Tatiana Teixeira Torres

List of Publications by Year in descending order

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38 papers

1,453 citations

393982 19 h-index 35 g-index

44 all docs

44 docs citations

44 times ranked 2725 citing authors

#	Article	IF	CITATIONS
1	Evidence of positive selection on six spider developmental genes. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2022, 338, 314-322.	0.6	2
2	Characterization of the mitochondrial genomes of <i>Bradysia hygida</i> , <i>Phytosciara flavipes</i> and <i>Trichosia splendens</i> (Diptera: Sciaridae) and novel insights on the control region of sciarid mitogenomes. Insect Molecular Biology, 2022, 31, 482-496.	1.0	2
3	Evolution of coding sequence and gene expression of blowflies and botflies with contrasting feeding habits. Genomics, 2021, 113, 699-706.	1.3	3
4	Genomic analysis on Brazilian strains of Anaplasma marginale. Brazilian Journal of Veterinary Parasitology, 2021, 30, e000421.	0.2	3
5	The steroid-hormone ecdysone coordinates parallel pupariation neuromotor and morphogenetic subprograms via epidermis-to-neuron Dilp8-Lgr3 signal induction. Nature Communications, 2021, 12, 3328.	5.8	7
6	Molecular basis of resistance to organophosphate insecticides in the New World screw-worm fly. Parasites and Vectors, 2020, 13, 562.	1.0	6
7	Genomic analyses of a livestock pest, the New World screwworm, find potential targets for genetic control programs. Communications Biology, 2020, 3, 424.	2.0	26
8	Evolution of Spiders and Silk Spinning: Mini Review of the Morphology, Evolution, and Development of Spiders' Spinnerets. Frontiers in Ecology and Evolution, 2020, 8, .	1.1	9
9	Detoxification mechanisms involved in ivermectin resistance in the cattle tick, Rhipicephalus (Boophilus) microplus. Scientific Reports, 2018, 8, 12401.	1.6	40
10	Traditional versus 3′ RNA-seq in a non-model species. Genomics Data, 2017, 11, 9-16.	1.3	35
11	Worldwide Phylogenetic Group Patterns of Escherichia coli from Commensal Human and Wastewater Treatment Plant Isolates. Frontiers in Microbiology, 2017, 8, 2512.	1.5	77
12	Carry on celebrating Mendel's legacy. Nature, 2016, 534, 475-475.	13.7	1
13	Evolution of genes involved in feeding preference and metabolic processes in Calliphoridae (Diptera:) Tj ETQq1 1	0.784314	rgBT Overlo
14	Novel variants in GNAI3 associated with auriculocondylar syndrome strengthen a common dominant negative effect. European Journal of Human Genetics, 2015, 23, 481-485.	1.4	21
15	Clustering of water bodies in unpolluted and polluted environments based on Escherichia coli phylogroup abundance using a simple interaction database. Genetics and Molecular Biology, 2014, 37, 694-701.	0.6	5
16	Selection and validation of reference genes for functional studies in the Calliphoridae family. Journal of Insect Science, 2014, 14, 2.	0.6	17
17	Selection and Validation of Reference Genes for Functional Studies in the Calliphoridae Family. Journal of Insect Science, 2014, 14, 1-15.	0.6	6
18	Bacterial diversity assessment in soil of an active Brazilian copper mine using high-throughput sequencing of 16S rDNA amplicons. Antonie Van Leeuwenhoek, 2014, 106, 879-890.	0.7	41

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19	Social Network Analysis Metrics and Their Application in Microbiological Network Studies. Studies in Computational Intelligence, 2014, , 251-260.	0.7	4
20	Bacterial communities and species-specific associations with the mucus of Brazilian coral species. Scientific Reports, 2013, 3, 1624.	1.6	110
21	The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the Environment. Journal of Heredity, 2013, 104, 595-600.	1.0	358
22	A transcriptomic analysis of gene expression in the venom gland of the snake Bothrops alternatus (urutu). BMC Genomics, 2010, 11, 605.	1.2	55
23	Deep sequencing of New World screw-worm transcripts to discover genes involved in insecticide resistance. BMC Genomics, 2010, 11, 695.	1.2	31
24	Microsatellite markers for population genetic studies of the blowfly Chrysomya putoria (Diptera:) Tj ETQq0 0 0	rgBT/Qver	lock 10 Tf 50
25	Expression profiling of Drosophila mitochondrial genes via deep mRNA sequencing. Nucleic Acids Research, 2009, 37, 7509-7518.	6.5	53
26	PanGEA: Identification of allele specific gene expression using the 454 technology. BMC Bioinformatics, 2009, 10, 143.	1.2	24
27	Population genetics of New World screwworm from the Caribbean: insights from microsatellite data. Medical and Veterinary Entomology, 2009, 23, 23-31.	0.7	22
28	Molecular characterization of esterase E3 gene associated with organophosphorus insecticide resistance in the New World screwworm fly, <i>Cochliomyia hominivorax</i> Entomology, 2009, 23, 86-91.	0.7	20
29	Development of polymorphic microsatellite markers for the human botfly, <i>Dermatobia hominis</i> (Diptera: Oestridae). Molecular Ecology Resources, 2009, 9, 409-411.	2.2	5
30	Gene expression profiling by massively parallel sequencing. Genome Research, 2008, 18, 172-177.	2.4	210
31	Characterization of polymorphic microsatellite markers for the blowfly <i>Chrysomya albiceps</i> (Diptera: Calliphoridae). Molecular Ecology Resources, 2008, 8, 208-210.	2.2	7
32	Isolation and characterization of polymorphic microsatellite loci for the horn fly, <i>Haematobia irritans</i> (L.) (Diptera: Muscidae). Molecular Ecology Resources, 2008, 8, 971-973.	2.2	0
33	Assessing Genetic Variation in New World Screwworm Cochliomyia hominivorax Populations from Uruguay., 2007,, 183-191.		11
34	A survey of mutations in the Cochliomyia hominivorax (Diptera: Calliphoridae) esterase E3 gene associated with organophosphate resistance and the molecular identification of mutant alleles. Veterinary Parasitology, 2006, 140, 344-351.	0.7	36
35	Development of new polymorphic microsatellite markers for the New World screw-worm Cochliomyia hominivorax (Diptera: Calliphoridae). Molecular Ecology Notes, 2005, 5, 815-817.	1.7	20
36	Isolation and characterization of microsatellite markers in the new world screw-worm Cochliomyia hominivorax (Diptera: Calliphoridae). Molecular Ecology Notes, 2004, 4, 182-184.	1.7	24

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37	The mitochondrial genome of the blowfly Chrysomya chloropyga (Diptera: Calliphoridae). Gene, 2004, 339, 7-15.	1.0	151
38	De novo construction of a transcriptome for the stink bug crop pest Chinavia impicticornis during late development. GigaByte, 0, 2020, 1-7.	0.0	0