite analysis of medfly bioinfestations in California. Molecular Ecology, 2001, 10, 2515-2524.	2.0	84
71	Microsatellite Polymorphism in Tsetse Flies (Diptera: Glossinidae). Journal of Medical Entomology, 2001, 38, 376-381.	0.9	40
72	Microsatellite polymorphism in the Mediterranean fruit fly, Ceratitis capitata. Insect Molecular Biology, 2000, 9, 251-261.	1.0	71

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73	Secondary Malaria Vectors of Sub-Saharan Africa: Threat to Malaria Elimination on the Continent?. , 0, , .		19