

# Luiz Coutinho

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5873088/publications.pdf>

Version: 2024-02-01

265  
papers

9,402  
citations

57752

44  
h-index

53222

85  
g-index

275  
all docs

275  
docs citations

275  
times ranked

9254  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of the genomes of two <i>Xanthomonas</i> pathogens with differing host specificities. <i>Nature</i> , 2002, 417, 459-463.	27.8	1,074
2	The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> . <i>Nature</i> , 2000, 406, 151-157.	27.8	827
3	Comparative Genomics of Two <i>Leptospira interrogans</i> Serovars Reveals Novel Insights into Physiology and Pathogenesis. <i>Journal of Bacteriology</i> , 2004, 186, 2164-2172.	2.2	406
4	Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of <i>Xylella fastidiosa</i> . <i>Journal of Bacteriology</i> , 2003, 185, 1018-1026.	2.2	307
5	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010, 20, 693-703.	5.5	280
6	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. <i>Genome Research</i> , 2003, 13, 2725-2735.	5.5	254
7	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18644-18649.	7.1	196
8	Liver transcriptomic networks reveal main biological processes associated with feed efficiency in beef cattle. <i>BMC Genomics</i> , 2015, 16, 1073.	2.8	161
9	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	10.3	142
10	Genome scan for meat quality traits in Nelore beef cattle. <i>Physiological Genomics</i> , 2013, 45, 1012-1020.	2.3	123
11	Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 39.	2.7	121
12	The Genome Sequence of the Gram-Positive Sugarcane Pathogen <i>Leifsonia xyli</i> subsp. <i>xyli</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 827-836.	2.6	119
13	Putative Regulatory Factors Associated with Intramuscular Fat Content. <i>PLoS ONE</i> , 2015, 10, e0128350.	2.5	116
14	Brazilian coffee genome project: an EST-based genomic resource. <i>Brazilian Journal of Plant Physiology</i> , 2006, 18, 95-108.	0.5	112
15	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	2.8	109
16	Discovery and profiling of bovine microRNAs from immune-related and embryonic tissues. <i>Physiological Genomics</i> , 2007, 29, 35-43.	2.3	104
17	MicroRNA transcriptome profiles during swine skeletal muscle development. <i>BMC Genomics</i> , 2009, 10, 77.	2.8	100
18	Complete Genome Sequence of <i>Sporisorium scitamineum</i> and Biotrophic Interaction Transcriptome with Sugarcane. <i>PLoS ONE</i> , 2015, 10, e0129318.	2.5	93

#	ARTICLE	IF	CITATIONS
19	Identification of genomic regions associated with feed efficiency in Nelore cattle. BMC Genetics, 2014, 15, 100.	2.7	87
20	De novo transcriptome analysis of Hevea brasiliensis tissues by RNA-seq and screening for molecular markers. BMC Genomics, 2014, 15, 236.	2.8	82
21	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
22	AP-1/jun binding sites mediate serum inducibility of the human vimentin promoter. Nucleic Acids Research, 1989, 17, 1619-1633.	14.5	79
23	Heat shock and structural proteins associated with meat tenderness in Nelore beef cattle, a Bos indicus breed. Meat Science, 2014, 96, 1318-1324.	5.5	79
24	Genome-wide association analysis of feed intake and residual feed intake in Nelore cattle. BMC Genetics, 2014, 15, 21.	2.7	78
25	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
26	Mapping QTLs on chicken chromosome 1 for performance and carcass traits in a broiler x layer cross. Animal Genetics, 2006, 37, 95-100.	1.7	74
27	Connectivity maintain mammal assemblages functional diversity within agricultural and fragmented landscapes. European Journal of Wildlife Research, 2016, 62, 431-446.	1.4	67
28	Comparative transcriptome analysis of early somatic embryo formation and seed development in Brazilian pine, Araucaria angustifolia (Bertol.) Kuntze. Plant Cell, Tissue and Organ Culture, 2015, 120, 903-915.	2.3	59
29	Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle. PLoS ONE, 2016, 11, e0157711.	2.5	59
30	Carcass and meat quality traits of chickens fed diets concurrently supplemented with vitamins C and E under constant heat stress. Animal, 2016, 10, 163-171.	3.3	58
31	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. Scientific Reports, 2016, 6, 39493.	3.3	57
32	High-throughput and Cost-effective Chicken Genotyping Using Next-Generation Sequencing. Scientific Reports, 2016, 6, 26929.	3.3	55
33	Candidate gene analysis of GH1 for effects on growth and carcass composition of cattle. Animal Genetics, 1998, 29, 194-201.	1.7	55
34	Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. BMC Genomics, 2016, 17, 961.	2.8	54
35	Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nelore Cattle. Frontiers in Genetics, 2018, 9, 441.	2.3	54
36	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

#	ARTICLE	IF	CITATIONS
37	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. <i>BMC Genomics</i> , 2018, 19, 126.	2.8	53
38	Genome wide scan for quantitative trait loci affecting tick resistance in cattle ( <i>Bos taurus</i> × <i>Bos Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i> )	2.8	51
39	Comparative muscle transcriptome associated with carcass traits of Nelore cattle. <i>BMC Genomics</i> , 2017, 18, 506.	2.8	51
40	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018, 19, 499.	2.8	51
41	Gene expression profile of intramuscular muscle in Nelore cattle with extreme values of fatty acid. <i>BMC Genomics</i> , 2016, 17, 972.	2.8	49
42	Integrative transcriptome analysis identifies deregulated microRNA-transcription factor networks in lung adenocarcinoma. <i>Oncotarget</i> , 2016, 7, 28920-28934.	1.8	49
43	Candidate genes for growth traits in beef cattle crosses <i>Bos taurus</i> × <i>Bos indicus</i> . <i>Journal of Animal Breeding and Genetics</i> , 2003, 120, 51-56.	2.0	48
44	Quantitative trait loci associated with fatness in a broiler × layer cross. <i>Animal Genetics</i> , 2009, 40, 729-736.	1.7	48
45	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
46	Quantitative trait loci for performance traits in a broiler × layer cross. <i>Animal Genetics</i> , 2009, 40, 200-208.	1.7	46
47	DNA methylation profiles in red blood cells of adult hens correlate to their rearing conditions. <i>Journal of Experimental Biology</i> , 2017, 220, 3579-3587.	1.7	46
48	Whole transcriptome analysis of the pectoralis major muscle reveals molecular mechanisms involved with white striping in broiler chickens. <i>Poultry Science</i> , 2019, 98, 590-601.	3.4	46
49	Mapping of quantitative trait loci controlling tick [ <i>Rhipicephalus</i> ( <i>Boophilus</i> ) <i>microplus</i> ] resistance on bovine chromosomes 5, 7 and 14. <i>Animal Genetics</i> , 2007, 38, 453-459.	1.7	44
50	MicroRNA expression profiles discriminate childhood <i>from</i> <i>acute</i> lymphoblastic leukemia. <i>Hematological Oncology</i> , 2019, 37, 103-112.	1.7	44
51	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. <i>Genetics Selection Evolution</i> , 2015, 47, 15.	3.0	40
52	The Receptive Endometrial Transcriptomic Signature Indicates an Earlier Shift from Proliferation to Metabolism at Early Diestrus in the Cow1. <i>Biology of Reproduction</i> , 2015, 93, 52.	2.7	40
53	QTL affecting body weight in a candidate region of cattle chromosome 5. <i>Genetics and Molecular Biology</i> , 2003, 26, 259-265.	1.3	39
54	Associations of myostatin gene polymorphisms with performance and mortality traits in broiler chickens. <i>Genetics Selection Evolution</i> , 2007, 39, 73-89.	3.0	39

#	ARTICLE	IF	CITATIONS
55	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.	2.8	39
56	Casein, lactoglobulin and growth hormone allele frequencies and genetic distances in Nelore, Gyr, Guzera, Caracu, Charolais, Canchim and Santa Gertrudis cattle. <i>Genetics and Molecular Biology</i> , 1999, 22, 539-541.	1.3	39
57	Evaluation of Monocot and Eudicot Divergence Using the Sugarcane Transcriptome. <i>Plant Physiology</i> , 2004, 134, 951-959.	4.8	38
58	Genetic parameters for milk fatty acids, milk yield and quality traits of a Holstein cattle population reared under tropical conditions. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 384-395.	2.0	38
59	Appetite regulating factors in pacu ( <i>Piaractus mesopotamicus</i> ): Tissue distribution and effects of food quantity and quality on gene expression. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2017, 203, 241-254.	1.8	38
60	Field study on nematode resistance in Nelore-breed cattle. <i>Veterinary Parasitology</i> , 2007, 148, 272-278.	1.8	37
61	Delayed somite formation in a quail line exhibiting myofiber hyperplasia is accompanied by delayed expression of myogenic regulatory factors and myosin heavy chain. <i>Development (Cambridge)</i> , 1993, 117, 563-569.	2.5	36
62	Microgeographic variation in <i>Caiman latirostris</i> . <i>The Journal of Experimental Zoology</i> , 2002, 294, 387-396.	1.4	35
63	The Transcriptome Signature of the Receptive Bovine Uterus Determined at Early Gestation. <i>PLoS ONE</i> , 2015, 10, e0122874.	2.5	35
64	A genomewide association mapping study using ultrasound-scanned information identifies potential genomic regions and candidate genes affecting carcass traits in Nelore cattle. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 420-427.	2.0	34
65	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.	2.8	34
66	Genetic characterization of Aberdeen Angus cattle using molecular markers. <i>Genetics and Molecular Biology</i> , 2003, 26, 133-137.	1.3	33
67	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2012–30 November 2012. <i>Molecular Ecology Resources</i> , 2013, 13, 341-343.	4.8	33
68	Genome-wide association study for performance traits in chickens using genotype by sequencing approach. <i>Scientific Reports</i> , 2017, 7, 41748.	3.3	33
69	The <i>Bos taurus</i> – <i>Bos indicus</i> balance in fertility and milk related genes. <i>PLoS ONE</i> , 2017, 12, e0181930.	2.5	33
70	Association of IGF1 and KDM5A polymorphisms with performance, fatness and carcass traits in chickens. <i>Journal of Applied Genetics</i> , 2013, 54, 103-112.	1.9	32
71	Large-scale SNP discovery and construction of a high-density genetic map of <i>Colossoma macropomum</i> through genotyping-by-sequencing. <i>Scientific Reports</i> , 2017, 7, 46112.	3.3	32
72	Cytokine gene expression in response to <i>Haemonchus placei</i> infections in Nelore cattle. <i>Veterinary Parasitology</i> , 2010, 171, 68-73.	1.8	31

#	ARTICLE	IF	CITATIONS
73	Genomic structure and marker-derived gene networks for growth and meat quality traits of Brazilian Nelore beef cattle. <i>BMC Genomics</i> , 2016, 17, 235.	2.8	31
74	Relationship of runs of homozygosity with adaptive and production traits in a paternal broiler line. <i>Animal</i> , 2018, 12, 1126-1134.	3.3	31
75	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.	2.8	31
76	Candidate gene analysis of GH1 for effects on growth and carcass composition of cattle. <i>Animal Genetics</i> , 1998, 29, 194-201.	1.7	31
77	Mutation dynamics of CpG dinucleotides during a recent event of vertebrate diversification. <i>Epigenetics</i> , 2019, 14, 685-707.	2.7	30
78	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
79	Immunological responses and cytokine gene expression analysis to <i>Cooperia punctata</i> infections in resistant and susceptible Nelore cattle. <i>Veterinary Parasitology</i> , 2008, 155, 95-103.	1.8	29
80	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple <i>Bos taurus</i> and <i>Bos indicus</i> breeds. <i>Frontiers in Genetics</i> , 2013, 4, 176.	2.3	29
81	Size of the Ovulatory Follicle Dictates Spatial Differences in the Oviductal Transcriptome in Cattle. <i>PLoS ONE</i> , 2015, 10, e0145321.	2.5	29
82	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
83	Variant discovery in a QTL region on chromosome 3 associated with fatness in chickens. <i>Animal Genetics</i> , 2015, 46, 141-147.	1.7	28
84	Linkage disequilibrium in Brazilian Santa In�s breed, <i>Ovis aries</i> . <i>Scientific Reports</i> , 2018, 8, 8851.	3.3	28
85	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
86	Identification of selection signatures involved in performance traits in a paternal broiler line. <i>BMC Genomics</i> , 2019, 20, 449.	2.8	28
87	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0161160.	2.5	28
88	Microsatellite DNA library for <i>Caiman latirostris</i> . <i>The Journal of Experimental Zoology</i> , 2002, 294, 346-351.	1.4	27
89	Real-time Polymerase Chain Reaction Quantification of <i>Porphyromonas gingivalis</i> and <i>Tannerella forsythia</i> in Primary Endodontic Infections. <i>Journal of Endodontics</i> , 2009, 35, 1518-1524.	3.1	27
90	Response of resistant and susceptible Brazilian Somalis crossbreed sheep naturally infected by <i>Haemonchus contortus</i> . <i>Parasitology Research</i> , 2014, 113, 1155-1161.	1.6	27

#	ARTICLE	IF	CITATIONS
91	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
92	Principal components analysis applied to performance and carcass traits in the chicken. <i>Animal Research</i> , 2006, 55, 419-425.	0.6	26
93	Quantification of bovine cytokine gene expression using real-time RT-PCR methodology. <i>Genetics and Molecular Biology</i> , 2007, 30, 575-579.	1.3	26
94	Genotypic characterization of microsatellite markers in broiler and layer selected chicken lines and their reciprocal F1s. <i>Scientia Agricola</i> , 2009, 66, 150-158.	1.2	26
95	Dynamic remodeling of endometrial extracellular matrix regulates embryo receptivity in cattle. <i>Reproduction</i> , 2017, 153, 49-61.	2.6	25
96	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	3.3	25
97	Genome-wide association study for milk production traits in a Brazilian Holstein population. <i>Journal of Dairy Science</i> , 2019, 102, 5305-5314.	3.4	25
98	Genome-wide association study for feedlot average daily gain in Nelore cattle ( <i>Bos indicus</i> ). <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 210-216.	2.0	24
99	Effects of hybrid, kernel maturity, and storage period on the bacterial community in high-moisture and rehydrated corn grain silages. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126131.	2.8	24
100	The use of an alternative feed additive, containing benzoic acid, thymol, eugenol, and piperine, improved growth performance, nutrient and energy digestibility, and gut health in weaned piglets. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	24
101	Identification and association of polymorphisms in CAPN1 and CAPN3 candidate genes related to performance and meat quality traits in chickens. <i>Genetics and Molecular Research</i> , 2013, 12, 472-482.	0.2	23
102	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
103	Exploring the genetic architecture of feed efficiency traits in chickens. <i>Scientific Reports</i> , 2021, 11, 4622.	3.3	23
104	Genome-wide detection of CNVs and their association with performance traits in broilers. <i>BMC Genomics</i> , 2021, 22, 354.	2.8	23
105	Parentage testing and effect of misidentification on the estimation of breeding value in Gir cattle. <i>Genetics and Molecular Biology</i> , 2002, 25, 389-394.	1.3	23
106	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
107	PCR screening and allele frequency estimation of bovine leukocyte adhesion deficiency in Holstein and Gir cattle in Brazil. <i>Genetics and Molecular Biology</i> , 2000, 23, 831-834.	1.3	21
108	Efeito do genótipo halotano, da ractopamina e do sexo do animal na qualidade da carne suína. <i>Revista Brasileira De Zootecnia</i> , 2006, 35, 2027-2033.	0.8	21

#	ARTICLE	IF	CITATIONS
109	SNP and INDEL detection in a QTL region on chicken chromosome 2 associated with muscle deposition. <i>Animal Genetics</i> , 2015, 46, 158-163.	1.7	21
110	RNA-Seq transcriptome analysis shows anti-tumor actions of melatonin in a breast cancer xenograft model. <i>Scientific Reports</i> , 2019, 9, 966.	3.3	21
111	Early pregnancy-induced transcripts in peripheral blood immune cells in <i>Bos indicus</i> heifers. <i>Scientific Reports</i> , 2020, 10, 13733.	3.3	21
112	Distribution of bovine lymphocyte antigen (BoLA-DRB3) alleles in Brazilian dairy Gir cattle ( <i>Bos indicus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.2	20
113	QTL for percentage of carcass and carcass parts in a broiler x layer cross. <i>Animal Genetics</i> , 2011, 42, 117-124.	1.7	20
114	On the Search for Markers of Tick Resistance in Bovines. <i>Developments in Biologicals</i> , 2008, 132, 225-230.	0.5	19
115	Expression of MyoD, myogenin, myostatin and Hsp70 transcripts in chicken embryos submitted to mild cold or heat. <i>Journal of Thermal Biology</i> , 2003, 28, 261-269.	2.5	18
116	Peanut genes identified during initial phase of <i>Cercosporidium personatum</i> infection. <i>Plant Science</i> , 2008, 174, 78-87.	3.6	18
117	A comprehensive manually-curated compendium of bovine transcription factors. <i>Scientific Reports</i> , 2018, 8, 13747.	3.3	18
118	Network analysis uncovers putative genes affecting resistance to tick infestation in Braford cattle skin. <i>BMC Genomics</i> , 2019, 20, 998.	2.8	18
119	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
120	Macrogeographic genetic variation in broad-snouted caiman ( <i>Caiman latirostris</i> ). <i>Journal of Experimental Zoology</i> , 2008, 309A, 628-636.	1.2	17
121	CNVranger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020, 36, 972-973.	4.1	17
122	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
123	Genotyping BoLA-DRB3 alleles in Brazilian Dairy Gir cattle ( <i>Bos indicus</i> ) by temperature-gradient gel electrophoresis (TGGE) and direct sequencing. <i>International Journal of Immunogenetics</i> , 2004, 31, 31-35.	1.2	16
124	Cross-species microsatellite amplification in South American Caimans ( <i>Caiman</i> spp and <i>Paleosuchus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.3	16
125	Genome-wide association study reveals genes associated with the absence of intermuscular bones in tambaqui ( <i>Colossoma macropomum</i> ). <i>Animal Genetics</i> , 2020, 51, 899-909.	1.7	16
126	Putative Epigenetic Biomarkers of Stress in Red Blood Cells of Chickens Reared Across Different Biomes. <i>Frontiers in Genetics</i> , 2020, 11, 508809.	2.3	16



#	ARTICLE	IF	CITATIONS
127	Selection for breed-specific growth hormone and IGF-I alleles in a synthetic beef cattle cross, Canchim. <i>Genetics and Molecular Biology</i> , 1999, 22, 531-537.	1.3	15
128	Heat and chemical stress modulate the expression of the $\beta$ -RZR gene in broiler chickens. <i>Genetics and Molecular Research</i> , 2010, 9, 1258-1266.	0.2	15
129	A genome-wide scan for selection signatures in Nelore cattle. <i>Animal Genetics</i> , 2014, 45, 771-781.	1.7	15
130	Identification of polymorphisms associated with production traits on chicken ( <i>Gallus gallus</i> ) chromosome 4. <i>Genetics and Molecular Research</i> , 2015, 14, 10717-10728.	0.2	15
131	Research Article Genomic regions and genes associated with carcass quality in Nelore cattle. <i>Genetics and Molecular Research</i> , 2019, 18, .	0.2	15
132	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
133	Whole mount in situ detection of low abundance transcripts of the myogenic factor qmf1 and myosin heavy chain protein in quail embryos. <i>BioTechniques</i> , 1992, 13, 722-4.	1.8	15
134	Land use and roles of soil bacterial community in the dissipation of atrazine. <i>Science of the Total Environment</i> , 2022, 827, 154239.	8.0	15
135	Caracterizaço molecular de animais da raa Nelore utilizando microssatlites e genes candidatos. <i>Revista Brasileira De Zootecnia</i> , 2000, 29, 1044-1049.	0.8	14
136	Quantitative trait loci associated with chemical composition of the chicken carcass. <i>Animal Genetics</i> , 2012, 43, 570-576.	1.7	14
137	Identification of <i>KCNJ11</i> as a functional candidate gene for bovine meat tenderness. <i>Physiological Genomics</i> , 2013, 45, 1215-1221.	2.3	14
138	Evaluation of reference genes for real-time PCR studies of Brazilian Somalis sheep infected by gastrointestinal nematodes. <i>Genetics and Molecular Biology</i> , 2010, 33, 486-490.	1.3	13
139	Impact of hormonal modulation at proestrus on ovarian responses and uterine gene expression of suckled anestrus beef cows. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 79.	5.3	13
140	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
141	Parentage test in broad-snouted caimans ( <i>Caiman latirostris</i> , <i>Crocodylidae</i> ) using microsatellite DNA. <i>Genetics and Molecular Biology</i> , 2009, 32, 874-881.	1.3	12
142	Impact of exposure time to harsh environments on physiology, mortality, and thermal comfort of day-old chickens in a simulated condition of transport. <i>International Journal of Biometeorology</i> , 2019, 63, 777-785.	3.0	12
143	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. <i>Genes</i> , 2021, 12, 67.	2.4	12
144	Stool and Ruminant Microbiome Components Associated With Methane Emission and Feed Efficiency in Nelore Beef Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	12

#	ARTICLE	IF	CITATIONS
145	Quantitative characterization of beta-adrenergic receptor subtypes in porcine adipocytes. <i>Comparative Biochemistry and Physiology Part C: Comparative Pharmacology</i> , 1992, 101, 481-485.	0.2	11
146	Genetic linkage map of chicken chromosome 1 from a Brazilian resource population. <i>Scientia Agricola</i> , 2005, 62, 12-17.	1.2	11
147	mRNA profile of Nelore calves after primary infection with <i>Haemonchus placei</i> . <i>Veterinary Parasitology</i> , 2011, 176, 195-200.	1.8	11
148	Polymorphisms in <i>FGFBP1</i> and <i>FGFBP2</i> genes associated with carcass and meat quality traits in chickens. <i>Genetics and Molecular Research</i> , 2013, 12, 208-222.	0.2	11
149	Single nucleotide polymorphisms in the growth hormone and IGF type-1 ( <i>IGF1</i> ) genes associated with carcass traits in Santa Ines sheep. <i>Animal</i> , 2019, 13, 460-468.	3.3	11
150	Immune status, well-being and gut microbiota in military supplemented with synbiotic ice cream and submitted to field training: a randomised clinical trial. <i>British Journal of Nutrition</i> , 2021, 126, 1794-1808.	2.3	11
151	Associations Between Microsatellite Markers and Traits Related to Performance, Carcass and Organs in Chickens. <i>International Journal of Poultry Science</i> , 2009, 8, 615-620.	0.1	11
152	Genetic effects of heat stress on milk fatty acids in Brazilian Holstein cattle. <i>Journal of Dairy Science</i> , 2022, 105, 3296-3305.	3.4	11
153	Identification and characterization of microRNAs expressed in chicken skeletal muscle. <i>Genetics and Molecular Research</i> , 2014, 13, 1465-1479.	0.2	10
154	Short Communication Genome-wide association with residual body weight gain in <i>Bos indicus</i> cattle. <i>Genetics and Molecular Research</i> , 2015, 14, 5229-5233.	0.2	10
155	Low-intensity resistance training with partial blood flow restriction and high-intensity resistance training induce similar changes in skeletal muscle transcriptome in elderly humans. <i>Applied Physiology, Nutrition and Metabolism</i> , 2019, 44, 216-220.	1.9	10
156	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
157	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
158	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
159	EST analysis of mRNAs expressed during embryogenesis in <i>Gallus gallus</i> . <i>International Journal of Developmental Biology</i> , 2004, 48, 333-337.	0.6	10
160	Genetic linkage maps of chicken chromosomes 6, 7, 8, 11 and 13 from a Brazilian resource population. <i>Scientia Agricola</i> , 2008, 65, 447-452.	1.2	10
161	Influence of the neural tube/notochord complex on MyoD expression and cellular proliferation in chicken embryos. <i>Brazilian Journal of Medical and Biological Research</i> , 2003, 36, 191-197.	1.5	9
162	<i>RGMA</i> and <i>RGMB</i> expression pattern during chicken development suggest unexpected roles for these repulsive guidance molecules in notochord formation, somitogenesis, and myogenesis. <i>Developmental Dynamics</i> , 2012, 241, 1886-1900.	1.8	9

#	ARTICLE	IF	CITATIONS
163	Genetic variants in glucocorticoid and mineralocorticoid receptors are associated with concentrations of plasma cortisol, muscle glycogen content, and meat quality traits in male Nelore cattle. <i>Domestic Animal Endocrinology</i> , 2015, 51, 105-113.	1.6	9
164	DNA methylation in canine brains is related to domestication and dog-breed formation. <i>PLoS ONE</i> , 2020, 15, e0240787.	2.5	9
165	CNV detection and their association with growth, efficiency and carcass traits in Santa In�as sheep. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 476-487.	2.0	9
166	Investigation of Leptin gene in broiler and layer chicken lines. <i>Scientia Agricola</i> , 2008, 65, 214-219.	1.2	8
167	Variation in <i>myogenin</i> mRNA abundance is associated with beef tenderness in Nelore cattle. <i>Animal Genetics</i> , 2016, 47, 491-494.	1.7	8
168	Oviductal transcriptional profiling of a bovine fertility model by next-generation sequencing. <i>Genomics Data</i> , 2017, 13, 27-29.	1.3	8
169	Comparative untargeted metabolome analysis of ruminal fluid and feces of Nelore steers (Bos Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.3	8
170	Liquid Biopsy as a Diagnostic and Prognostic Tool for Women and Female Dogs with Breast Cancer. <i>Cancers</i> , 2021, 13, 5233.	3.7	8
171	Delayed somite formation in a quail line exhibiting myofiber hyperplasia is accompanied by delayed expression of myogenic regulatory factors and myosin heavy chain. <i>Development (Cambridge)</i> , 1993, 117, 563-9.	2.5	8
172	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
173	Strategic marker selection to detect quantitative trait loci in chicken. <i>Scientia Agricola</i> , 2005, 62, 111-116.	1.2	7
174	Leptin and hypothalamic gene expression in early- and late-maturing <i>Bos indicus</i> Nelore heifers. <i>Genetics and Molecular Biology</i> , 2008, 31, 657-664.	1.3	7
175	Gene expression profile suggesting immunological dysregulation in two Brazilian Bloom's syndrome cases. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2020, 8, e1133.	1.2	7
176	Does algae $\beta$ -glucan affect the fecal bacteriome in dairy calves?. <i>PLoS ONE</i> , 2021, 16, e0258069.	2.5	7
177	Single Loci and Haplotypes in <i>CAPN1</i> and <i>CAST</i> Genes are Associated with Growth, Biometrics, and <i>in Vivo</i> Carcass Traits in Santa In�as Sheep. <i>Annals of Animal Science</i> , 2020, 20, 465-483.	1.6	7
178	Molecular cloning of $\beta$ -RZR hotspot region 1 from broiler chicken. <i>Brazilian Archives of Biology and Technology</i> , 2009, 52, 225-231.	0.5	6
179	Gene expression of beta-adrenergic receptors and myosin heavy chain isoforms induced by ractopamine feeding duration in pigs not carrying the ryanodine receptor mutation. <i>Livestock Science</i> , 2015, 172, 91-95.	1.6	6
180	Genetic parameters for growth characteristics of free-range chickens under univariate random regression models. <i>Poultry Science</i> , 2016, 95, 1989-1998.	3.4	6

#	ARTICLE	IF	CITATIONS
181	Quantitative trait loci with sex-specific effects for internal organs weights and hematocrit value in a broiler-layer cross. <i>Journal of Applied Genetics</i> , 2016, 57, 215-224.	1.9	6
182	Genome-Enabled Prediction of Breeding Values for Feedlot Average Daily Weight Gain in Nelore Cattle. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1855-1859.	1.8	6
183	Next-Generation Sequencing of the Complete Mitochondrial Genome of the Endangered Species Black Lion Tamarin <i>Leontopithecus chrysopygus</i> (Primates) and Mitogenomic Phylogeny Focusing on the Callitrichidae Family. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1985-1991.	1.8	6
184	Data from proteomic analysis of bovine <i>Longissimus dorsi</i> muscle associated with intramuscular fat content. <i>Data in Brief</i> , 2018, 19, 1314-1317.	1.0	6
185	Variants in myostatin and MyoD family genes are associated with meat quality traits in Santa Inês sheep. <i>Animal Biotechnology</i> , 2022, 33, 201-213.	1.5	6
186	Sulfadiazine dissipation as a function of soil bacterial diversity. <i>Environmental Pollution</i> , 2021, 271, 116374.	7.5	6
187	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
188	Alpha-2 adrenergic receptor activity in porcine adipocytes is androgen and age/cell size dependent. <i>Comparative Biochemistry and Physiology A, Comparative Physiology</i> , 1993, 105, 333-339.	0.6	5
189	Standard-curve competitive RT-PCR quantification of myogenic regulatory factors in chicken embryos. <i>Brazilian Journal of Medical and Biological Research</i> , 2003, 36, 1629-1641.	1.5	5
190	Characterization of open reading frame-expressed sequence tags generated from <i>Bos indicus</i> and <i>B. taurus</i> mammary gland cDNA libraries. <i>Animal Genetics</i> , 2004, 35, 213-219.	1.7	5
191	Identification of genomic regions related to tenderness in Nelore beef cattle. <i>Advances in Animal Biosciences</i> , 2017, 8, s42-s44.	1.0	5
192	Investigation of mechanisms involved in regulation of progesterone catabolism using an overfed versus underfed ewe lamb model. <i>Journal of Animal Science</i> , 2017, 95, 5537-5546.	0.5	5
193	Genotypic and allelic frequencies of gene polymorphisms associated with meat tenderness in Nelore beef cattle. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.2	5
194	Carcass and commercial cut yield of Santa Ines sheep affected by polymorphisms of the LEP gene. <i>Small Ruminant Research</i> , 2018, 166, 121-128.	1.2	5
195	Heat and chemical stress modulate the expression of the $\beta$ -Ryr gene in broiler chickens. <i>Genetics and Molecular Research</i> , 2010, 9, 1258-1266.	0.2	5
196	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. <i>Animals</i> , 2022, 12, 1632.	2.3	5
197	A new member of the chalcone synthase (CHS) family in sugarcane. <i>Genetics and Molecular Biology</i> , 2001, 24, 257-261.	1.3	4
198	Molecular evolution of ribosomal intergenic spacers in <i>Odontophrynus americanus</i> and <i>4n</i> (Amphibia: Anura). <i>Genome</i> , 2002, 45, 71-81.	2.0	4

#	ARTICLE	IF	CITATIONS
199	Quantitative trait locus affecting birth weight on bovine chromosome 5 in a F2 Gyr x Holstein population. <i>Genetics and Molecular Biology</i> , 2005, 28, 670-676.	1.3	4
200	Molecular marker heterozygosities and genetic distances as correlates of production traits in F1 bovine crosses. <i>Genetics and Molecular Biology</i> , 2005, 28, 218-224.	1.3	4
201	Mapping quantitative trait loci in <i>Gallus gallus</i> using principal components. <i>Revista Brasileira De Zootecnia</i> , 2010, 39, 2434-2441.	0.8	4
202	Repulsive Guidance Molecules a, b and c Are Skeletal Muscle Proteins, and Repulsive Guidance Molecule a Promotes Cellular Hypertrophy and Is Necessary for Myotube Fusion. <i>Cells Tissues Organs</i> , 2014, 200, 326-338.	2.3	4
203	Endometrial transcriptional profiling of a bovine fertility model by Next-Generation Sequencing. <i>Genomics Data</i> , 2016, 7, 26-28.	1.3	4
204	0340 Differentially expressed miRNAs in skeletal muscle related to feed efficiency in Nelore cattle. <i>Journal of Animal Science</i> , 2016, 94, 163-164.	0.5	4
205	Variants in GH, IGF1, and LEP genes associated with body traits in Santa Inês sheep. <i>Scientia Agricola</i> , 2021, 78, .	1.2	4
206	Genome-wide association for plasma urea concentration in sheep. <i>Livestock Science</i> , 2021, 248, 104483.	1.6	4
207	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
208	Differentially expressed genes in the femur cartilage transcriptome clarify the understanding of femoral head separation in chickens. <i>Scientific Reports</i> , 2021, 11, 17965.	3.3	4
209	Abundance of MyoD and myostatin transcripts in chicken embryos submitted to distinct incubation temperatures and timing exposures. <i>Brazilian Journal of Biology</i> , 2011, 71, 563-564.	0.9	4
210	Potential Association Between Microsatellite Markers on Chicken Chromosomes 6, 7 and 8 and Body Weight. <i>International Journal of Poultry Science</i> , 2009, 8, 696-699.	0.1	4
211	Precision of distances and ordering of microsatellite markers in consensus linkage maps of chromosomes 1, 3 and 4 from two reciprocal chicken populations using bootstrap sampling. <i>Genetics and Molecular Research</i> , 2010, 9, 1357-1376.	0.2	4
212	Efeito da ractopamina e do gÃnero no desempenho e na carcaÃsa de suÃnos de diferentes genÃtipos halotano. <i>Semina:Ciencias Agrarias</i> , 2008, 29, 713.	0.3	4
213	GBS-MeDIP: A protocol for parallel identification of genetic and epigenetic variation in the same reduced fraction of genomes across individuals. <i>STAR Protocols</i> , 2022, 3, 101202.	1.2	4
214	The 18S rRNA from <i>Odontophrynus americanus</i> 2n and 4n (Amphibia, Anura) reveals unusual extra sequences in the variable region V2. <i>Genome</i> , 2004, 47, 421-428.	2.0	3
215	Effect of growth hormone on fatty acid synthase gene expression in porcine adipose tissue cultures. <i>Genetics and Molecular Biology</i> , 2006, 29, 180-186.	1.3	3
216	Contributions and perspectives of chicken genomics in Brazil: from biological model to export commodity. <i>World's Poultry Science Journal</i> , 2007, 63, 597-610.	3.0	3

#	ARTICLE	IF	CITATIONS
217	Quantitative trait loci (QTL) mapping for growth traits on bovine chromosome 14. <i>Genetics and Molecular Biology</i> , 2007, 30, 364-369.	1.3	3
218	<i>Biotecnologia animal. Estudos Avancados</i> , 2010, 24, 123-147.	0.5	3
219	Whole-genome analysis for backfat thickness in a tropically adapted, composite cattle breed from Brazil. <i>Animal Genetics</i> , 2012, 43, 518-524.	1.7	3
220	Evaluation of imputation accuracy using the combination of two high-density panels in Nelore beef cattle. <i>Scientific Reports</i> , 2019, 9, 17920.	3.3	3
221	Genome assembly and annotation of the tambaqui ( <i>Colossoma macropomum</i> ): an emblematic fish of the Amazon River Basin. <i>GigaByte</i> , 0, 2021, 1-14.	0.0	3
222	In situ detection of transcripts of the myogenic factor MyoD in whole chicken embryos. <i>Genetics and Molecular Biology</i> , 2000, 23, 145-148.	1.3	3
223	Genomic Signatures of Divergent Ecological Strategies in a Recent Radiation of Neotropical Wild Cats. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	3
224	Gene expression profiling by high throughput sequencing to determine signatures for the bovine receptive uterus at early gestation. <i>Genomics Data</i> , 2015, 5, 94-96.	1.3	2
225	Allele- and parent-of-origin-specific effects on expression of the KCNJ11 gene: A candidate for meat tenderness in cattle. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	2
226	EDA mutation by exome sequencing in non-syndromic X-linked oligodontia. <i>Clinical Genetics</i> , 2017, 92, 227-229.	2.0	2
227	Assessing the accuracy of prediction for milk fatty acids by using a small reference population of tropical Holstein cows. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 453-463.	2.0	2
228	Quantitative trait loci for morphometric and mineral composition traits of the tibia bone in a broiler A-layer cross. <i>Animal</i> , 2019, 13, 1563-1569.	3.3	2
229	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
230	Ruminal and Fecal Bacteriome of Dairy Calves Fed Different Levels and Sources of NDF. <i>Animals</i> , 2021, 11, 2705.	2.3	2
231	Liquid biopsy can detect BRCA2 gene variants in female dogs with mammary neoplasia. <i>Veterinary and Comparative Oncology</i> , 2021, , .	1.8	2
232	Regiões genômicas associadas a características de desempenho e carcassa no cromossomo 5 de linhagens Brasileiras de galinha. <i>Pesquisa Agropecuária Brasileira</i> , 2011, 46, 229-238.	0.9	2
233	Polymorphisms in MyoD1, MyoG, Myf5, Myf6, and MSTN genes in Santa Inês sheep. <i>Pesquisa Agropecuária Brasileira</i> , 0, 54, .	0.9	2
234	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

#	ARTICLE	IF	CITATIONS
235	Transcriptomic characterization of the molecular mechanisms induced by RGMa during skeletal muscle nuclei accretion and hypertrophy. <i>BMC Genomics</i> , 2022, 23, 188.	2.8	2
236	In situ DNA transfer to chicken embryos by biolistics. <i>Genetics and Molecular Biology</i> , 1999, 22, 525-529.	1.3	1
237	Temporal expression pattern of myostatin transcripts during chicken embryogenesis. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2006, 58, 940-943.	0.4	1
238	Assignment <sup>1</sup> of the bovine <i>PTGFR</i> and <i>HSD3B1</i> genes to bovine chromosome 3 with somatic and radiation hybrid panel mapping. <i>Cytogenetic and Genome Research</i> , 2006, 114, 94E-94E.	1.1	1
239	Expression of 1alpha-HYD and 24-HYD in bovine kidney mediated by vitamin D3 supplementation. <i>Genetics and Molecular Research</i> , 2013, 12, 6611-6618.	0.2	1
240	Composite interval mapping and mixed models reveal QTL associated with performance and carcass traits on chicken chromosomes 1, 3, and 4. <i>Journal of Applied Genetics</i> , 2014, 55, 97-103.	1.9	1
241	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
242	0903 Differentially expressed genes in genetically divergent Nellore steers for calcium content in the Longissimus dorsi muscle. <i>Journal of Animal Science</i> , 2016, 94, 435-435.	0.5	1
243	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
244	KCNJ11 gene expression is associated to feed consumption and growth traits in Nelore beef cattle. <i>Agri Gene</i> , 2018, 9, 1-4.	1.9	1
245	Transcriptome changes in muscle of Nellore cows submitted to recovery weight gain under grazing condition. <i>Animal</i> , 2019, 13, 333-340.	3.3	1
246	SAP30 Gene Is a Probable Regulator of Muscle Hypertrophy in Chickens. <i>Frontiers in Genetics</i> , 2021, 12, 709937.	2.3	1
247	Identification of proliferating cells in chicken embryos using 5-bromo- 2'-deoxyuridine immunohistochemical detection. <i>Genetics and Molecular Biology</i> , 2000, 23, 149-153.	1.3	1
248	ESTs and putative line-specific (broiler and layer) SNPs identified in genes expressed in Gallus gallus pituitary and hypothalamus. <i>Genetics and Molecular Biology</i> , 2007, 30, 1077-1081.	1.3	1
249	Associations of myostatin gene polymorphisms with performance and mortality traits in broiler chickens. <i>Genetics Selection Evolution</i> , 2007, 39, 73-89.	3.0	1
250	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
251	EEF1A1 transcription cofactor gene polymorphism is associated with muscle gene expression and residual feed intake in Nelore cattle. <i>Mammalian Genome</i> , 2022, 33, 619-628.	2.2	1
252	A biolistic process for in vitro gene transfer into chicken embryos. <i>Brazilian Journal of Medical and Biological Research</i> , 2001, 34, 1115-1124.	1.5	0



#	ARTICLE	IF	CITATIONS
253	Assignment <sup>1</sup> of the subunit C of succinate dehydrogenase complex (SDHC) gene to bovine chromosome 2 with somatic and radiation hybrid panel mapping. <i>Cytogenetic and Genome Research</i> , 2006, 114, 93D-93D.	1.1	0
254	Temporal expression pattern of the insulin-like growth factor II and fibroblast growth factor transcripts in avian embryogenesis. <i>Brazilian Archives of Biology and Technology</i> , 2008, 51, 949-955.	0.5	0
255	03-P075 The repulsive guidance molecule (RGM) family in chicken. <i>Mechanisms of Development</i> , 2009, 126, S88-S89.	1.7	0
256	A single nucleotide polymorphism in NEUROD1 is associated with production traits in Nelore beef cattle. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	0
257	0339 Gene network regulated by microRNAs suggests modulation of fat deposition in cattle. <i>Journal of Animal Science</i> , 2016, 94, 163-163.	0.5	0
258	Genome-wide association for plasma albumin concentration in sheep. <i>Animal Genetics</i> , 2021, 52, 898-900.	1.7	0
259	Chicken skeletal muscle-associated macroarray for gene discovery. <i>Genetics and Molecular Research</i> , 2010, 9, 188-207.	0.2	0
260	Abstract 2751: Identification of predisposition genes involved in thyroid and breast carcinomas in patients with family history of these tumors by whole exome sequencing. , 2015, , .		0
261	Abstract P1-05-28: Melatonin treatment: A transcriptomic networks in a xenograft model of breast cancer. , 2017, , .		0
262	PSIX-1 Fecal microbiome of dairy calves fed with fresh or frozen maternal colostrum or colostrum powder. <i>Journal of Animal Science</i> , 2020, 98, 419-419.	0.5	0
263	PSIX-6 Gastrointestinal microbiome of calves fed solid diets containing different levels and sources of NDF. <i>Journal of Animal Science</i> , 2020, 98, 418-419.	0.5	0
264	PSVI-22 Fecal microbiome of dairy calves fed with different liquid diets. <i>Journal of Animal Science</i> , 2020, 98, 431-431.	0.5	0
265	Expression of calpain system transcripts responds inversely to beef tenderization after vitamin D3 supplementation in Nelore cattle. <i>Revista Brasileira De Saude E Producao Animal</i> , 0, 23, .	0.3	0