

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

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315739

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42
all docs

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docs citations

42
times ranked

3518
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010, 42, 1140-1143.	21.4	504
2	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
3	Evolution and Population Structure of <i>Salmonella enterica</i> Serovar Newport. <i>Journal of Bacteriology</i> , 2010, 192, 6465-6476.	2.2	109
4	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
5	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
6	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
7	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
8	Canine distemper virus in the Serengeti ecosystem: molecular adaptation to different carnivore species. <i>Molecular Ecology</i> , 2017, 26, 2111-2130.	3.9	56
9	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
10	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
11	Molecular characterization of canine kobuvirus in wild carnivores and the domestic dog in Africa. <i>Virology</i> , 2015, 477, 89-97.	2.4	32
12	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
13	The Transcriptome of <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) Male Reproductive Organs. <i>PLoS ONE</i> , 2012, 7, e34495.	2.5	32
14	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
15	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
16	Molecular Evolution of the period Gene in Sandflies. <i>Journal of Molecular Evolution</i> , 2002, 55, 553-562.	1.8	25
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	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

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19	Multilocus analysis of introgression between two sand fly vectors of leishmaniasis. BMC Evolutionary Biology, 2008, 8, 141.	3.2	23
20	Estimation of divergence time between two sibling species of the Anopheles (Kerteszia) cruzii complex using a multilocus approach. BMC Evolutionary Biology, 2010, 10, 91.	3.2	21
21	GARSA: genomic analysis resources for sequence annotation. Bioinformatics, 2005, 21, 4302-4303.	4.1	20
22	Molecular polymorphism, differentiation and introgression in the period gene between Lutzomyia intermedia and Lutzomyia whitmani. BMC Evolutionary Biology, 2006, 6, 85.	3.2	16
23	High adaptive variability and virus-driven selection on major histocompatibility complex (MHC) genes in invasive wild rabbits in Australia. Biological Invasions, 2017, 19, 1255-1271.	2.4	15
24	Whole genome sequencing and methylome analysis of the wild guinea pig. BMC Genomics, 2014, 15, 1036.	2.8	14
25	Resistance to RHD virus in wild Australian rabbits: Comparison of susceptible and resistant individuals using a genomewide approach. Molecular Ecology, 2017, 26, 4551-4561.	3.9	14
26	New Genetic Insights About Hybridization and Population Structure of Hawksbill and Loggerhead Turtles From Brazil. Journal of Heredity, 2020, 111, 444-456.	2.4	13
27	Sequence diversity between class I MHC loci of African native and introduced Bos taurus cattle in Theileria parva endemic regions: in silico peptide binding prediction identifies distinct functional clusters. Immunogenetics, 2016, 68, 339-352.	2.4	12
28	A novel endogenous betaretrovirus group characterized from polar bears (Ursus maritimus) and giant pandas (Ailuropoda melanoleuca). Virology, 2013, 443, 1-10.	2.4	11
29	PCR Strategies for Complete Allele Calling in Multigene Families Using High-Throughput Sequencing Approaches. PLoS ONE, 2016, 11, e0157402.	2.5	11
30	Spatial pattern of adaptive and neutral genetic diversity across different biomes in the lesser anteater (<i>Tamandua tetradactyla</i>). Ecology and Evolution, 2015, 5, 4932-4948.	1.9	10
31	Polar Bear Encephalitis: Establishment of a Comprehensive Next-generation Pathogen Analysis Pipeline for Captive and Free-living Wildlife. Journal of Comparative Pathology, 2014, 150, 474-488.	0.4	9
32	Manatee genomics supports a special conservation area along the Guianas coastline under the influence of the Amazon River plume. Estuarine, Coastal and Shelf Science, 2019, 226, 106286.	2.1	9
33	Evidence for selection maintaining MHC diversity in a rodent species despite strong density fluctuations. Immunogenetics, 2016, 68, 429-437.	2.4	8
34	Manatee genomics supports a special conservation area along the Guianas coastline under the influence of the Amazon River plume. Estuarine, Coastal and Shelf Science, 2019, 231, 106436.	2.1	8
35	Demography and selection shape transcriptomic divergence in field crickets. Evolution; International Journal of Organic Evolution, 2018, 72, 553-567.	2.3	6
36	Endogenous murine leukemia retroviral variation across wild European and inbred strains of house mouse. BMC Genomics, 2015, 16, 613.	2.8	4

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37	Transcriptome profiling of ontogeny in the acridid grasshopper <i>Chorthippus biguttulus</i> . PLoS ONE, 2017, 12, e0177367.	2.5	4
38	Comparing PreXMRV-2 gag sequence diversity in laboratory and wild mice using deep sequencing. Virus Research, 2012, 169, 30-37.	2.2	1