

Luciana Ca Regitano

List of Publications by Year in descending order

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131
papers

3,703
citations

136885

32
h-index

168321

53
g-index

144
all docs

144
docs citations

144
times ranked

3399
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of genomic predictions for Angus cattle in Brazil incorporating genotypes from related American sires. <i>Journal of Animal Science</i> , 2022, , .	0.2	1
2	Cross-population selection signatures in Canchim composite beef cattle. <i>PLoS ONE</i> , 2022, 17, e0264279.	1.1	7
3	DNA methylation may affect beef tenderness through signal transduction in <i>Bos indicus</i> . <i>Epigenetics and Chromatin</i> , 2022, 15, 15.	1.8	6
4	Stool and Ruminal Microbiome Components Associated With Methane Emission and Feed Efficiency in Nelore Beef Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	12
5	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. <i>Animals</i> , 2022, 12, 1632.	1.0	5
6	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.	1.0	1
7	Nasopharyngeal Microbial Communities of Patients Infected With SARS-CoV-2 That Developed COVID-19. <i>Frontiers in Microbiology</i> , 2021, 12, 637430.	1.5	53
8	Muscle allele-specific expression QTLs may affect meat quality traits in <i>Bos indicus</i> . <i>Scientific Reports</i> , 2021, 11, 7321.	1.6	10
9	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	1.3	10
10	Comparative untargeted metabolome analysis of ruminal fluid and feces of Nelore steers (<i>Bos</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382	1.6	8
11	Genome-Wide Analyses Reveal the Genetic Architecture and Candidate Genes of Indicine, Taurine, Synthetic Crossbreds, and Locally Adapted Cattle in Brazil. <i>Frontiers in Genetics</i> , 2021, 12, 702822.	1.1	10
12	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. <i>Genes</i> , 2021, 12, 67.	1.0	12
13	Overlapping haplotype blocks indicate shared genomic regions between a composite beef cattle breed and its founder breeds. <i>Livestock Science</i> , 2021, 254, 104747.	0.6	0
14	CNVranger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020, 36, 972-973.	1.8	17
15	FABP1 and SLC2A5 expression levels affect feed efficiency-related traits. <i>Agri Gene</i> , 2020, 15, 100100.	1.9	3
16	Potential Biomarkers for Feed Efficiency-Related Traits in Nelore Cattle Identified by Co-expression Network and Integrative Genomics Analyses. <i>Frontiers in Genetics</i> , 2020, 11, 189.	1.1	23
17	Allele-specific expression is widespread in <i>Bos indicus</i> muscle and affects meat quality candidate genes. <i>Scientific Reports</i> , 2020, 10, 10204.	1.6	13
18	The structure of microbial populations in Nelore GIT reveals inter-dependency of methanogens in feces and rumen. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 6.	2.1	28

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19	Proteome alterations associated with the oleic acid and cis-9, trans-11 conjugated linoleic acid content in bovine skeletal muscle. <i>Journal of Proteomics</i> , 2020, 222, 103792.	1.2	2
20	Genetic regulators of mineral amount in Nelore cattle muscle predicted by a new co-expression and regulatory impact factor approach. <i>Scientific Reports</i> , 2020, 10, 8436.	1.6	10
21	Interplay among miR-29 family, mineral metabolism, and gene regulation in <i>Bos indicus</i> muscle. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1113-1127.	1.0	2
22	Tournaments between markers as a strategy to enhance genomic predictions. <i>PLoS ONE</i> , 2019, 14, e0217283.	1.1	4
23	Co-Expression Networks Reveal Potential Regulatory Roles of miRNAs in Fatty Acid Composition of Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 651.	1.1	22
24	Cross talk between mineral metabolism and meat quality: a systems biology overview. <i>Physiological Genomics</i> , 2019, 51, 529-538.	1.0	12
25	CRUMBLER: A tool for the prediction of ancestry in cattle. <i>PLoS ONE</i> , 2019, 14, e0221471.	1.1	7
26	Muscle transcriptome analysis reveals genes and metabolic pathways related to mineral concentration in <i>Bos indicus</i> . <i>Scientific Reports</i> , 2019, 9, 12715.	1.6	15
27	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 210.	1.1	27
28	PSVIII-38 Genomic prediction for tick resistance in Angus cattle. <i>Journal of Animal Science</i> , 2019, 97, 263-263.	0.2	0
29	Evaluation of imputation accuracy using the combination of two high-density panels in Nelore beef cattle. <i>Scientific Reports</i> , 2019, 9, 17920.	1.6	3
30	Network analysis uncovers putative genes affecting resistance to tick infestation in Braford cattle skin. <i>BMC Genomics</i> , 2019, 20, 998.	1.2	18
31	Gene co-expression networks associated with carcass traits reveal new pathways for muscle and fat deposition in Nelore cattle. <i>BMC Genomics</i> , 2019, 20, 32.	1.2	34
32	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
33	Prospecting genes associated with navel length, coat and scrotal circumference traits in Canchim cattle. <i>Livestock Science</i> , 2018, 210, 33-38.	0.6	6
34	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	1.6	25
35	Longissimus dorsi muscle label-free quantitative proteomic reveals biological mechanisms associated with intramuscular fat deposition. <i>Journal of Proteomics</i> , 2018, 179, 30-41.	1.2	53
36	A comprehensive manually-curated compendium of bovine transcription factors. <i>Scientific Reports</i> , 2018, 8, 13747.	1.6	18

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37	An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. <i>Scientific Reports</i> , 2018, 8, 17072.	1.6	47
38	Gene Co-expression Analysis Indicates Potential Pathways and Regulators of Beef Tenderness in Nelore Cattle. <i>Frontiers in Genetics</i> , 2018, 9, 441.	1.1	54
39	Data from proteomic analysis of bovine Longissimus dorsi muscle associated with intramuscular fat content. <i>Data in Brief</i> , 2018, 19, 1314-1317.	0.5	6
40	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
41	Integrative analysis of microRNAs and mRNAs revealed regulation of composition and metabolism in Nelore cattle. <i>BMC Genomics</i> , 2018, 19, 126.	1.2	53
42	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018, 19, 499.	1.2	51
43	HSF1 and HSPA6 as functional candidate genes associated with heat tolerance in Angus cattle. <i>Revista Brasileira De Zootecnia</i> , 2018, 47, .	0.3	17
44	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.	0.8	6
45	Candidate genes for male and female reproductive traits in Canchim beef cattle. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 67.	2.1	32
46	Tissue Tropism in Host Transcriptional Response to Members of the Bovine Respiratory Disease Complex. <i>Scientific Reports</i> , 2017, 7, 17938.	1.6	28
47	Genomewide association study for production and meat quality traits in Canchim beef cattle ¹ . <i>Journal of Animal Science</i> , 2017, 95, 3381-3390.	0.2	12
48	Comparative muscle transcriptome associated with carcass traits of Nelore cattle. <i>BMC Genomics</i> , 2017, 18, 506.	1.2	51
49	Genomewide association mapping and pathway analysis of meat tenderness in Polled Nelore cattle ¹ . <i>Journal of Animal Science</i> , 2017, 95, 1945-1956.	0.2	6
50	Study on the introgression of beef breeds in Canchim cattle using single nucleotide polymorphism markers. <i>PLoS ONE</i> , 2017, 12, e0171660.	1.1	11
51	Genotypic and allelic frequencies of gene polymorphisms associated with meat tenderness in Nelore beef cattle. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	5
52	The <i>Bos taurus</i> – <i>Bos indicus</i> balance in fertility and milk related genes. <i>PLoS ONE</i> , 2017, 12, e0181930.	1.1	33
53	Genomewide association mapping and pathway analysis of meat tenderness in Polled Nelore cattle. <i>Journal of Animal Science</i> , 2017, 95, 1945.	0.2	19
54	Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle. <i>PLoS ONE</i> , 2016, 11, e0157711.	1.1	59

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55	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, .	0.3	2
56	Differences in the skeletal muscle transcriptome profile associated with extreme values of fatty acids content. <i>BMC Genomics</i> , 2016, 17, 961.	1.2	54
57	Variation in <i>myogenic differentiation 1</i> mRNA abundance is associated with beef tenderness in Nelore cattle. <i>Animal Genetics</i> , 2016, 47, 491-494.	0.6	8
58	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. <i>Scientific Reports</i> , 2016, 6, 39493.	1.6	57
59	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.	1.2	31
60	Selection signatures in Canchim beef cattle. <i>Journal of Animal Science and Biotechnology</i> , 2016, 7, 29.	2.1	49
61	Comparison of Sequence Variants in the PDK4 and COX4I2 Genes Between Racing and Cutting Lines of Quarter Horses and Associations With the Speed Index. <i>Journal of Equine Veterinary Science</i> , 2016, 39, 1-6.	0.4	9
62	MSTN , CKM , and DMRT3 Gene Variants in Different Lines of Quarter Horses. <i>Journal of Equine Veterinary Science</i> , 2016, 39, 33-37.	0.4	18
63	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0161160.	1.1	28
64	Candidate genes for carcass traits in a tropical-adapted Brazilian composite beef breed. <i>Genetics and Molecular Research</i> , 2015, 14, 16667-16674.	0.3	3
65	Putative Regulatory Factors Associated with Intramuscular Fat Content. <i>PLoS ONE</i> , 2015, 10, e0128350.	1.1	116
66	Polymorphisms in TOX and NCOA2 genes and their associations with reproductive traits in cattle. <i>Reproduction, Fertility and Development</i> , 2015, 27, 523.	0.1	14
67	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. <i>Genetics Selection Evolution</i> , 2015, 47, 15.	1.2	40
68	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	1.2	109
69	Strategies for genotype imputation in composite beef cattle. <i>BMC Genetics</i> , 2015, 16, 99.	2.7	17
70	Allele substitution effects of IGF1, GH and PIT1 markers on estimated breeding values for weight and reproduction traits in Canchim beef cattle. <i>Livestock Science</i> , 2015, 180, 78-83.	0.6	1
71	Effect of IGF1, GH, and PIT1 markers on the genetic parameters of growth and reproduction traits in Canchim cattle. <i>Molecular Biology Reports</i> , 2015, 42, 245-251.	1.0	15
72	Sequenciamento parcial dos genes TOX e NCOA2 em bubalinos. <i>Archivos De Zootecnia</i> , 2015, 64, 75-78.	0.2	1

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73	Short Communication Single nucleotide polymorphisms in candidate genes associated with gastrointestinal nematode infection in goats. <i>Genetics and Molecular Research</i> , 2014, 13, 8530-8536.	0.3	10
74	Identification of genomic regions associated with feed efficiency in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 100.	2.7	87
75	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	1.5	391
76	Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 39.	2.7	121
77	Inheritance of AFLP markers and genetic linkage analysis in two full-sib families of the marine shrimp <i>Litopenaeus vannamei</i> (Crustacea, Decapoda). <i>Advances in Bioscience and Biotechnology (Print)</i> , 2014, 05, 273-281.	0.3	3
78	Calcium and potassium content in beef: Influences on tenderness and associations with molecular markers in Nelore cattle. <i>Meat Science</i> , 2014, 96, 436-440.	2.7	43
79	Quantitative study of <i>Babesia bovis</i> infection in beef cattle from São Paulo state, Brazil. <i>Ticks and Tick-borne Diseases</i> , 2014, 5, 234-238.	1.1	25
80	Association between JY-1 gene polymorphisms and reproductive traits in beef cattle. <i>Gene</i> , 2014, 533, 477-480.	1.0	15
81	Genomics in the United States beef industry. <i>Livestock Science</i> , 2014, 166, 84-93.	0.6	17
82	A genome-wide scan for selection signatures in Nelore cattle. <i>Animal Genetics</i> , 2014, 45, 771-781.	0.6	15
83	Heat shock and structural proteins associated with meat tenderness in Nelore beef cattle, a <i>Bos indicus</i> breed. <i>Meat Science</i> , 2014, 96, 1318-1324.	2.7	79
84	Bovine NR1I3 gene polymorphisms and its association with feed efficiency traits in Nelore cattle. <i>Meta Gene</i> , 2014, 2, 206-217.	0.3	17
85	Linkage disequilibrium and haplotype block structure in a composite beef cattle breed. <i>BMC Genomics</i> , 2014, 15, S6.	1.2	48
86	Genome-Wide Association for Growth Traits in Canchim Beef Cattle. <i>PLoS ONE</i> , 2014, 9, e94802.	1.1	53
87	<i>Babesia bovis</i> infection in cattle in the southwestern Brazilian Amazon. <i>Ticks and Tick-borne Diseases</i> , 2013, 4, 78-82.	1.1	5
88	Genome-wide association study for backfat thickness in Canchim beef cattle using Random Forest approach. <i>BMC Genetics</i> , 2013, 14, 47.	2.7	32
89	Identification of <i>KCNJ11</i> as a functional candidate gene for bovine meat tenderness. <i>Physiological Genomics</i> , 2013, 45, 1215-1221.	1.0	14
90	Characterization of the Exonic Regions of the <i>JY-1</i> Gene in Zebu Cattle and Buffaloes. <i>Reproduction in Domestic Animals</i> , 2013, 48, 918-922.	0.6	7

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91	Genome scan for meat quality traits in Nelore beef cattle. <i>Physiological Genomics</i> , 2013, 45, 1012-1020.	1.0	123
92	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.	1.1	29
93	Polymorphism and parent-of-origin effects on gene expression of CAST, leptin and DGAT1 in cattle. <i>Meat Science</i> , 2012, 90, 507-510.	2.7	4
94	A SNP in ASAP1 gene is associated with meat quality and production traits in Nelore breed. <i>Meat Science</i> , 2012, 92, 855-857.	2.7	33
95	First polymorphisms in JY-1 gene in cattle (<i>Bos taurus indicus</i>) and their association with sexual precocity and growth traits. <i>Molecular Biology Reports</i> , 2012, 39, 10105-10109.	1.0	10
96	Candidate genes for production traits in Nelore beef cattle. <i>Genetics and Molecular Research</i> , 2012, 11, 4138-4144.	0.3	10
97	Resistance of cattle of various genetic groups to the tick <i>Rhipicephalus microplus</i> and the relationship with coat traits. <i>Veterinary Parasitology</i> , 2012, 186, 425-430.	0.7	52
98	Whole-genome analysis for backfat thickness in a tropically adapted, composite cattle breed from Brazil. <i>Animal Genetics</i> , 2012, 43, 518-524.	0.6	3
99	Association of CSSM066 and ILSTS011 microsatellite markers and thyroglobulin gene SNP with backfat in Canchim cattle. <i>Scientia Agricola</i> , 2012, 69, 1-5.	0.6	2
100	Candidate gene region for control of rib eye area in Canchim beef cattle. <i>Genetics and Molecular Research</i> , 2011, 10, 1220-1226.	0.3	3
101	mRNA profile of Nelore calves after primary infection with <i>Haemonchus placei</i> . <i>Veterinary Parasitology</i> , 2011, 176, 195-200.	0.7	11
102	Genetic variability among the wild boars (<i>Sus scrofa scrofa</i>), crossbred animals and pigs using microsatellite markers (STRs). <i>Brazilian Archives of Biology and Technology</i> , 2011, 54, 301-306.	0.5	1
103	Genome wide scan for quantitative trait loci affecting tick resistance in cattle (<i>Bos taurus</i> × <i>Bos</i> Tj ETQq1 1 0.784314 rgBT/Overlo 1.2 51		
104	Infestação natural de fêmeas bovinas de corte por ectoparasitas na Região Sudeste do Brasil. <i>Revista Brasileira De Zootecnia</i> , 2010, 39, 1477-1482.	0.3	20
105	Prospecting candidate SNPs for backfat in Canchim beef cattle. <i>Genetics and Molecular Research</i> , 2010, 9, 1997-2003.	0.3	10
106	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010, 20, 693-703.	2.4	280
107	Efeitos de ambiente e estimativas de parâmetros genéticos para características de carcaça em bovinos da raça Canchim criados em pastagem. <i>Revista Brasileira De Zootecnia</i> , 2010, 39, 1437-1442.	0.3	17
108	Parentage test in broad-snouted caimans (<i>Caiman latirostris</i> , Crocodylidae) using microsatellite DNA. <i>Genetics and Molecular Biology</i> , 2009, 32, 874-881.	0.6	12

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109	Characterization of mitochondrial genotypes in the foundation herd of the Canchim beef cattle breed. <i>Genetics and Molecular Research</i> , 2009, 8, 261-267.	0.3	3
110	Detection of <i>Babesia bigemina</i> in cattle of different genetic groups and in <i>Rhipicephalus (Boophilus)</i> microplus tick. <i>Veterinary Parasitology</i> , 2008, 155, 281-286.	0.7	25
111	Association of an <i>insulin-like growth factor 1</i> gene microsatellite with phenotypic variation and estimated breeding values of growth traits in Canchim cattle. <i>Animal Genetics</i> , 2008, 39, 480-485.	0.6	37
112	Genotype characterization of the <i>Haematobia irritans</i> (diptera: muscidae) from Brazil, Dominican Republic and Colombia based on randomly amplified polymorphic dna (rapd) analysis. <i>Brazilian Journal of Veterinary Parasitology</i> , 2008, 17, 179-184.	0.2	4
113	Association of PIT1 genotypes with growth traits in Canchim cattle. <i>Scientia Agricola</i> , 2008, 65, 116-121.	0.6	12
114	Growth hormone 1 gene (GH1) polymorphisms as possible markers of the production potential of beef cattle using the Brazilian Canchim breed as a model. <i>Genetics and Molecular Biology</i> , 2008, 31, 874-879.	0.6	8
115	Quantitative trait loci (QTL) mapping for growth traits on bovine chromosome 14. <i>Genetics and Molecular Biology</i> , 2007, 30, 364-369.	0.6	3
116	Genotype characterization of <i>Haematobia irritans</i> from different Brazilian geographic regions based on randomly amplified polymorphic DNA (RAPD) analysis. <i>Pesquisa Veterinaria Brasileira</i> , 2007, 27, 1-5.	0.5	2
117	Artificial infestation of <i>Boophilus microplus</i> in beef cattle heifers of four genetic groups. <i>Genetics and Molecular Biology</i> , 2007, 30, 1150-1155.	0.6	31
118	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.	0.6	44
119	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.	0.6	4
120	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.	0.6	4
121	Association of GH and IGF-1 polymorphisms with growth traits in a synthetic beef cattle breed. <i>Genetics and Molecular Biology</i> , 2005, 28, 230-236.	0.6	43
122	Ajuste de modelos não-lineares em estudos de associação entre polimorfismos genéticos e crescimento em bovinos de corte. <i>Revista Brasileira De Zootecnia</i> , 2004, 33, 1416-1425.	0.3	11
123	Lack of Genetic Structuring among Tropical Brazilian Wood Stork Populations and Low Genetic Differentiation from North American Populations. <i>Biotropica</i> , 2004, 36, 248-258.	0.8	9
124	Semiquantitative determination of <i>Alicyclobacillus acidoterrestris</i> in orange juice by reverse-transcriptase polymerase chain reaction and capillary electrophoresis - laser induced fluorescence using microchip technology. <i>Electrophoresis</i> , 2004, 25, 3860-3864.	1.3	23
125	Candidate genes for growth traits in beef cattle crosses <i>Bos taurus</i> x <i>Bos indicus</i> . <i>Journal of Animal Breeding and Genetics</i> , 2003, 120, 51-56.	0.8	48
126	QTL affecting body weight in a candidate region of cattle chromosome 5. <i>Genetics and Molecular Biology</i> , 2003, 26, 259-265.	0.6	39

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127	Genetic characterization of Aberdeen Angus cattle using molecular markers. Genetics and Molecular Biology, 2003, 26, 133-137.	0.6	33
128	Prevalência de rotavírus do grupo A em fezes diarreicas de bezerros de corte em sistema semi-intensivo de produção. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2003, 55, 266-270.	0.1	13
129	Caracterização molecular de animais da raça Nelore utilizando microssatélites e genes candidatos. Revista Brasileira De Zootecnia, 2000, 29, 1044-1049.	0.3	14
130	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.	0.6	15
131	Casein, κ -lactoglobulin and growth hormone allele frequencies and genetic distances in Nelore, Gyr, Guzerá, Caracu, Charolais, Canchim and Santa Gertrudis cattle. Genetics and Molecular Biology, 1999, 22, 539-541.	0.6	39