

Camila J Mazzoni

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

2,033
citations

361413

20
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315739

38
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42
docs citations

42
times ranked

3518
citing authors

#	ARTICLE	IF	CITATIONS
1	New Genetic Insights About Hybridization and Population Structure of Hawksbill and Loggerhead Turtles From Brazil. <i>Journal of Heredity</i> , 2020, 111, 444-456.	2.4	13
2	Manatee genomics supports a special conservation area along the Guianas coastline under the influence of the Amazon River plume. <i>Estuarine, Coastal and Shelf Science</i> , 2019, 226, 106286.	2.1	9
3	Combining the 5.8S and ITS2 to improve classification of fungi. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1702-1711.	5.2	27
4	Manatee genomics supports a special conservation area along the Guianas coastline under the influence of the Amazon River plume. <i>Estuarine, Coastal and Shelf Science</i> , 2019, 231, 106436.	2.1	8
5	Demography and selection shape transcriptomic divergence in field crickets. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 553-567.	2.3	6
6	A new hybrid approach for MHC genotyping: high-throughput NGS and long read MinION nanopore sequencing, with application to the non-model vertebrate Alpine chamois (<i>Rupicapra rupicapra</i>). <i>Heredity</i> , 2018, 121, 293-303.	2.6	25
7	Long-read DNA metabarcoding of ribosomal RNA in the analysis of fungi from aquatic environments. <i>Molecular Ecology Resources</i> , 2018, 18, 1500-1514.	4.8	103
8	High adaptive variability and virus-driven selection on major histocompatibility complex (MHC) genes in invasive wild rabbits in Australia. <i>Biological Invasions</i> , 2017, 19, 1255-1271.	2.4	15
9	Canine distemper virus in the Serengeti ecosystem: molecular adaptation to different carnivore species. <i>Molecular Ecology</i> , 2017, 26, 2111-2130.	3.9	56
10	Resistance to RHD virus in wild Australian rabbits: Comparison of susceptible and resistant individuals using a genomewide approach. <i>Molecular Ecology</i> , 2017, 26, 4551-4561.	3.9	14
11	Transcriptome profiling of ontogeny in the acridid grasshopper <i>Chorthippus biguttulus</i> . <i>PLoS ONE</i> , 2017, 12, e0177367.	2.5	4
12	A genes eye view of ontogeny: <i>de novo</i> assembly and profiling of the <i>Gryllus rubens</i> transcriptome. <i>Molecular Ecology Resources</i> , 2016, 16, 1478-1490.	4.8	37
13	Sequence diversity between class I MHC loci of African native and introduced <i>Bos taurus</i> cattle in <i>Theileria parva</i> endemic regions: in silico peptide binding prediction identifies distinct functional clusters. <i>Immunogenetics</i> , 2016, 68, 339-352.	2.4	12
14	Evidence for selection maintaining MHC diversity in a rodent species despite strong density fluctuations. <i>Immunogenetics</i> , 2016, 68, 429-437.	2.4	8
15	PCR Strategies for Complete Allele Calling in Multigene Families Using High-Throughput Sequencing Approaches. <i>PLoS ONE</i> , 2016, 11, e0157402.	2.5	11
16	Spatial pattern of adaptive and neutral genetic diversity across different biomes in the lesser anteater (<i>Tamandua tetradactyla</i>). <i>Ecology and Evolution</i> , 2015, 5, 4932-4948.	1.9	10
17	A population genomic scan in <i>Chorthippus</i> grasshoppers unveils previously unknown phenotypic divergence. <i>Molecular Ecology</i> , 2015, 24, 3918-3930.	3.9	25
18	Molecular characterization of canine kobuvirus in wild carnivores and the domestic dog in Africa. <i>Virology</i> , 2015, 477, 89-97.	2.4	32

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19	A Novel Endogenous Betaretrovirus in the Common Vampire Bat (<i>Desmodus rotundus</i>) Suggests Multiple Independent Infection and Cross-Species Transmission Events. <i>Journal of Virology</i> , 2015, 89, 5180-5184.	3.4	32
20	Endogenous murine leukemia retroviral variation across wild European and inbred strains of house mouse. <i>BMC Genomics</i> , 2015, 16, 613.	2.8	4
21	Whole genome sequencing and methylome analysis of the wild guinea pig. <i>BMC Genomics</i> , 2014, 15, 1036.	2.8	14
22	Polar Bear Encephalitis: Establishment of a Comprehensive Next-generation Pathogen Analysis Pipeline for Captive and Free-living Wildlife. <i>Journal of Comparative Pathology</i> , 2014, 150, 474-488.	0.4	9
23	MHC genotyping of non-model organisms using next-generation sequencing: a new methodology to deal with artefacts and allelic dropout. <i>BMC Genomics</i> , 2013, 14, 542.	2.8	107
24	A novel endogenous betaretrovirus group characterized from polar bears (<i>Ursus maritimus</i>) and giant pandas (<i>Ailuropoda melanoleuca</i>). <i>Virology</i> , 2013, 443, 1-10.	2.4	11
25	Cyanobacterial diversity in the hot spring, pelagic and benthic habitats of a tropical soda lake. <i>FEMS Microbiology Ecology</i> , 2013, 85, 389-401.	2.7	71
26	Multilocus Analysis of Divergence and Introgression in Sympatric and Allopatric Sibling Species of the <i>Lutzomyia longipalpis</i> Complex in Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2495.	3.0	30
27	Comparing PreXMRV-2 gag sequence diversity in laboratory and wild mice using deep sequencing. <i>Virus Research</i> , 2012, 169, 30-37.	2.2	1
28	The Transcriptome of <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) Male Reproductive Organs. <i>PLoS ONE</i> , 2012, 7, e34495.	2.5	32
29	Population structure of the <i>Yersinia pseudotuberculosis</i> complex according to multilocus sequence typing. <i>Environmental Microbiology</i> , 2011, 13, 3114-3127.	3.8	84
30	Estimation of divergence time between two sibling species of the <i>Anopheles</i> (<i>Kerteszia</i>) <i>cruzi</i> complex using a multilocus approach. <i>BMC Evolutionary Biology</i> , 2010, 10, 91.	3.2	21
31	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010, 42, 1140-1143.	21.4	504
32	Evolution and Population Structure of <i>Salmonella enterica</i> Serovar Newport. <i>Journal of Bacteriology</i> , 2010, 192, 6465-6476.	2.2	109
33	A multiplex single nucleotide polymorphism typing assay for detecting mutations that result in decreased fluoroquinolone susceptibility in <i>Salmonella enterica</i> serovars Typhi and Paratyphi A. <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 1631-1641.	3.0	36
34	High-throughput sequencing provides insights into genome variation and evolution in <i>Salmonella</i> Typhi. <i>Nature Genetics</i> , 2008, 40, 987-993.	21.4	453
35	Multilocus analysis of introgression between two sand fly vectors of leishmaniasis. <i>BMC Evolutionary Biology</i> , 2008, 8, 141.	3.2	23
36	Molecular polymorphism, differentiation and introgression in the period gene between <i>Lutzomyia intermedia</i> and <i>Lutzomyia whitmani</i> . <i>BMC Evolutionary Biology</i> , 2006, 6, 85.	3.2	16

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37	GARSA: genomic analysis resources for sequence annotation. <i>Bioinformatics</i> , 2005, 21, 4302-4303.	4.1	20
38	Molecular Evolution of the period Gene in Sandflies. <i>Journal of Molecular Evolution</i> , 2002, 55, 553-562.	1.8	25