

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	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	1.5	391
2	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010, 20, 693-703.	2.4	280
3	Genome scan for meat quality traits in Nelore beef cattle. <i>Physiological Genomics</i> , 2013, 45, 1012-1020.	1.0	123
4	Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 39.	2.7	121
5	Putative Regulatory Factors Associated with Intramuscular Fat Content. <i>PLoS ONE</i> , 2015, 10, e0128350.	1.1	116
6	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	1.2	109
7	Identification of genomic regions associated with feed efficiency in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 100.	2.7	87
8	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
9	Genome-Wide Detection of CNVs and Their Association with Meat Tenderness in Nelore Cattle. <i>PLoS ONE</i> , 2016, 11, e0157711.	1.1	59
10	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
11	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
12	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
13	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
14	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
15	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
16	Genome-Wide Association for Growth Traits in Canchim Beef Cattle. <i>PLoS ONE</i> , 2014, 9, e94802.	1.1	53
17	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
18	Genome wide scan for quantitative trait loci affecting tick resistance in cattle (<i>Bos taurus</i> × <i>Bos Tj</i>) <i>ETQq0 0 0 rgBTj/Overlock 10 Tf 50</i>	1.2	51

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19	Comparative muscle transcriptome associated with carcass traits of Nelore cattle. BMC Genomics, 2017, 18, 506.	1.2	51
20	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC Genomics, 2018, 19, 499.	1.2	51
21	Selection signatures in Canchim beef cattle. Journal of Animal Science and Biotechnology, 2016, 7, 29.	2.1	49
22	Candidate genes for growth traits in beef cattle crosses Bos taurus x Bos indicus. Journal of Animal Breeding and Genetics, 2003, 120, 51-56.	0.8	48
23	Linkage disequilibrium and haplotype block structure in a composite beef cattle breed. BMC Genomics, 2014, 15, S6.	1.2	48
24	An integrative transcriptome analysis indicates regulatory mRNA-miRNA networks for residual feed intake in Nelore cattle. Scientific Reports, 2018, 8, 17072.	1.6	47
25	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.	0.6	44
26	Association of GH and IGF-1 polymorphisms with growth traits in a synthetic beef cattle breed. Genetics and Molecular Biology, 2005, 28, 230-236.	0.6	43
27	Calcium and potassium content in beef: Influences on tenderness and associations with molecular markers in Nelore cattle. Meat Science, 2014, 96, 436-440.	2.7	43
28	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. Genetics Selection Evolution, 2015, 47, 15.	1.2	40
29	QTL affecting body weight in a candidate region of cattle chromosome 5. Genetics and Molecular Biology, 2003, 26, 259-265.	0.6	39
30	Casein, β -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
31	Association of an insulin-like growth factor 1 gene microsatellite with phenotypic variation and estimated breeding values of growth traits in Canchim cattle. Animal Genetics, 2008, 39, 480-485.	0.6	37
32	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
33	Genetic characterization of Aberdeen Angus cattle using molecular markers. Genetics and Molecular Biology, 2003, 26, 133-137.	0.6	33
34	A SNP in ASAP1 gene is associated with meat quality and production traits in Nelore breed. Meat Science, 2012, 92, 855-857.	2.7	33
35	The Bos taurus-Bos indicus balance in fertility and milk related genes. PLoS ONE, 2017, 12, e0181930.	1.1	33
36	Genome-wide association study for backfat thickness in Canchim beef cattle using Random Forest approach. BMC Genomics, 2013, 14, 47.	2.7	32

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37	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
38	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
39	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
40	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
41	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
42	Tissue Tropism in Host Transcriptional Response to Members of the Bovine Respiratory Disease Complex. <i>Scientific Reports</i> , 2017, 7, 17938.	1.6	28
43	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
44	Iron Content Affects Lipogenic Gene Expression in the Muscle of Nelore Beef Cattle. <i>PLoS ONE</i> , 2016, 11, e0161160.	1.1	28
45	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
46	Detection of <i>Babesia bigemina</i> in cattle of different genetic groups and in <i>Rhipicephalus</i> (<i>Boophilus</i>) microplus tick. <i>Veterinary Parasitology</i> , 2008, 155, 281-286.	0.7	25
47	Quantitative study of <i>Babesia bovis</i> infection in beef cattle from SÃ£o Paulo state, Brazil. <i>Ticks and Tick-borne Diseases</i> , 2014, 5, 234-238.	1.1	25
48	Widespread modulation of gene expression by copy number variation in skeletal muscle. <i>Scientific Reports</i> , 2018, 8, 1399.	1.6	25
49	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
50	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
51	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
52	InfestaÃ§Ã£o natural de fÃªmeas bovinas de corte por ectoparasitas na RegiÃ£o Sudeste do Brasil. <i>Revista Brasileira De Zootecnia</i> , 2010, 39, 1477-1482.	0.3	20
53	Genomewide association mapping and pathway analysis of meat tenderness in Polled Nellore cattle. <i>Journal of Animal Science</i> , 2017, 95, 1945.	0.2	19
54	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

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55	A comprehensive manually-curated compendium of bovine transcription factors. <i>Scientific Reports</i> , 2018, 8, 13747.	1.6	18
56	Network analysis uncovers putative genes affecting resistance to tick infestation in Braford cattle skin. <i>BMC Genomics</i> , 2019, 20, 998.	1.2	18
57	Genomics in the United States beef industry. <i>Livestock Science</i> , 2014, 166, 84-93.	0.6	17
58	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
59	Strategies for genotype imputation in composite beef cattle. <i>BMC Genetics</i> , 2015, 16, 99.	2.7	17
60	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
61	CNVranger: association analysis of CNVs with gene expression and quantitative phenotypes. <i>Bioinformatics</i> , 2020, 36, 972-973.	1.8	17
62	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
63	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.	0.6	15
64	Association between JY-1 gene polymorphisms and reproductive traits in beef cattle. <i>Gene</i> , 2014, 533, 477-480.	1.0	15
65	A genome-wide scan for selection signatures in Nelore cattle. <i>Animal Genetics</i> , 2014, 45, 771-781.	0.6	15
66	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
67	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
68	Caracterização molecular de animais da raça Nelore utilizando microssatélites e genes candidatos. <i>Revista Brasileira De Zootecnia</i> , 2000, 29, 1044-1049.	0.3	14
69	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
70	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
71	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
72	Prevalência de rotavírus do grupo A em fezes diarreicas de bezerros de corte em sistema semi-intensivo de produção. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2003, 55, 266-270.	0.1	13

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73	Association of PIT1 genotypes with growth traits in Canchim cattle. <i>Scientia Agricola</i> , 2008, 65, 116-121.	0.6	12
74	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
75	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
76	Cross talk between mineral metabolism and meat quality: a systems biology overview. <i>Physiological Genomics</i> , 2019, 51, 529-538.	1.0	12
77	Multi-Omics Approach Reveals miR-SNPs Affecting Muscle Fatty Acids Profile in Nelore Cattle. <i>Genes</i> , 2021, 12, 67.	1.0	12
78	Stool and Ruminant Microbiome Components Associated With Methane Emission and Feed Efficiency in Nelore Beef Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	12
79	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
80	mRNA profile of Nelore calves after primary infection with <i>Haemonchus placei</i> . <i>Veterinary Parasitology</i> , 2011, 176, 195-200.	0.7	11
81	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
82	Prospecting candidate SNPs for backfat in Canchim beef cattle. <i>Genetics and Molecular Research</i> , 2010, 9, 1997-2003.	0.3	10
83	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
84	Candidate genes for production traits in Nelore beef cattle. <i>Genetics and Molecular Research</i> , 2012, 11, 4138-4144.	0.3	10
85	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
86	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
87	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	1.3	10
88	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
89	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
90	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

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91	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
92	Variation in <i>myogenin</i> mRNA abundance is associated with beef tenderness in Nelore cattle. <i>Animal Genetics</i> , 2016, 47, 491-494.	0.6	8
93	Comparative untargeted metabolome analysis of ruminal fluid and feces of Nelore steers (Bos Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.6	8
94	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
95	Characterization of the Exonic Regions of the <i>JY</i> Gene in Zebu Cattle and Buffaloes. <i>Reproduction in Domestic Animals</i> , 2013, 48, 918-922.	0.6	7
96	CRUMBLER: A tool for the prediction of ancestry in cattle. <i>PLoS ONE</i> , 2019, 14, e0221471.	1.1	7
97	Cross-population selection signatures in Canchim composite beef cattle. <i>PLoS ONE</i> , 2022, 17, e0264279.	1.1	7
98	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
99	Genomewide association mapping and pathway analysis of meat tenderness in Polled Nellore cattle. <i>Journal of Animal Science</i> , 2017, 95, 1945-1956.	0.2	6
100	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
101	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.	0.5	6
102	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
103	<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
104	Genotypic and allelic frequencies of gene polymorphisms associated with meat tenderness in Nellore beef cattle. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	5
105	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. <i>Animals</i> , 2022, 12, 1632.	1.0	5
106	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
107	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
108	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

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109	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
110	Tournaments between markers as a strategy to enhance genomic predictions. <i>PLoS ONE</i> , 2019, 14, e0217283.	1.1	4
111	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
112	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
113	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
114	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
115	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
116	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
117	FABP1 and SLC2A5 expression levels affect feed efficiency-related traits. <i>Agri Gene</i> , 2020, 15, 100100.	1.9	3
118	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
119	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
120	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
121	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
122	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
123	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
124	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
125	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
126	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

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127	Sequenciamento parcial dos genes TOX e NCOA2 em bubalinos. Archivos De Zootecnia, 2015, 64, 75-78.	0.2	1
128	Development of genomic predictions for Angus cattle in Brazil incorporating genotypes from related American sires. Journal of Animal Science, 2022, , .	0.2	1
129	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
130	PSVIII-38 Genomic prediction for tick resistance in Angus cattle. Journal of Animal Science, 2019, 97, 263-263.	0.2	0
131	Overlapping haplotype blocks indicate shared genomic regions between a composite beef cattle breed and its founder breeds. Livestock Science, 2021, 254, 104747.	0.6	0