Luiz Coutinho

List of Publications by Year
in descending order

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264 papers	9,402 citations	66250 44 h-index	60403 85 g-index
275 all docs	275 docs citations	275 times ranked	10026 citing authors

#	Article	IF	Citations
1	Variants in myostatin and MyoD family genes are associated with meat quality traits in Santa InÃªs sheep. Animal Biotechnology, 2022, 33, 201-213.	0.7	6
2	Genetic effects of heat stress on milk fatty acids in Brazilian Holstein cattle. Journal of Dairy Science, 2022, 105, 3296-3305.	1.4	11
3	CNV detection and their association with growth, efficiency and carcass traits in Santa InÃªs sheep. Journal of Animal Breeding and Genetics, 2022, 139, 476-487.	0.8	9
4	GBS-MeDIP: A protocol for parallel identification of genetic and epigenetic variation in the same reduced fraction of genomes across individuals. STAR Protocols, 2022, 3, 101202.	0.5	4
5	Transcriptomic characterization of the molecular mechanisms induced by RGMa during skeletal muscle nuclei accretion and hypertrophy. BMC Genomics, 2022, 23, 188.	1.2	2
6	Land use and roles of soil bacterial community in the dissipation of atrazine. Science of the Total Environment, 2022, 827, 154239.	3.9	15
7	DNA methylation may affect beef tenderness through signal transduction in Bos indicus. Epigenetics and Chromatin, 2022, 15, 15.	1.8	6
8	Stool and Ruminal Microbiome Components Associated With Methane Emission and Feed Efficiency in Nelore Beef Cattle. Frontiers in Genetics, 2022, 13, .	1.1	12
9	Genomic Signatures of Divergent Ecological Strategies in a Recent Radiation of Neotropical Wild Cats. Molecular Biology and Evolution, 2022, 39, .	3.5	3
10	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. Animals, 2022, 12, 1632.	1.0	5
11	Effect of dietary soybean oil inclusion on liver-related transcription factors in a pig model for metabolic diseases. Scientific Reports, 2022, 12, .	1.6	8
12	Prune homolog 2 with BCH domain (PRUNE2) gene expression is associated with feed efficiency-related traits in Nelore steers. Mammalian Genome, 2022, 33, 629-641.	1.0	1
13	EEF1A1 transcription cofactor gene polymorphism is associated with muscle gene expression and residual feed intake in Nelore cattle. Mammalian Genome, 2022, 33, 619-628.	1.0	1
14	Variants in GH, IGF1, and LEP genes associated with body traits in Santa InÃªs sheep. Scientia Agricola, 2021, 78, .	0.6	4
15	Sulfadiazine dissipation as a function of soil bacterial diversity. Environmental Pollution, 2021, 271, 116374.	3.7	6
16	Exploring the genetic architecture of feed efficiency traits in chickens. Scientific Reports, 2021, 11, 4622.	1.6	23
17	Immune status, well-being and gut microbiota in military supplemented with synbiotic ice cream and submitted to field training: a randomised clinical trial. British Journal of Nutrition, 2021, 126, 1794-1808.	1.2	11
18	Muscle allele-specific expression QTLs may affect meat quality traits in Bos indicus. Scientific Reports, 2021, 11, 7321.	1.6	10

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19	Genome-wide detection of CNVs and their association with performance traits in broilers. BMC Genomics, 2021, 22, 354.	1.2	23
20	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. Livestock Science, 2021, 248, 104515.	0.6	18
21	Genome-wide association for plasma urea concentration in sheep. Livestock Science, 2021, 248, 104483.	0.6	4
22	Comparative untargeted metabolome analysis of ruminal fluid and feces of Nelore steers (Bos) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	1.6	8
23	A Missense Mutation in the MYBPH Gene Is Associated With Abdominal Fat Traits in Meat-Type Chickens. Frontiers in Genetics, 2021, 12, 698163.	1.1	4
24	Differentially expressed genes in the femur cartilage transcriptome clarify the understanding of femoral head separation in chickens. Scientific Reports, 2021, 11, 17965.	1.6	4
25	Ruminal and Fecal Bacteriome of Dairy Calves Fed Different Levels and Sources of NDF. Animals, 2021, 11, 2705.	1.0	2
26	Liquid biopsy can detect BRCA2 gene variants in female dogs with mammary neoplasia. Veterinary and Comparative Oncology, 2021, , .	0.8	2
27	SAP30 Gene Is a Probable Regulator of Muscle Hypertrophy in Chickens. Frontiers in Genetics, 2021, 12, 709937.	1.1	1
28	Does algae Î²-glucan affect the fecal bacteriome in dairy calves?. PLoS ONE, 2021, 16, e0258069.	1.1	7
29	Genomeâ€wide association for plasma albumin concentration in sheep. Animal Genetics, 2021, 52, 898-900.	0.6	0
30	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. Genes, 2021, 12, 67.	1.0	12
31	Liquid Biopsy as a Diagnostic and Prognostic Tool for Women and Female Dogs with Breast Cancer. Cancers, 2021, 13, 5233.	1.7	8
32	CNVRanger: association analysis of CNVs with gene expression and quantitative phenotypes. Bioinformatics, 2020, 36, 972-973.	1.8	17
33	Genomeâ€wide association study reveals genes associated with the absence of intermuscular bones in tambaqui (Colossoma macropomum). Animal Genetics, 2020, 51, 899-909.	0.6	16
34	Effects of hybrid, kernel maturity, and storage period on the bacterial community in high-moisture and rehydrated corn grain silages. Systematic and Applied Microbiology, 2020, 43, 126131.	1.2	24
35	Putative Epigenetic Biomarkers of Stress in Red Blood Cells of Chickens Reared Across Different Biomes. Frontiers in Genetics, 2020, 11, 508809.	1.1	16
36	Early pregnancy-induced transcripts in peripheral blood immune cells in Bos indicus heifers. Scientific Reports, 2020, 10, 13733.	1.6	21

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37	Potential Biomarkers for Feed Efficiency-Related Traits in Nelore Cattle Identified by Co-expression Network and Integrative Genomics Analyses. Frontiers in Genetics, 2020, 11, 189.	1.1	23
38	Allele-specific expression is widespread in Bos indicus muscle and affects meat quality candidate genes. Scientific Reports, 2020, 10, 10204.	1.6	13
39	Gene expression profile suggesting immunological dysregulation in two Brazilian Bloom's syndrome cases. Molecular Genetics & Genomic Medicine, 2020, 8, e1133.	0.6	7
40	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. Journal of Animal Science, 2020, 98, .	0.2	24
41	Proteome alterations associated with the oleic acid and cis-9, trans-11 conjugated linoleic acid content in bovine skeletal muscle. Journal of Proteomics, 2020, 222, 103792.	1.2	2
42	Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach. Scientific Reports, 2020, 10, 8436.	1.6	10
43	DNA methylation in canine brains is related to domestication and dog-breed formation. PLoS ONE, 2020, 15, e0240787.	1.1	9
44	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 InÃªs Sheep. Annals of Animal Science, 2020, 20, 465-483.	0.6	7
45	Interplay among miR-29 family, mineral metabolism, and gene regulation in Bos indicus muscle. Molecular Genetics and Genomics, 2020, 295, 1113-1127.	1.0	2
46	PSIX-1 Fecal microbiome of dairy calves fed with fresh or frozen maternal colostrum or colostrum powder. Journal of Animal Science, 2020, 98, 419-419.	0.2	0
47	PSIX-6 Gastrointestinal microbiome of calves fed solid diets containing different levels and sources of NDF. Journal of Animal Science, 2020, 98, 418-419.	0.2	0
48	PSVI-22 Fecal microbiome of dairy calves fed with different liquid diets. Journal of Animal Science, 2020, 98, 431-431.	0.2	0
49	Single nucleotide polymorphisms in the growth hormone and IGF type-1 (IGF1) genes associated with carcass traits in Santa Ines sheep. Animal, 2019, 13, 460-468.	1.3	11
50	Transcriptome changes in muscle of Nellore cows submitted to recovery weight gain under grazing condition. Animal, 2019, 13, 333-340.	1.3	1
51	Low-intensity resistance training with partial blood flow restriction and high-intensity resistance training induce similar changes in skeletal muscle transcriptome in elderly humans. Applied Physiology, Nutrition and Metabolism, 2019, 44, 216-220.	0.9	10
52	Co-Expression Networks Reveal Potential Regulatory Roles of miRNAs in Fatty Acid Composition of Nelore Cattle. Frontiers in Genetics, 2019, 10, 651.	1.1	22
53	Research Article Genomic regions and genes associated with carcass quality in Nelore cattle. Genetics and Molecular Research, 2019, 18, .	0.3	15
54	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. BMC Genetics, 2019, 20, 83.	2.7	10

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55	Assessing the accuracy of prediction for milk fatty acids by using a small reference population of tropical Holstein cows. Journal of Animal Breeding and Genetics, 2019, 136, 453-463.	0.8	2
56	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. BMC Genomics, 2019, 20, 669.	1.2	17
57	Muscle transcriptome analysis reveals genes and metabolic pathways related to mineral concentration in Bos indicus. Scientific Reports, 2019, 9, 12715.	1.6	15
58	RNA-Seq transcriptome analysis shows anti-tumor actions of melatonin in a breast cancer xenograft model. Scientific Reports, 2019, 9, 966.	1.6	21
59	Mutation dynamics of CpG dinucleotides during a recent event of vertebrate diversification. Epigenetics, 2019, 14, 685-707.	1.3	30
60	Identification of selection signatures involved in performance traits in a paternal broiler line. BMC Genomics, 2019, 20, 449.	1.2	28
61	Genome-wide association study for milk production traits in a Brazilian Holstein population. Journal of Dairy Science, 2019, 102, 5305-5314.	1.4	25
62	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. Frontiers in Genetics, 2019, 10, 210.	1.1	27
63	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.	1.3	12
64	Evaluation of imputation accuracy using the combination of two high-density panels in Nelore beef cattle. Scientific Reports, 2019, 9, 17920.	1.6	3
65	Network analysis uncovers putative genes affecting resistance to tick infestation in Braford cattle skin. BMC Genomics, 2019, 20, 998.	1.2	18
66	Quantitative trait loci for morphometric and mineral composition traits of the tibia bone in a broiler Ã— layer cross. Animal, 2019, 13, 1563-1569.	1.3	2
67	Gene co-expression networks associated with carcass traits reveal new pathways for muscle and fat deposition in Nelore cattle. BMC Genomics, 2019, 20, 32.	1.2	34
68	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
69	MicroRNA expression profiles discriminate childhood Tâ€•from Bâ€•acute lymphoblastic leukemia. Hematological Oncology, 2019, 37, 103-112.	0.8	44
70	Whole transcriptome analysis of the pectoralis major muscle reveals molecular mechanisms involved with white striping in broiler chickens. Poultry Science, 2019, 98, 590-601.	1.5	46
71	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. G3: Genes, Genomes, Genetics, 2018, 8, 1985-1991.	0.8	6
72	Widespread modulation of gene expression by copy number variation in skeletal muscle. Scientific Reports, 2018, 8, 1399.	1.6	25

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73	Longissimus dorsi muscle label-free quantitative proteomic reveals biological mechanisms associated with intramuscular fat deposition. Journal of Proteomics, 2018, 179, 30-41.	1.2	53
74	Relationship of runs of homozygosity with adaptive and production traits in a paternal broiler line. Animal, 2018, 12, 1126-1134.	1.3	31
75	A comprehensive manually-curated compendium of bovine transcription factors. Scientific Reports, 2018, 8, 13747.	1.6	18
76	An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. Scientific Reports, 2018, 8, 17072.	1.6	47
77	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. Scientific Reports, 2018, 8, 16222.	1.6	29
78	Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nellore Cattle. Frontiers in Genetics, 2018, 9, 441.	1.1	54
79	Genome-wide characterization of genetic variants and putative regions under selection in meat and egg-type chicken lines. BMC Genomics, 2018, 19, 83.	1.2	39
80	Linkage disequilibrium in Brazilian Santa InÃªs breed, Ovis aries. Scientific Reports, 2018, 8, 8851.	1.6	28
81	Data from proteomic analysis of bovine Longissimus dorsi muscle associated with intramuscular fat content. Data in Brief, 2018, 19, 1314-1317.	0.5	6
82	Carcass and commercial cut yield of Santa Ines sheep affected by polymorphisms of the LEP gene. Small Ruminant Research, 2018, 166, 121-128.	0.6	5
83	KCNJ11 gene expression is associated to feed consumption and growth traits in Nelore beef cattle. Agri Gene, 2018, 9, 1-4.	1.9	1
84	Estimates of genomic heritability and genome-wide association study for fatty acids profile in Santa InÃªs sheep. BMC Genomics, 2018, 19, 375.	1.2	31
85	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. BMC Genomics, 2018, 19, 126.	1.2	53
86	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC Genomics, 2018, 19, 499.	1.2	51
87	A genome-wide association study reveals novel genomic regions and positional candidate genes for fat deposition in broiler chickens. BMC Genomics, 2018, 19, 374.	1.2	28
88	EDA mutation by exome sequencing in nonâ€•syndromic Xâ€•linked oligodontia. Clinical Genetics, 2017, 92, 227-229.	1.0	2
89	Genome-wide association study for performance traits in chickens using genotype by sequencing approach. Scientific Reports, 2017, 7, 41748.	1.6	33
90	Genome-Enabled Prediction of Breeding Values for Feedlot Average Daily Weight Gain in Nelore Cattle. G3: Genes, Genomes, Genetics, 2017, 7, 1855-1859.	0.8	6

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91	Large-scale SNP discovery and construction of a high-density genetic map of Colossoma macropomum through genotyping-by-sequencing. Scientific Reports, 2017, 7, 46112.	1.6	32
92	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. Science Advances, 2017, 3, e1700299.	4.7	142
93	DNA methylation profiles in red blood cells of adult hens correlate to their rearing conditions. Journal of Experimental Biology, 2017, 220, 3579-3587.	0.8	46
94	Identification of genomic regions related to tenderness in Nellore beef cattle. Advances in Animal Biosciences, 2017, 8, s42-s44.	1.0	5
95	Oviductal transcriptional profiling of a bovine fertility model by next-generation sequencing. Genomics Data, 2017, 13, 27-29.	1.3	8
96	Dynamic remodeling of endometrial extracellular matrix regulates embryo receptivity in cattle. Reproduction, 2017, 153, 49-61.	1.1	25
97	Appetite regulating factors in pacu (Piaractus mesopotamicus): 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.	0.8	38
98	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.	2.1	13
99	Comparative muscle transcriptome associated with carcass traits of Nellore cattle. BMC Genomics, 2017, 18, 506.	1.2	51
100	Supplementation with small-extracellular vesicles from ovarian follicular fluid during in vitro production modulates bovine embryo development. PLoS ONE, 2017, 12, e0179451.	1.1	80
101	Investigation of mechanisms involved in regulation of progesterone catabolism using an overfed versus underfed eweâ€“lamb model1. Journal of Animal Science, 2017, 95, 5537-5546.	0.2	5
102	Genotypic and allelic frequencies of gene polymorphisms associated with meat tenderness in Nellore beef cattle. Genetics and Molecular Research, 2017, 16, .	0.3	5
103	The Bos taurusâ€“Bos indicus balance in fertility and milk related genes. PLoS ONE, 2017, 12, e0181930.	1.1	33
104	Abstract P1-05-28: Melatonin treatment: A transcriptomic networks in a xenograft model of breast cancer. , 2017, , .		0
105	Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle. PLoS ONE, 2016, 11, e0157711.	1.1	59
106	A single nucleotide polymorphism in NEUROD1 is associated with production traits in Nelore beef cattle. Genetics and Molecular Research, 2016, 15, .	0.3	0
107	Allele- and parent-of-origin-specific effects on expression of the KCNJ11 gene: A candidate for meat tenderness in cattle. Genetics and Molecular Research, 2016, 15, .	0.3	2
108	0318 PRUNE2 gene has a potential effect on residual feed intake in Nellore cattle. Journal of Animal Science, 2016, 94, 152-153.	0.2	1

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109	Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. BMC Genomics, 2016, 17, 961.	1.2	54
110	Gene expression profile of intramuscular muscle in Nellore cattle with extreme values of fatty acid. BMC Genomics, 2016, 17, 972.	1.2	49
111	0903 Differentially expressed genes in genetically divergent Nellore steers for calcium content in the Longissimus dorsi muscle. Journal of Animal Science, 2016, 94, 435-435.	0.2	1
112	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.	0.8	38
113	Variation in<i>myogenic differentiation 1</i>mRNA abundance isÂassociated with beef tenderness in Nelore cattle. Animal Genetics, 2016, 47, 491-494.	0.6	8
114	0339 Gene network regulated by microRNAs suggests modulation of fat deposition in cattle. Journal of Animal Science, 2016, 94, 163-163.	0.2	0
115	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. Scientific Reports, 2016, 6, 39493.	1.6	57
116	0893 Label-free MSE proteomic analysis of the bovine skeletal muscle: New approach for meat tenderness evaluation. Journal of Animal Science, 2016, 94, 429-429.	0.2	1
117	Endometrial transcriptional profiling of a bovine fertility model by Next-Generation Sequencing. Genomics Data, 2016, 7, 26-28.	1.3	4
118	Connectivity maintain mammal assemblages functional diversity within agricultural and fragmented landscapes. European Journal of Wildlife Research, 2016, 62, 431-446.	0.7	67
119	Genomic structure and marker-derived gene networks for growth and meat quality traits of Brazilian Nelore beef cattle. BMC Genomics, 2016, 17, 235.	1.2	31
120	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.	1.3	58
121	High-throughput and Cost-effective Chicken Genotyping Using Next-Generation Sequencing. Scientific Reports, 2016, 6, 26929.	1.6	55
122	0340 Differentially expressed miRNAs in skeletal muscle related to feed efficiency in Nellore cattle. Journal of Animal Science, 2016, 94, 163-164.	0.2	4
123	Genetic parameters for growth characteristics of free-range chickens under univariate random regression models. Poultry Science, 2016, 95, 1989-1998.	1.5	6
124	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.	1.0	78
125	Quantitative trait loci with sex-specific effects for internal organs weights and hematocrit value in a broiler-layer cross. Journal of Applied Genetics, 2016, 57, 215-224.	1.0	6
126	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. PLoS ONE, 2016, 11, e0161160.	1.1	28

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127	Integrative transcriptome analysis identifies deregulated microRNA-transcription factor networks in lung adenocarcinoma. Oncotarget, 2016, 7, 28920-28934.	0.8	49
128	Liver transcriptomic networks reveal main biological processes associated with feed efficiency in beef cattle. BMC Genomics, 2015, 16, 1073.	1.2	161
129	A genomewide association mapping study using ultrasoundâ€scanned information identifies potential genomic regions and candidate genes affecting carcass traits in Nellore cattle. Journal of Animal Breeding and Genetics, 2015, 132, 420-427.	0.8	34
130	Short Communication Genome-wide association with residual body weight gain in Bos indicus cattle. Genetics and Molecular Research, 2015, 14, 5229-5233.	0.3	10
131	Identification of polymorphisms associated with production traits on chicken (Gallus gallus) chromosome 4. Genetics and Molecular Research, 2015, 14, 10717-10728.	0.3	15
132	Putative Regulatory Factors Associated with Intramuscular Fat Content. PLoS ONE, 2015, 10, e0128350.	1.1	116
133	Size of the Ovulatory Follicle Dictates Spatial Differences in the Oviductal Transcriptome in Cattle. PLoS ONE, 2015, 10, e0145321.	1.1	29
134	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.	0.8	9
135	Gene expression of beta-adrenergic receptors and myosin heavy chain isoforms induced by ractopamine feeding duration in pigs not carrying the ryanodine receptor mutation. Livestock Science, 2015, 172, 91-95.	0.6	6
136	Gene expression profiling by high throughput sequencing to determine signatures for the bovine receptive uterus at early gestation. Genomics Data, 2015, 5, 94-96.	1.3	2
137	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. Genetics Selection Evolution, 2015, 47, 15.	1.2	40
138	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. BMC Genomics, 2015, 16, 242.	1.2	109
139	SNP and INDEL detection in a QTL region on chicken chromosome 2 associated with muscle deposition. Animal Genetics, 2015, 46, 158-163.	0.6	21
140	Variant discovery in a QTL region on chromosome 3 associated with fatness in chickens. Animal Genetics, 2015, 46, 141-147.	0.6	28
141	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.	1.2	40
142	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.	1.2	59
143	The Transcriptome Signature of the Receptive Bovine Uterus Determined at Early Gestation. PLoS ONE, 2015, 10, e0122874.	1.1	35
144	Complete Genome Sequence of Sporisorium scitamineum and Biotrophic Interaction Transcriptome with Sugarcane. PLoS ONE, 2015, 10, e0129318.	1.1	93

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145	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
146	Identification and characterization of microRNAs expressed in chicken skeletal muscle. Genetics and Molecular Research, 2014, 13, 1465-1479.	0.3	10
147	Identification of genomic regions associated with feed efficiency in Nelore cattle. BMC Genetics, 2014, 15, 100.	2.7	87
148	Genomeâ€•wide association study for feedlot average daily gain in Nellore cattle (<i>Bos indicus</i>). Journal of Animal Breeding and Genetics, 2014, 131, 210-216.	0.8	24
149	Genome-wide association study for intramuscular fat deposition and composition in Nellore cattle. BMC Genetics, 2014, 15, 39.	2.7	121
150	Response of resistant and susceptible Brazilian Somalis crossbreed sheep naturally infected by Haemonchus contortus. Parasitology Research, 2014, 113, 1155-1161.	0.6	27
151	Genome-wide association analysis of feed intake and residual feed intake in Nellore cattle. BMC Genetics, 2014, 15, 21.	2.7	78
152	Composite interval mapping and mixed models reveal QTL associated with performance and carcass traits on chicken chromosomes 1, 3, and 4. Journal of Applied Genetics, 2014, 55, 97-103.	1.0	1
153	A genomeâ€•wide scan for selection signatures in <scp>N</scp>ellore cattle. Animal Genetics, 2014, 45, 771-781.	0.6	15
154	De novo transcriptome analysis of Hevea brasiliensistissues by RNA-seq and screening for molecular markers. BMC Genomics, 2014, 15, 236.	1.2	82
155	Heat shock and structural proteins associated with meat tenderness in Nellore beef cattle, a Bos indicus breed. Meat Science, 2014, 96, 1318-1324.	2.7	79
156	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. Cells Tissues Organs, 2014, 200, 326-338.	1.3	4
157	Association of IGF1 and KDM5A polymorphisms with performance, fatness and carcass traits in chickens. Journal of Applied Genetics, 2013, 54, 103-112.	1.0	32
158	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2012â€“30 November 2012. Molecular Ecology Resources, 2013, 13, 341-343.	2.2	33
159	Identification of <i>KCNJ11</i> as a functional candidate gene for bovine meat tenderness. Physiological Genomics, 2013, 45, 1215-1221.	1.0	14
160	Genome scan for meat quality traits in Nelore beef cattle. Physiological Genomics, 2013, 45, 1012-1020.	1.0	123
161	Expression of 1alpha-HYD and 24-HYD in bovine kidney mediated by vitamin D3 supplementation. Genetics and Molecular Research, 2013, 12, 6611-6618.	0.3	1
162	Identification and association of polymorphisms in CAPN1 and CAPN3 candidate genes related to performance and meat quality traits in chickens. Genetics and Molecular Research, 2013, 12, 472-482.	0.3	23

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163	Polymorphisms in FGFBP1 and FGFBP2 genes associated with carcass and meat quality traits in chickens. Genetics and Molecular Research, 2013, 12, 208-222.	0.3	11
164	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.	1.1	29
165	<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. Developmental Dynamics, 2012, 241, 1886-1900.	0.8	9
166	Wholeâ€genome analysis for backfat thickness in a tropically adapted, composite cattle breed from Brazil. Animal Genetics, 2012, 43, 518-524.	0.6	3
167	Quantitative trait loci associated with chemical composition of the chicken carcass. Animal Genetics, 2012, 43, 570-576.	0.6	14
168	QTL for percentage of carcass and carcass parts in a broiler x layer cross. Animal Genetics, 2011, 42, 117-124.	0.6	20
169	mRNA profile of Nellore calves after primary infection with Haemonchus placei. Veterinary Parasitology, 2011, 176, 195-200.	0.7	11
170	RegiÃµes genÃ´micas associadas a caracterÃsticas de desempenho e carcaÃ§a no cromossomo 5 de linhagens Brasileiras de galinha. Pesquisa Agropecuaria Brasileira, 2011, 46, 229-238.	0.9	2
171	Abundance of MyoD and myostatin transcripts in chicken embryos submitted to distinct incubation temperatures and timing exposures. Brazilian Journal of Biology, 2011, 71, 563-564.	0.4	4
172	Genome wide scan for quantitative trait loci affecting tick resistance in cattle (Bos taurus Ã— Bos) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.2	51
173	Cytokine gene expression in response to Haemonchus placei infections in Nelore cattle. Veterinary Parasitology, 2010, 171, 68-73.	0.7	31
174	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.	0.6	13
175	Mapping quantitative trait loci in Gallus gallus using principal components. Revista Brasileira De Zootecnia, 2010, 39, 2434-2441.	0.3	4
176	Heat and chemical stress modulate the expression of the Î±-RYR gene in broiler chickens. Genetics and Molecular Research, 2010, 9, 1258-1266.	0.3	15
177	Biotecnologia animal. Estudos Avancados, 2010, 24, 123-147.	0.2	3
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