

Luiz Coutinho

List of Publications by Year in descending order

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265
papers

9,402
citations

57758

44
h-index

53230

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

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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 Nellore 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 Nellore 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 Nellore 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

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37	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. BMC Genomics, 2018, 19, 126.	2.8	53
38	Genome wide scan for quantitative trait loci affecting tick resistance in cattle (Bos taurus × Bos Tj ETQq0 0 0 rgBT/Overlook 10 Tf 50	2.8	51
39	Comparative muscle transcriptome associated with carcass traits of Nelore cattle. BMC Genomics, 2017, 18, 506.	2.8	51
40	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC Genomics, 2018, 19, 499.	2.8	51
41	Gene expression profile of intramuscular muscle in Nelore cattle with extreme values of fatty acid. BMC Genomics, 2016, 17, 972.	2.8	49
42	Integrative transcriptome analysis identifies deregulated microRNA-transcription factor networks in lung adenocarcinoma. Oncotarget, 2016, 7, 28920-28934.	1.8	49
43	Candidate genes for growth traits in beef cattle crosses Bos taurus x Bos indicus. Journal of Animal Breeding and Genetics, 2003, 120, 51-56.	2.0	48
44	Quantitative trait loci associated with fatness in a broiler × layer cross. Animal Genetics, 2009, 40, 729-736.	1.7	48
45	An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. Scientific Reports, 2018, 8, 17072.	3.3	47
46	Quantitative trait loci for performance traits in a broiler × layer cross. Animal Genetics, 2009, 40, 200-208.	1.7	46
47	DNA methylation profiles in red blood cells of adult hens correlate to their rearing conditions. Journal of Experimental Biology, 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. Poultry Science, 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. Animal Genetics, 2007, 38, 453-459.	1.7	44
50	MicroRNA expression profiles discriminate childhood T- from B-acute lymphoblastic leukemia. Hematological Oncology, 2019, 37, 103-112.	1.7	44
51	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. Genetics Selection Evolution, 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. Biology of Reproduction, 2015, 93, 52.	2.7	40
53	QTL affecting body weight in a candidate region of cattle chromosome 5. Genetics and Molecular Biology, 2003, 26, 259-265.	1.3	39
54	Associations of myostatin gene polymorphisms with performance and mortality traits in broiler chickens. Genetics Selection Evolution, 2007, 39, 73-89.	3.0	39

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55	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
56	Casein, κ -lactoglobulin and growth hormone allele frequencies and genetic distances in Nelore, Gyr, Guzzeri, Caracu, Charolais, Canchim and Santa Gertrudis cattle. Genetics and Molecular Biology, 1999, 22, 539-541.	1.3	39
57	Evaluation of Monocot and Eudicot Divergence Using the Sugarcane Transcriptome. Plant Physiology, 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. Journal of Animal Breeding and Genetics, 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. Comparative Biochemistry and Physiology Part A, Molecular & Integrative Physiology, 2017, 203, 241-254.	1.8	38
60	Field study on nematode resistance in Nelore-breed cattle. Veterinary Parasitology, 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. Development (Cambridge), 1993, 117, 563-569.	2.5	36
62	Microgeographic variation in <i>Caiman latirostris</i> . The Journal of Experimental Zoology, 2002, 294, 387-396.	1.4	35
63	The Transcriptome Signature of the Receptive Bovine Uterus Determined at Early Gestation. PLoS ONE, 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. Journal of Animal Breeding and Genetics, 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. BMC Genomics, 2019, 20, 32.	2.8	34
66	Genetic characterization of Aberdeen Angus cattle using molecular markers. Genetics and Molecular Biology, 2003, 26, 133-137.	1.3	33
67	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2012–30 November 2012. Molecular Ecology Resources, 2013, 13, 341-343.	4.8	33
68	Genome-wide association study for performance traits in chickens using genotype by sequencing approach. Scientific Reports, 2017, 7, 41748.	3.3	33
69	The <i>Bos taurus</i> – <i>Bos indicus</i> balance in fertility and milk related genes. PLoS ONE, 2017, 12, e0181930.	2.5	33
70	Association of IGF1 and KDM5A polymorphisms with performance, fatness and carcass traits in chickens. Journal of Applied Genetics, 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. Scientific Reports, 2017, 7, 46112.	3.3	32
72	Cytokine gene expression in response to <i>Haemonchus placei</i> infections in Nelore cattle. Veterinary Parasitology, 2010, 171, 68-73.	1.8	31

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73	Genomic structure and marker-derived gene networks for growth and meat quality traits of Brazilian Nelore beef cattle. BMC Genomics, 2016, 17, 235.	2.8	31
74	Relationship of runs of homozygosity with adaptive and production traits in a paternal broiler line. Animal, 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. BMC Genomics, 2018, 19, 375.	2.8	31
76	Candidate gene analysis of GH1 for effects on growth and carcass composition of cattle. Animal Genetics, 1998, 29, 194-201.	1.7	31
77	Mutation dynamics of CpG dinucleotides during a recent event of vertebrate diversification. Epigenetics, 2019, 14, 685-707.	2.7	30
78	MiRNAs differentially expressed in skeletal muscle of animals with divergent estimated breeding values for beef tenderness. BMC Molecular Biology, 2019, 20, 1.	3.0	30
79	Immunological responses and cytokine gene expression analysis to Cooperia punctata infections in resistant and susceptible Nelore cattle. Veterinary Parasitology, 2008, 155, 95-103.	1.8	29
80	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple Bos taurus and Bos indicus breeds. Frontiers in Genetics, 2013, 4, 176.	2.3	29
81	Size of the Ovulatory Follicle Dictates Spatial Differences in the Oviductal Transcriptome in Cattle. PLoS ONE, 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. Scientific Reports, 2018, 8, 16222.	3.3	29
83	Variant discovery in a QTL region on chromosome 3 associated with fatness in chickens. Animal Genetics, 2015, 46, 141-147.	1.7	28
84	Linkage disequilibrium in Brazilian Santa In�s breed, Ovis aries. Scientific Reports, 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. BMC Genomics, 2018, 19, 374.	2.8	28
86	Identification of selection signatures involved in performance traits in a paternal broiler line. BMC Genomics, 2019, 20, 449.	2.8	28
87	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. PLoS ONE, 2016, 11, e0161160.	2.5	28
88	Microsatellite DNA library for Caiman latirostris. The Journal of Experimental Zoology, 2002, 294, 346-351.	1.4	27
89	Real-time Polymerase Chain Reaction Quantification of Porphyromonas gingivalis and Tannerella forsythia in Primary Endodontic Infections. Journal of Endodontics, 2009, 35, 1518-1524.	3.1	27
90	Response of resistant and susceptible Brazilian Somalis crossbreed sheep naturally infected by Haemonchus contortus. Parasitology Research, 2014, 113, 1155-1161.	1.6	27

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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 Nellore 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

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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 T	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

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127	Selection for breed-specific growth hormone and IGF-I alleles in a synthetic beef cattle cross, Canchim. Genetics and Molecular Biology, 1999, 22, 531-537.	1.3	15
128	Heat and chemical stress modulate the expression of the β -Ryr gene in broiler chickens. Genetics and Molecular Research, 2010, 9, 1258-1266.	0.2	15
129	A genome-wide scan for selection signatures in Nelore cattle. Animal Genetics, 2014, 45, 771-781.	1.7	15
130	Identification of polymorphisms associated with production traits on chicken (Gallus gallus) chromosome 4. Genetics and Molecular Research, 2015, 14, 10717-10728.	0.2	15
131	Research Article Genomic regions and genes associated with carcass quality in Nelore cattle. Genetics and Molecular Research, 2019, 18, .	0.2	15
132	Muscle transcriptome analysis reveals genes and metabolic pathways related to mineral concentration in Bos indicus. Scientific Reports, 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. BioTechniques, 1992, 13, 722-4.	1.8	15
134	Land use and roles of soil bacterial community in the dissipation of atrazine. Science of the Total Environment, 2022, 827, 154239.	8.0	15
135	Caracteriza��o molecular de animais da ra��a Nelore utilizando microssat��lites e genes candidatos. Revista Brasileira De Zootecnia, 2000, 29, 1044-1049.	0.8	14
136	Quantitative trait loci associated with chemical composition of the chicken carcass. Animal Genetics, 2012, 43, 570-576.	1.7	14
137	Identification of <i>KCNJ11</i> as a functional candidate gene for bovine meat tenderness. Physiological Genomics, 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. Genetics and Molecular Biology, 2010, 33, 486-490.	1.3	13
139	Impact of hormonal modulation at proestrus on ovarian responses and uterine gene expression of suckled anestrous beef cows. Journal of Animal Science and Biotechnology, 2017, 8, 79.	5.3	13
140	Allele-specific expression is widespread in Bos indicus muscle and affects meat quality candidate genes. Scientific Reports, 2020, 10, 10204.	3.3	13
141	Parentage test in broad-snouted caimans (Caiman latirostris, Crocodylidae) using microsatellite DNA. Genetics and Molecular Biology, 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. International Journal of Biometeorology, 2019, 63, 777-785.	3.0	12
143	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. Genes, 2021, 12, 67.	2.4	12
144	Stool and Ruminant Microbiome Components Associated With Methane Emission and Feed Efficiency in Nelore Beef Cattle. Frontiers in Genetics, 2022, 13, .	2.3	12

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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 Nellore calves after primary infection with <i>Haemonchus placei</i> . <i>Veterinary Parasitology</i> , 2011, 176, 195-200.	1.8	11
148	Polymorphisms in FGFBP1 and FGFBP2 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 (IGF1) 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

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163	Genetic variants in glucocorticoid and mineralocorticoid receptors are associated with concentrations of plasma cortisol, muscle glycogen content, and meat quality traits in male Nellore cattle. Domestic Animal Endocrinology, 2015, 51, 105-113.	1.6	9
164	DNA methylation in canine brains is related to domestication and dog-breed formation. PLoS ONE, 2020, 15, e0240787.	2.5	9
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