

Marcos Mateo Miretti

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

2,968
citations

516710

16
h-index

580821

25
g-index

27
all docs

27
docs citations

27
times ranked

5992
citing authors

#	ARTICLE	IF	CITATIONS
1	Expression-based analysis of genes related to single nucleotide polymorphism hits associated with bovine leukemia virus proviral load in Argentinean dairy cattle. <i>Journal of Dairy Science</i> , 2021, 104, 1993-2007.	3.4	3
2	Health-Related Quality of Life in Neurological Disorders Most Commonly Associated With Zika-Virus Infection: A Systematic Review. <i>Value in Health</i> , 2020, 23, 969-976.	0.3	2
3	CRISPR-based platform for carbapenemases and emerging viruses detection using Cas12a (Cpf1) effector nuclease. <i>Emerging Microbes and Infections</i> , 2020, 9, 1140-1148.	6.5	25
4	Arbovirus vectors of epidemiological concern in the Americas: A scoping review of entomological studies on Zika, dengue and chikungunya virus vectors. <i>PLoS ONE</i> , 2020, 15, e0220753.	2.5	48
5	Genome-wide scan for commons SNPs affecting bovine leukemia virus infection level in dairy cattle. <i>BMC Genomics</i> , 2018, 19, 142.	2.8	18
6	Yerba mate (<i>Ilex paraguariensis</i> , A. St.-Hil.) de novo transcriptome assembly based on tissue specific genomic expression profiles. <i>BMC Genomics</i> , 2018, 19, 891.	2.8	9
7	Molecular characterization of yerba mate chlorosis-associated virus, a putative cytorhabdovirus infecting yerba mate (<i>Ilex paraguariensis</i>). <i>Archives of Virology</i> , 2017, 162, 2481-2484.	2.1	13
8	<i>BOLA</i> gene polymorphisms influence bovine leukaemia virus infection levels in Holstein and Holstein–Jersey crossbreed dairy cattle. <i>Animal Genetics</i> , 2017, 48, 420-430.	1.7	32
9	A unifying study of phenotypic and molecular genetic variability in natural populations of <i>Anadenanthera colubrina</i> var. <i>cebil</i> from Yungas and Paranaense biogeographic provinces in Argentina. <i>Journal of Genetics</i> , 2014, 93, 123-132.	0.7	9
10	Genetic diversity of the Brazilian Creole cattle PÃ©-duro assessed by microsatellites and mitochondrial DNA. <i>Revista Brasileira De Zootecnia</i> , 2012, 41, 2316-2322.	0.8	1
11	Human platelet antigen typing of neonatal alloimmune thrombocytopenia patients using whole genome amplified DNA and a 5â€²â€”nuclease assay. <i>Transfusion</i> , 2009, 49, 953-958.	1.6	3
12	Variation analysis and gene annotation of eight MHC haplotypes: The MHC Haplotype Project. <i>Immunogenetics</i> , 2008, 60, 1-18.	2.4	286
13	Generation of a genomic tiling array of the human Major Histocompatibility Complex (MHC) and its application for DNA methylation analysis. <i>BMC Medical Genomics</i> , 2008, 1, 19.	1.5	24
14	A Bayesian deconvolution strategy for immunoprecipitation-based DNA methylome analysis. <i>Nature Biotechnology</i> , 2008, 26, 779-785.	17.5	619
15	Germline rates of de novo meiotic deletions and duplications causing several genomic disorders. <i>Nature Genetics</i> , 2008, 40, 90-95.	21.4	276
16	Association of Smoking Behavior with an Odorant Receptor Allele Telomeric to the Human Major Histocompatibility Complex. <i>Genetic Testing and Molecular Biomarkers</i> , 2008, 12, 481-486.	1.7	13
17	An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs). <i>Genome Research</i> , 2008, 18, 1518-1529.	5.5	350
18	Structure and genetic relationships between Brazilian naturalized and exotic purebred goat domestic goat (<i>Capra hircus</i>) breeds based on microsatellites. <i>Genetics and Molecular Biology</i> , 2007, 30, 356-363.	1.3	17

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19	Immunogenomics: Molecular hide and seek. <i>Human Genomics</i> , 2006, 2, 244.	2.9	5
20	The LRC haplotype project: a resource for killer immunoglobulin-like receptor-linked association studies. <i>Tissue Antigens</i> , 2006, 68, 450-452.	1.0	8
21	A high-resolution HLA and SNP haplotype map for disease association studies in the extended human MHC. <i>Nature Genetics</i> , 2006, 38, 1166-1172.	21.4	686
22	Genetic Analysis of Completely Sequenced Disease-Associated MHC Haplotypes Identifies Shuffling of Segments in Recent Human History. <i>PLoS Genetics</i> , 2006, 2, e9.	3.5	156
23	A comparison of tagging methods and their tagging space. <i>Human Molecular Genetics</i> , 2005, 14, 2757-2767.	2.9	36
24	A High-Resolution Linkage-Disequilibrium Map of the Human Major Histocompatibility Complex and First Generation of Tag Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2005, 76, 634-646.	6.2	237
25	Predominant African-Derived mtDNA in Caribbean and Brazilian Creole Cattle is also Found in Spanish Cattle (<i>Bos taurus</i>). <i>Journal of Heredity</i> , 2004, 95, 450-453.	2.4	46
26	African-Derived Mitochondria in South American Native Cattle Breeds (<i>Bos taurus</i>): Evidence of a New Taurine Mitochondrial Lineage. , 2002, 93, 323-330.		29
27	Restriction fragment length polymorphism (RFLP) in exon 2 of the BoLA-DRB3 gene in South American cattle. <i>Biochemical Genetics</i> , 2001, 39, 311-324.	1.7	17