

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

236925

25
h-index

330143

37
g-index

66
all docs

66
docs citations

66
times ranked

1527
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle. BMC Genetics, 2014, 15, 39.	2.7	121
2	Putative Regulatory Factors Associated with Intramuscular Fat Content. PLoS ONE, 2015, 10, e0128350.	2.5	116
3	Identification of genomic regions associated with feed efficiency in Nelore cattle. BMC Genetics, 2014, 15, 100.	2.7	87
4	Supplementation with small-extracellular vesicles from ovarian follicular fluid during in vitro production modulates bovine embryo development. PLoS ONE, 2017, 12, e0179451.	2.5	80
5	Copy number variations and genome-wide associations reveal putative genes and metabolic pathways involved with the feed conversion ratio in beef cattle. Journal of Applied Genetics, 2016, 57, 495-504.	1.9	78
6	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. Scientific Reports, 2016, 6, 39493.	3.3	57
7	Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. BMC Genomics, 2016, 17, 961.	2.8	54
8	Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nelore Cattle. Frontiers in Genetics, 2018, 9, 441.	2.3	54
9	Longissimus dorsi muscle label-free quantitative proteomic reveals biological mechanisms associated with intramuscular fat deposition. Journal of Proteomics, 2018, 179, 30-41.	2.4	53
10	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. BMC Genomics, 2018, 19, 126.	2.8	53
11	Comparative muscle transcriptome associated with carcass traits of Nelore cattle. BMC Genomics, 2017, 18, 506.	2.8	51
12	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC Genomics, 2018, 19, 499.	2.8	51
13	Gene expression profile of intramuscular muscle in Nelore cattle with extreme values of fatty acid. BMC Genomics, 2016, 17, 972.	2.8	49
14	An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. Scientific Reports, 2018, 8, 17072.	3.3	47
15	Feed efficiency indexes and their relationships with carcass, non-carcass and meat quality traits in Nelore steers. Meat Science, 2016, 116, 78-85.	5.5	40
16	Genome-wide characterization of genetic variants and putative regions under selection in meat and egg-type chicken lines. BMC Genomics, 2018, 19, 83.	2.8	39
17	Gene co-expression networks associated with carcass traits reveal new pathways for muscle and fat deposition in Nelore cattle. BMC Genomics, 2019, 20, 32.	2.8	34
18	Estimates of genomic heritability and genome-wide association study for fatty acids profile in Santa In�s sheep. BMC Genomics, 2018, 19, 375.	2.8	31

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19	Copy number variation regions in Nelore cattle: Evidences of environment adaptation. <i>Livestock Science</i> , 2018, 207, 51-58.	1.6	30
20	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
21	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.	3.3	29
22	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.	2.8	28
23	Identification of selection signatures involved in performance traits in a paternal broiler line. <i>BMC Genomics</i> , 2019, 20, 449.	2.8	28
24	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0161160.	2.5	28
25	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 210.	2.3	27
26	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	3.3	25
27	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
28	Genome-wide detection of CNVs and their association with performance traits in broilers. <i>BMC Genomics</i> , 2021, 22, 354.	2.8	23
29	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
30	Influence of Chinese breeds on pork quality of commercial pig lines. <i>Genetics and Molecular Research</i> , 2010, 9, 727-733.	0.2	18
31	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.	1.6	18
32	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.	2.8	17
33	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
34	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. <i>Genes</i> , 2021, 12, 67.	2.4	12
35	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
36	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

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37	Effect of consanguinity on Argentinean Angus beef DNA traceability. <i>Meat Science</i> , 2010, 85, 671-675.	5.5	8
38	Influence of the halothane gene (HAL) on pork quality in two commercial crossbreeds. <i>Genetics and Molecular Research</i> , 2011, 10, 1479-1489.	0.2	8
39	Effect of dietary soybean oil inclusion on liver-related transcription factors in a pig model for metabolic diseases. <i>Scientific Reports</i> , 2022, 12, .	3.3	8
40	Fine mapping of genomic regions associated with female fertility in Nellore beef cattle based on sequence variants from segregating sires. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 97.	5.3	7
41	Data from proteomic analysis of bovine Longissimus dorsi muscle associated with intramuscular fat content. <i>Data in Brief</i> , 2018, 19, 1314-1317.	1.0	6
42	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. <i>Animals</i> , 2022, 12, 1632.	2.3	5
43	0340 Differentially expressed miRNAs in skeletal muscle related to feed efficiency in Nellore cattle. <i>Journal of Animal Science</i> , 2016, 94, 163-164.	0.5	4
44	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.	2.3	4
45	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
46	PIT1 gene polymorphism in Pietrain and Large White pigs after divergent selection. <i>Genetics and Molecular Research</i> , 2009, 8, 1008-1012.	0.2	3
47	0891 Genome-wide efficient mixed-model study for meat quality in Nellore cattle. <i>Journal of Animal Science</i> , 2016, 94, 428-429.	0.5	2
48	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.	2.4	2
49	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.	2.1	2
50	0318 PRUNE2 gene has a potential effect on residual feed intake in Nellore cattle. <i>Journal of Animal Science</i> , 2016, 94, 152-153.	0.5	1
51	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.	0.5	1
52	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
53	Obese gene polymorphism in Pietrain and large white pigs after a divergent selection. <i>Genetics and Molecular Research</i> , 2008, 7, 1217-1222.	0.2	1
54	Estimation of taurindicine hybridization of American Zebu cattle in Brazil. <i>Genetics and Molecular Research</i> , 2012, 11, 393-403.	0.2	1

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55	0341 miRNAs related to fatty acids composition in Nelore cattle. Journal of Animal Science, 2016, 94, 164-164.	0.5	1
56	Editorial: Gene Regulation Explored by Systems Biology in Livestock Science. Frontiers in Genetics, 2022, 13, 859061.	2.3	1
57	P3032 Association of skeletal muscle transcripts with fatty acid content in Nelore cattle. Journal of Animal Science, 2016, 94, 68-68.	0.5	0
58	A single nucleotide polymorphism in NEUROD1 is associated with production traits in Nelore beef cattle. Genetics and Molecular Research, 2016, 15, .	0.2	0
59	0339 Gene network regulated by microRNAs suggests modulation of fat deposition in cattle. Journal of Animal Science, 2016, 94, 163-163.	0.5	0
60	Nuclear and mitochondrial DNA markers in traceability of retail beef samples. Pesquisa Veterinaria Brasileira, 2010, 30, 783-786.	0.5	0