

Andressa Lima

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2619842/publications.pdf>

Version: 2024-02-01

10
papers

246
citations

1307594

7
h-index

1372567

10
g-index

10
all docs

10
docs citations

10
times ranked

493
citing authors

#	ARTICLE	IF	CITATIONS
1	Network Analyses Predict Small RNAs That Might Modulate Gene Expression in the Testis and Epididymis of <i>Bos indicus</i> Bulls. <i>Frontiers in Genetics</i> , 2021, 12, 610116.	2.3	7
2	Single nucleotide polymorphisms affect miRNA target prediction in bovine. <i>PLoS ONE</i> , 2021, 16, e0249406.	2.5	5
3	Potential Biomarkers for Feed Efficiency-Related Traits in Nelore Cattle Identified by Co-expression Network and Integrative Genomics Analyses. <i>Frontiers in Genetics</i> , 2020, 11, 189.	2.3	23
4	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
5	Muscle transcriptome analysis reveals genes and metabolic pathways related to mineral concentration in <i>Bos indicus</i> . <i>Scientific Reports</i> , 2019, 9, 12715.	3.3	15
6	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
7	Allele- and parent-of-origin-specific effects on expression of the <i>KCNJ11</i> gene: A candidate for meat tenderness in cattle. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	2
8	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
9	Linkage disequilibrium and haplotype block structure in a composite beef cattle breed. <i>BMC Genomics</i> , 2014, 15, S6.	2.8	48
10	Genome-wide association study for backfat thickness in Canchim beef cattle using Random Forest approach. <i>BMC Genetics</i> , 2013, 14, 47.	2.7	32