

Adhemar Zerlotini

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

2,621
citations

394421

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414414

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43
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43
docs citations

43
times ranked

3278
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation may affect beef tenderness through signal transduction in <i>Bos indicus</i> . <i>Epigenetics and Chromatin</i> , 2022, 15, 15.	3.9	6
2	Prune homolog 2 with BCH domain (PRUNE2) gene expression is associated with feed efficiency-related traits in Nelore steers. <i>Mammalian Genome</i> , 2022, 33, 629-641.	2.2	1
3	Plant Co-expression Annotation Resource: a web server for identifying targets for genetically modified crop breeding pipelines. <i>BMC Bioinformatics</i> , 2021, 22, 46.	2.6	0
4	Muscle allele-specific expression QTLs may affect meat quality traits in <i>Bos indicus</i> . <i>Scientific Reports</i> , 2021, 11, 7321.	3.3	10
5	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. <i>Genes</i> , 2021, 12, 67.	2.4	12
6	Machado: Open source genomics data integration framework. <i>GigaScience</i> , 2020, 9, .	6.4	5
7	Allele-specific expression is widespread in <i>Bos indicus</i> muscle and affects meat quality candidate genes. <i>Scientific Reports</i> , 2020, 10, 10204.	3.3	13
8	Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach. <i>Scientific Reports</i> , 2020, 10, 8436.	3.3	10
9	Co-Expression Networks Reveal Potential Regulatory Roles of miRNAs in Fatty Acid Composition of Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 651.	2.3	22
10	A comprehensive manually-curated compendium of bovine transcription factors. <i>Scientific Reports</i> , 2018, 8, 13747.	3.3	18
11	An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. <i>Scientific Reports</i> , 2018, 8, 17072.	3.3	47
12	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018, 19, 499.	2.8	51
13	Whole genome sequencing of Guzerat cattle reveals genetic variants in candidate genes for production, disease resistance, and heat tolerance. <i>Mammalian Genome</i> , 2017, 28, 66-80.	2.2	15
14	Single nucleotide variants and InDels identified from whole-genome re-sequencing of Guzerat, Gyr, Girolando and Holstein cattle breeds. <i>PLoS ONE</i> , 2017, 12, e0173954.	2.5	47
15	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. <i>Scientific Reports</i> , 2016, 6, 39493.	3.3	57
16	Synergy of Omeprazole and Praziquantel In Vitro Treatment against <i>Schistosoma mansoni</i> Adult Worms. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004086.	3.0	17
17	POTION: an end-to-end pipeline for positive Darwinian selection detection in genome-scale data through phylogenetic comparison of protein-coding genes. <i>BMC Genomics</i> , 2015, 16, 567.	2.8	44
18	Significant variance in genetic diversity among populations of <i>Schistosoma haematobium</i> detected using microsatellite DNA loci from a genome-wide database. <i>Parasites and Vectors</i> , 2013, 6, 300.	2.5	26

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19	Complete genome sequence of <i>Streptococcus agalactiae</i> strain SA20-06, a fish pathogen associated to meningoencephalitis outbreaks. <i>Standards in Genomic Sciences</i> , 2013, 8, 188-197.	1.5	33
20	A Systematically Improved High Quality Genome and Transcriptome of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1455.	3.0	400
21	Chromatin structure changes around satellite repeats on the <i>Schistosoma mansoni</i> female sex chromosome suggest a possible mechanism for sex chromosome emergence. <i>Genome Biology</i> , 2012, 13, R14.	9.6	28
22	The <i>Schistosoma mansoni</i> phylome: using evolutionary genomics to gain insight into a parasite's biology. <i>BMC Genomics</i> , 2012, 13, 617.	2.8	28
23	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	21.4	383
24	SchistoDB: an updated genome resource for the three key schistosomes of humans. <i>Nucleic Acids Research</i> , 2012, 41, D728-D731.	14.5	45
25	Evidence for Reductive Genome Evolution and Lateral Acquisition of Virulence Functions in Two <i>Corynebacterium pseudotuberculosis</i> Strains. <i>PLoS ONE</i> , 2011, 6, e18551.	2.5	75
26	Evolutionary histories of expanded peptidase families in <i>Schistosoma mansoni</i> . <i>Memorias Do Instituto Oswaldo Cruz</i> , 2011, 106, 864-877.	1.6	12
27	Eukaryotic Protein Kinases (ePKs) of the Helminth Parasite <i>Schistosoma mansoni</i> . <i>BMC Genomics</i> , 2011, 12, 215.	2.8	90
28	Identification of <i>Schistosoma mansoni</i> microRNAs. <i>BMC Genomics</i> , 2011, 12, 47.	2.8	62
29	The contributions of the Genome Project to the study of schistosomiasis. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2010, 105, 367-369.	1.6	6
30	SchistoDB: a <i>Schistosoma mansoni</i> genome resource. <i>Nucleic Acids Research</i> , 2009, 37, D579-D582.	14.5	72
31	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	27.8	945
32	Single nucleotide polymorphisms identification in expressed genes of <i>Schistosoma mansoni</i> . <i>Molecular and Biochemical Parasitology</i> , 2007, 154, 134-140.	1.1	22