

A S M Cesar

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

1,563
citations

236612

25
h-index

329751

37
g-index

66
all docs

66
docs citations

66
times ranked

1527
citing authors

#	ARTICLE	IF	CITATIONS
1	Editorial: Gene Regulation Explored by Systems Biology in Livestock Science. <i>Frontiers in Genetics</i> , 2022, 13, 859061.	1.1	1
2	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. <i>Animals</i> , 2022, 12, 1632.	1.0	5
3	Effect of dietary soybean oil inclusion on liver-related transcription factors in a pig model for metabolic diseases. <i>Scientific Reports</i> , 2022, 12, .	1.6	8
4	Fatty acid profile in brain and hepatic tissues from pigs supplemented with canola oil. <i>Revista Brasileira De Agrotecnologia</i> , 2021, 11, 414-420.	0.0	3
5	Effects of dietary oil inclusion on meat quality of immunocastrated male pigs. <i>Revista Brasileira De Agrotecnologia</i> , 2021, 11, 382-385.	0.0	1
6	Genome-wide detection of CNVs and their association with performance traits in broilers. <i>BMC Genomics</i> , 2021, 22, 354.	1.2	23
7	Effects of increasing dietary oil inclusion from different sources on growth performance, carcass and meat quality traits, and fatty acid profile in genetically lean immunocastrated male pigs. <i>Livestock Science</i> , 2021, 248, 104515.	0.6	18
8	A Missense Mutation in the MYBPH Gene Is Associated With Abdominal Fat Traits in Meat-Type Chickens. <i>Frontiers in Genetics</i> , 2021, 12, 698163.	1.1	4
9	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. <i>Genes</i> , 2021, 12, 67.	1.0	12
10	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.	1.1	23
11	Allele-specific expression is widespread in <i>Bos indicus</i> muscle and affects meat quality candidate genes. <i>Scientific Reports</i> , 2020, 10, 10204.	1.6	13
12	Proteome alterations associated with the oleic acid and cis-9, trans-11 conjugated linoleic acid content in bovine skeletal muscle. <i>Journal of Proteomics</i> , 2020, 222, 103792.	1.2	2
13	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.	1.6	10
14	Interplay among miR-29 family, mineral metabolism, and gene regulation in <i>Bos indicus</i> muscle. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1113-1127.	1.0	2
15	Co-Expression Networks Reveal Potential Regulatory Roles of miRNAs in Fatty Acid Composition of Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 651.	1.1	22
16	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. <i>BMC Genetics</i> , 2019, 20, 83.	2.7	10
17	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. <i>BMC Genomics</i> , 2019, 20, 669.	1.2	17
18	Identification of selection signatures involved in performance traits in a paternal broiler line. <i>BMC Genomics</i> , 2019, 20, 449.	1.2	28

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19	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 210.	1.1	27
20	Fine mapping of genomic regions associated with female fertility in Nelore beef cattle based on sequence variants from segregating sires. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 97.	2.1	7
21	Gene co-expression networks associated with carcass traits reveal new pathways for muscle and fat deposition in Nelore cattle. <i>BMC Genomics</i> , 2019, 20, 32.	1.2	34
22	MiRNAs differentially expressed in skeletal muscle of animals with divergent estimated breeding values for beef tenderness. <i>BMC Molecular Biology</i> , 2019, 20, 1.	3.0	30
23	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	1.6	25
24	Longissimus dorsi muscle label-free quantitative proteomic reveals biological mechanisms associated with intramuscular fat deposition. <i>Journal of Proteomics</i> , 2018, 179, 30-41.	1.2	53
25	Copy number variation regions in Nelore cattle: Evidences of environment adaptation. <i>Livestock Science</i> , 2018, 207, 51-58.	0.6	30
26	An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. <i>Scientific Reports</i> , 2018, 8, 17072.	1.6	47
27	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. <i>Scientific Reports</i> , 2018, 8, 16222.	1.6	29
28	Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nelore Cattle. <i>Frontiers in Genetics</i> , 2018, 9, 441.	1.1	54
29	Genome-wide characterization of genetic variants and putative regions under selection in meat and egg-type chicken lines. <i>BMC Genomics</i> , 2018, 19, 83.	1.2	39
30	Data from proteomic analysis of bovine Longissimus dorsi muscle associated with intramuscular fat content. <i>Data in Brief</i> , 2018, 19, 1314-1317.	0.5	6
31	Estimates of genomic heritability and genome-wide association study for fatty acids profile in Santa In�s sheep. <i>BMC Genomics</i> , 2018, 19, 375.	1.2	31
32	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. <i>BMC Genomics</i> , 2018, 19, 126.	1.2	53
33	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018, 19, 499.	1.2	51
34	A genome-wide association study reveals novel genomic regions and positional candidate genes for fat deposition in broiler chickens. <i>BMC Genomics</i> , 2018, 19, 374.	1.2	28
35	Comparative muscle transcriptome associated with carcass traits of Nelore cattle. <i>BMC Genomics</i> , 2017, 18, 506.	1.2	51
36	Supplementation with small-extracellular vesicles from ovarian follicular fluid during in vitro production modulates bovine embryo development. <i>PLoS ONE</i> , 2017, 12, e0179451.	1.1	80

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37	P3032 Association of skeletal muscle transcripts with fatty acid content in Nelore cattle. <i>Journal of Animal Science</i> , 2016, 94, 68-68.	0.2	0
38	A single nucleotide polymorphism in NEUROD1 is associated with production traits in Nelore beef cattle. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.3	0
39	0318 PRUNE2 gene has a potential effect on residual feed intake in Nelore cattle. <i>Journal of Animal Science</i> , 2016, 94, 152-153.	0.2	1
40	Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. <i>BMC Genomics</i> , 2016, 17, 961.	1.2	54
41	Gene expression profile of intramuscular muscle in Nelore cattle with extreme values of fatty acid. <i>BMC Genomics</i> , 2016, 17, 972.	1.2	49
42	0339 Gene network regulated by microRNAs suggests modulation of fat deposition in cattle. <i>Journal of Animal Science</i> , 2016, 94, 163-163.	0.2	0
43	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. <i>Scientific Reports</i> , 2016, 6, 39493.	1.6	57
44	0893 Label-free MSE proteomic analysis of the bovine skeletal muscle: New approach for meat tenderness evaluation. <i>Journal of Animal Science</i> , 2016, 94, 429-429.	0.2	1
45	0340 Differentially expressed miRNAs in skeletal muscle related to feed efficiency in Nelore cattle. <i>Journal of Animal Science</i> , 2016, 94, 163-164.	0.2	4
46	0891 Genome-wide efficient mixed-model study for meat quality in Nelore cattle. <i>Journal of Animal Science</i> , 2016, 94, 428-429.	0.2	2
47	Copy number variations and genome-wide associations reveal putative genes and metabolic pathways involved with the feed conversion ratio in beef cattle. <i>Journal of Applied Genetics</i> , 2016, 57, 495-504.	1.0	78
48	Feed efficiency indexes and their relationships with carcass, non-carcass and meat quality traits in Nelore steers. <i>Meat Science</i> , 2016, 116, 78-85.	2.7	40
49	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0161160.	1.1	28
50	0341 miRNAs related to fatty acids composition in Nelore cattle. <i>Journal of Animal Science</i> , 2016, 94, 164-164.	0.2	1
51	Putative Regulatory Factors Associated with Intramuscular Fat Content. <i>PLoS ONE</i> , 2015, 10, e0128350.	1.1	116
52	Identification of genomic regions associated with feed efficiency in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 100.	2.7	87
53	Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 39.	2.7	121
54	Estimation of taurindicine hybridization of American Zebu cattle in Brazil. <i>Genetics and Molecular Research</i> , 2012, 11, 393-403.	0.3	1

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55	Influence of the halothane gene (HAL) on pork quality in two commercial crossbreeds. Genetics and Molecular Research, 2011, 10, 1479-1489.	0.3	8
56	Influence of Chinese breeds on pork quality of commercial pig lines. Genetics and Molecular Research, 2010, 9, 727-733.	0.3	18
57	Effect of consanguinity on Argentinean Angus beef DNA traceability. Meat Science, 2010, 85, 671-675.	2.7	8
58	Nuclear and mitochondrial DNA markers in traceability of retail beef samples. Pesquisa Veterinaria Brasileira, 2010, 30, 783-786.	0.5	0
59	PIT1 gene polymorphism in Pietrain and Large White pigs after divergent selection. Genetics and Molecular Research, 2009, 8, 1008-1012.	0.3	3
60	Obese gene polymorphism in Pietrain and large white pigs after a divergent selection. Genetics and Molecular Research, 2008, 7, 1217-1222.	0.3	1