Fernando Baldi

List of Publications by Year
in descending order

194 papers	3,490 citations	159358 30 h-index	233125 45 g-index
199 all docs	199 docs citations	199 times ranked	2554 citing authors

#	Article	IF	Citations
1	Runs of homozygosity: current knowledge and applications in livestock. Animal Genetics, 2017, 48, 255-271.	0.6	242
2	Assessment of runs of homozygosity islands and estimates of genomic inbreeding in Gyr (Bos indicus) dairy cattle. BMC Genomics, 2018, 19, 34.	1.2	124
3	Study of whole genome linkage disequilibrium in Nellore cattle. BMC Genomics, 2013, 14, 305.	1.2	106
4	Genome-Wide Association Study for Indicator Traits of Sexual Precocity in Nellore Cattle. PLoS ONE, 2016, 11, e0159502.	1.1	82
5	Genome-Wide Association Study of Meat Quality Traits in Nellore Cattle. PLoS ONE, 2016, 11, e0157845.	1.1	76
6	Genome-Wide Association Study for Carcass Traits in an Experimental Nelore Cattle Population. PLoS ONE, 2017, 12, e0169860.	1.1	71
7	Genome-wide association between single nucleotide polymorphisms with beef fatty acid profile in Nellore cattle using the single step procedure. BMC Genomics, 2016, 17, 213.	1.2	66
8	Genomic Regions Associated with Feed Efficiency Indicator Traits in an Experimental Nellore Cattle Population. PLoS ONE, 2016, 11, e0164390.	1.1	65
9	Accuracies of genomic prediction of feed efficiency traits using different prediction and validation methods in an experimental Nelore cattle population1. Journal of Animal Science, 2016, 94, 3613-3623.	0.2	55
10	Sliding window haplotype approaches overcome single SNP analysis limitations in identifying genes for meat tenderness in Nelore cattle. BMC Genetics, 2019, 20, 8.	2.7	53
11	Association between single-nucleotide polymorphisms and milk production traits in buffalo. Genetics and Molecular Research, 2014, 13, 10256-10268.	0.3	53
12	Gene expression profile of intramuscular muscle in Nellore cattle with extreme values of fatty acid. BMC Genomics, 2016, 17, 972.	1.2	49
13	Genomic prediction of breeding values for carcass traits in Nellore cattle. Genetics Selection Evolution, 2016, 48, 7.	1.2	48
14	Effect of body condition and suckling restriction with and without presence of the calf on cow and calf performance. Animal Production Science, 2010, 50, 931.	0.6	47
15	Genetic associations between stayability and reproductive and growth traits in Canchim beef cattle. Livestock Science, 2010, 132, 107-112.	0.6	45
16	Estimates of genetic parameters for growth, reproductive, and carcass traits in Nelore cattle using the single step genomic BLUP procedure. Livestock Science, 2018, 216, 203-209.	0.6	45
17	Genetic parameters for buffalo milk yield and milk quality traits using Bayesian inference. Journal of Dairy Science, 2010, 93, 2195-2201.	1.4	44
18	Genetic Architecture of Carcass and Meat Quality Traits in Montana TropicalÂ® Composite Beef Cattle. Frontiers in Genetics, 2020, 11, 123.	1.1	42

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19	Mechanical and structural characterization of POSS-modified polyamide 6. Journal of Applied Polymer Science, 2006, 100, 3409-3414.	1.3	41
20	Genetic association between body composition measured by ultrasound and visual scores in Brazilian Nelore cattle1. Journal of Animal Science, 2012, 90, 4223-4229.	0.2	40
21	Genetic associations between scrotal circumference and female reproductive traits in Nelore cattle1. Journal of Animal Science, 2015, 93, 2706-2713.	0.2	40
22	Genetic correlations between mature cow weight and productive and reproductive traits in Nellore cattle. Genetics and Molecular Research, 2012, 11, 2979-2986.	0.3	39
23	Genomic regions and pathways associated with gastrointestinal parasites resistance in Santa InÃªs breed adapted to tropical climate. Journal of Animal Science and Biotechnology, 2017, 8, 73.	2.1	35
24	SNP detection using RNA-sequences of candidate genes associated with puberty in cattle. Genetics and Molecular Research, 2017, 16, .	0.3	35
25	Autozygosity islands and ROH patterns in Nellore lineages: evidence of selection for functionally important traits. BMC Genomics, 2018, 19, 680.	1.2	34
26	Genetic associations between flight speed and growth traits in Nellore cattle1. Journal of Animal Science, 2012, 90, 3427-3432.	0.2	33
27	Genetic parameter estimates for feed efficiency and dry matter intake and their association with growth and carcass traits in Nellore cattle. Livestock Science, 2014, 167, 80-85.	0.6	33
28	Growth performance, and carcass and meat quality traits in progeny of Poll Nellore, Angus and Brahman sires under tropical conditions. Animal Production Science, 2015, 55, 1295.	0.6	32
29	Genome-wide association study of reproductive traits in Nellore heifers using Bayesian inference. Genetics Selection Evolution, 2015, 47, 67.	1.2	32
30	Differences in global gene expression in muscle tissue of Nellore cattle with divergent meat tenderness. BMC Genomics, 2017, 18, 945.	1.2	32
31	Genetic parameter estimates for carcass traits and visual scores including or not genomic information1. Journal of Animal Science, 2016, 94, 1821-1826.	0.2	31
32	Genome scan for postmortem carcass traits in Nellore cattle1. Journal of Animal Science, 2016, 94, 4087-4095.	0.2	31
33	Gene expression profiling and identification of hub genes in Nellore cattle with different marbling score levels. Genomics, 2020, 112, 873-879.	1.3	31
34	Genome-Wide Association Study between Single Nucleotide Polymorphisms and Flight Speed in Nellore Cattle. PLoS ONE, 2016, 11, e0156956.	1.1	31
35	Rubber toughening of polyamide 6/organoclay nanocomposites obtained by melt blending. Journal of Applied Polymer Science, 2006, 99, 3406-3416.	1.3	30
36	Genetic association of growth traits with carcass and meat traits in Nellore cattle. Genetics and Molecular Research, 2015, 14, 18713-18719.	0.3	30

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37	Copy number variation regions in Nellore cattle: Evidences of environment adaptation. Livestock Science, 2018, 207, 51-58.	0.6	30
38	Weighted singleâ€step genomeâ€wide association study and pathway analyses for feed efficiency traits in Nellore cattle. Journal of Animal Breeding and Genetics, 2021, 138, 23-44.	0.8	30
39	Genotype Ã— environment interaction for age at first calving, scrotal circumference, and yearling weight in Nellore cattle using reaction norms in multitrait random regression models. Journal of Animal Science, 2015, 93, 1503-1510.	0.2	29
40	Association study between copy number variation and beef fatty acid profile of Nellore cattle. Journal of Applied Genetics, 2018, 59, 203-223.	1.0	29
41	Genetic parameters and relationships between growth traits and scrotal circumference measured at different ages in Nellore cattle. Genetics and Molecular Biology, 2011, 34, 225-230.	0.6	27
42	Random regression models on Legendre polynomials to estimate genetic parameters for weights from birth to adult age in Canchim cattle*. Journal of Animal Breeding and Genetics, 2010, 127, 289-299.	0.8	26
43	Genetic and phenotypic parameters of carcass and organ traits of broiler chickens. Genetics and Molecular Research, 2014, 13, 10294-10300.	0.3	24
44	Prediction of hub genes associated with intramuscular fat content in Nelore cattle. BMC Genomics, 2019, 20, 520.	1.2	24
45	Genome-wide association study for growth traits in Nelore cattle. Animal, 2018, 12, 1358-1362.	1.3	23
46	Genome-wide scan reveals population stratification and footprints of recent selection in Nelore cattle. Genetics Selection Evolution, 2018, 50, 22.	1.2	23
47	Gender status effect on carcass and meat quality traits of feedlot AngusÂÃ—ÂNellore cattle. Animal Science Journal, 2019, 90, 1078-1089.	0.6	23
48	Genomic selection for meat quality traits in Nelore cattle. Meat Science, 2019, 148, 32-37.	2.7	23
49	Genetic parameter estimates for buffalo milk yield, milk quality and mozzarella production and Bayesian inference analysis of their relationships. Genetics and Molecular Research, 2010, 9, 1636-1644.	0.3	22
50	Meat quality traits of Nellore bulls according to different degrees of backfat thickness: a multivariate approach. Animal Production Science, 2017, 57, 363.	0.6	22
51	Estimation of genetic parameters for milk yield in Murrah buffaloes by Bayesian inference. Journal of Dairy Science, 2010, 93, 784-791.	1.4	21
52	Genetic variability for temperament indicators of Nellore cattle1. Journal of Animal Science, 2013, 91, 3532-3537.	0.2	21
53	Study of lipid metabolism-related genes as candidate genes of sexual precocity in Nellore cattle. Genetics and Molecular Research, 2015, 14, 234-243.	0.3	21
54	Reaction norm for yearling weight in beef cattle using single-step genomic evaluation1. Journal of Animal Science, 2018, 96, 27-34.	0.2	21

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55	Growth, meat and feed efficiency traits of lambs born to ewes submitted to energy restriction during mid-gestation. Animal, 2018, 12, 256-264.	1.3	21
56	Genomeâ€wide scan for runs of homozygosity in the composite Montana Tropical^{Â®} beef cattle. Journal of Animal Breeding and Genetics, 2020, 137, 155-165.	0.8	21
57	Spliced genes in muscle from Nelore Cattle and their association with carcass and meat quality. Scientific Reports, 2020, 10, 14701.	1.6	21
58	Expression of genes related to mitochondrial function in Nellore cattle divergently ranked on residual feed intake. Molecular Biology Reports, 2015, 42, 559-565.	1.0	20
59	Assessing the value of phenotypic information from non-genotyped animals for QTL mapping of complex traits in real and simulated populations. BMC Genetics, 2016, 17, 89.	2.7	20
60	Genetic correlation estimates between beef fatty acid profile with meat and carcass traits in Nellore cattle finished in feedlot. Journal of Applied Genetics, 2017, 58, 123-132.	1.0	20
61	Genetic association between different criteria to define sexual precocious heifers with growth, carcass, reproductive and feed efficiency indicator traits in Nellore cattle using genomic information. Journal of Animal Breeding and Genetics, 2019, 136, 15-22.	0.8	20
62	Genomic prediction for beef fatty acid profile in Nellore cattle. Meat Science, 2017, 128, 60-67.	2.7	19
63	Random regression analyses using B-spline functions to model growth of Nellore cattle. Animal, 2012, 6, 212-220.	1.3	18
64	Associations between single nucleotide polymorphisms and carcass traits in Nellore cattle using high-density panels. Genetics and Molecular Research, 2015, 14, 11133-11144.	0.3	18
65	Genomeâ€wide association study for age at puberty in young Nelore bulls. Journal of Animal Breeding and Genetics, 2020, 137, 234-244.	0.8	18
66	ParÃ¢metros genÃ©ticos para caracterÃsticas de tamanho e condiÃ§Ã£o corporal, eficiÃªncia reprodutiva e longevidade em fÃªmeas da raÃ§a Canchim. Revista Brasileira De Zootecnia, 2008, 37, 247-253.	0.3	18
67	Random regression analyses using Bâ€splines functions to model growth from birth to adult age in Canchim cattle*. Journal of Animal Breeding and Genetics, 2010, 127, 433-441.	0.8	17
68	Polymorphisms in candidate genes and their association with carcass traits and meat quality in Nellore cattle. Pesquisa Agropecuaria Brasileira, 2014, 49, 364-371.	0.9	17
69	Identification of novel mRNA isoforms associated with meat tenderness using RNA sequencing data in beef cattle. Meat Science, 2021, 173, 108378.	2.7	17
70	Effect of lactation length adjustment procedures on genetic parameter estimates for buffalo milk yield. Genetics and Molecular Biology, 2011, 34, 62-67.	0.6	16
71	Genetic associations between temperament and performance traits in Nellore beef cattle. Journal of Animal Breeding and Genetics, 2015, 132, 42-50.	0.8	16
72	Genetic analysis of carcass and meat quality traits in Nelore cattle1. Journal of Animal Science, 2018, 96, 3558-3564.	0.2	16

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73	Random regression models to estimate genetic parameters for testâ€day milk yield in Brazilian Murrah buffaloes. Journal of Animal Breeding and Genetics, 2010, 127, 369-376.	0.8	15
74	Association between JY-1 gene polymorphisms and reproductive traits in beef cattle. Gene, 2014, 533, 477-480.	1.0	15
75	Genetic parameter estimates for temperament, heifer rebreeding, and stayability in Nellore cattle. Livestock Science, 2017, 206, 45-50.	0.6	15
76	Prediction of meat quality traits in Nelore cattle by near-infrared reflectance spectroscopy1. Journal of Animal Science, 2018, 96, 4229-4237.	0.2	15
77	Research Article Genomic regions and genes associated with carcass quality in Nelore cattle. Genetics and Molecular Research, 2019, 18, .	0.3	15
78	Improving genomic prediction accuracy for meat tenderness in Nellore cattle using artificial neural networks. Journal of Animal Breeding and Genetics, 2020, 137, 438-448.	0.8	15
79	Polymorphisms in TOX and NCOA2 genes and their associations with reproductive traits in cattle. Reproduction, Fertility and Development, 2015, 27, 523.	0.1	14
80	Fat Deposition, Fatty Acid Composition, and Its Relationship with Meat Quality and Human Health. , 0, , .		14
81	Application of single step genomic BLUP under different uncertain paternity scenarios using simulated data. PLoS ONE, 2017, 12, e0181752.	1.1	14
82	Genetic parameters for test-day yield of milk, fat and protein in buffaloes estimated by random regression models. Journal of Dairy Research, 2012, 79, 272-279.	0.7	13
83	Water buffalo genome characterization by the Illumina BovineHD BeadChip. Genetics and Molecular Research, 2014, 13, 4202-4215.	0.3	13
84	Genetic association between temperament and sexual precocity indicator traits in Nellore cattle. Journal of Applied Genetics, 2015, 56, 349-354.	1.0	13
85	Association between single nucleotide polymorphisms and sexual precocity in Nellore heifers. Animal Reproduction Science, 2017, 177, 88-96.	0.5	13
86	Genome Association Study for Visual Scores in Nellore Cattle Measured at Weaning. BMC Genomics, 2019, 20, 150.	1.2	13
87	Transcriptome profiling of muscle in Nelore cattle phenotypically divergent for the ribeye muscle area. Genomics, 2020, 112, 1257-1263.	1.3	13
88	Genomic reaction norm models exploiting genotypeÂÃ—Âenvironment interaction on sexual precocity indicator traits in Nellore cattle. Animal Genetics, 2020, 51, 210-223.	0.6	13
89	Performance of growing cattle grazing moderate quality legume - grass temperate pastures when offered varying forage allowance with or without grain supplementation. Australian Journal of Experimental Agriculture, 2006, 46, 793.	1.0	12
90	Multiple-trait random regression models for the estimation of genetic parameters for milk, fat, and protein yield in buffaloes. Journal of Dairy Science, 2013, 96, 5923-5932.	1.4	12

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91	Reaction norms for the study of genotype-environment interaction for growth and indicator traits of sexual precocity in Nellore cattle. Genetics and Molecular Research, 2015, 14, 7151-7162.	0.3	12
92	Genome-wide association study provides insights into genes related with horn development in Nelore beef cattle. PLoS ONE, 2018, 13, e0202978.	1.1	12
93	Effects of supplementation strategies during the growing phase on meat quality of beef cattle finished in different systems. Livestock Science, 2021, 247, 104465.	0.6	12
94	Estimativas de parÃ¢metros genÃ©ticos para caracterÃsticas de crescimento em bovinos da raÃ§a Canchim utilizando modelos de dimensÃ£o finita. Revista Brasileira De Zootecnia, 2010, 39, 2409-2417.	0.3	11
95	Milk fatty acid characterization and genetic parameter estimates for milk conjugated linoleic acid in buffaloes. Journal of Dairy Research, 2011, 78, 178-183.	0.7	11
96	Genetic parameter estimates for live weight and daily live weight gain obtained for Nellore bulls in a test station using different models. Livestock Science, 2012, 144, 148-156.	0.6	11
97	Genome-wide associations and detection of candidate genes for direct and maternal genetic effects influencing growth traits in the Montana TropicalÂ® Composite population. Livestock Science, 2019, 229, 64-76.	0.6	11
98	Effects of n-3 and n-6 feeding sources on the quality and lipid oxidation of meat from feedlot-finished Bos indicus steers. Meat Science, 2020, 161, 107966.	2.7	11
99	Genetic correlation estimates between age at puberty and growth, reproductive, and carcass traits in young Nelore bulls. Livestock Science, 2020, 241, 104266.	0.6	11
100	Genomic prediction ability for feed efficiency traits using different models and pseudo-phenotypes under several validation strategies in Nelore cattle. Animal, 2021, 15, 100085.	1.3	11
101	Genome-enabled prediction of meat and carcass traits using Bayesian regression, single-step genomic best linear unbiased prediction and blending methods in Nelore cattle. Animal, 2021, 15, 100006.	1.3	11
102	Genomic analysis of stayability in Nellore cattle. PLoS ONE, 2017, 12, e0179076.	1.1	11
103	First polymorphisms in JY-1 gene in cattle (Bos taurus indicus) and their association with sexual precocity and growth traits. Molecular Biology Reports, 2012, 39, 10105-10109.	1.0	10
104	Genetic parameters and investigation of genotype Ã— environment interactions in Nellore Ã— Hereford crossbred for resistance to cattle ticks in different regions of Brazil. Journal of Applied Genetics, 2015, 56, 107-113.	1.0	10
105	Genetic parameters for fatty acids in intramuscular fat from feedlot-finished Nelore carcasses. Animal Production Science, 2018, 58, 234.	0.6	10
106	Genomic regions and enrichment analyses associated with carcass composition indicator traits in Nellore cattle. Journal of Animal Breeding and Genetics, 2019, 136, 118-133.	0.8	10
107	Comparison between haplotypeâ€based and individual snpâ€based genomic predictions for beef fatty acid profile in Nelore cattle. Journal of Animal Breeding and Genetics, 2020, 137, 468-476.	0.8	10
108	Genome-wide detection of signatures of selection in indicine and Brazilian locally adapted taurine cattle breeds using whole-genome re-sequencing data. BMC Genomics, 2020, 21, 624.	1.2	10

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109	Use of gene expression profile to identify potentially relevant transcripts to myofibrillar fragmentation index trait. Functional and Integrative Genomics, 2020, 20, 609-619.	1.4	10
110	Duration of phase II of labour negatively affects maternal behaviour and lamb viability in wool-type primiparous ewes under extensive rearing. Applied Animal Behaviour Science, 2021, 234, 105207.	0.8	10
111	Genome-wide association study for beef fatty acid profile using haplotypes in Nellore cattle. Livestock Science, 2021, 245, 104396.	0.6	10
112	ParÃ¢metros genÃ©ticos de caracterÃsticas de carcaÃ§a e de crescimento de bovinos da raÃ§a Nelore. Archivos De Zootecnia, 2013, 62, 123-129.	0.2	10
113	Ivermectin Prophylaxis Used for COVID-19: A Citywide, Prospective, Observational Study of 223,128 Subjects Using Propensity Score Matching. Cureus, 2022, 14, e21272.	0.2	10
114	Characterization of novel lncRNA muscle expression profiles associated with meat quality in beef cattle. Evolutionary Applications, 2022, 15, 706-718.	1.5	10
115	Estimates of genetic parameters for scrotal circumference using random regression models in Nelore cattle. Livestock Science, 2011, 137, 205-209.	0.6	9
116	Genetic parameters of total milk yield and factors describing the shape of lactation curve in dairy buffaloes. Journal of Dairy Research, 2012, 79, 60-65.	0.7	9
117	Effects of supplementation frequency on the ruminal fermentation and enteric methane production of beef cattle grazing in tropical pastures. Revista Brasileira De Zootecnia, 2014, 43, 590-600.	0.3	9
118	Association between ACTA1 candidate gene and performance, organs and carcass traits in broilers. Poultry Science, 2015, 94, 2863-2869.	1.5	9
119	Genetic contribution of cytoplasmic lineage effect on feed efficiency in Nellore cattle. Livestock Science, 2017, 198, 52-57.	0.6	9
120	Whole cottonseed, vitamin E and finishing period affect the fatty acid profile and sensory traits of meat products from Nellore cattle. Meat Science, 2018, 138, 15-22.	2.7	8
121	Effect of growth path on the performance and carcass traits of Hereford steers finished either on pasture or in feedlot. Animal Production Science, 2018, 58, 1341.	0.6	8
122	Genetic parameter estimates for gastrointestinal nematode parasite resistance and maternal efficiency indicator traits in Santa InÃªs breed. Journal of Animal Breeding and Genetics, 2019, 136, 495-504.	0.8	8
123	Prediction of genomic breeding values for reproductive traits in Nellore heifers. Theriogenology, 2019, 125, 12-17.	0.9	8
124	Selection criteria for feed efficiency-related traits and their association with growth, reproductive and carcass traits in Nelore cattle. Animal Production Science, 2021, 61, 1633-1642.	0.6	8
125	Early growth, backfat thickness and body condition has major effect on early heifer pregnancy in Nellore cattle. Anais Da Academia Brasileira De Ciencias, 2022, 94, e20191559.	0.3	8
126	Characterization of the Exonic Regions of the <scp>JY</scp>â€1 Gene in Zebu Cattle and Buffaloes. Reproduction in Domestic Animals, 2013, 48, 918-922.	0.6	7

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127	Genomic study for maternal related traits in Santa InÃªs sheep breed. Livestock Science, 2018, 217, 76-84.	0.6	7
128	Differentially expressed genes identified through RNAâ€seq with extreme values of principal components for beef fatty acid in Nelore cattle. Journal of Animal Breeding and Genetics, 2021, 138, 80-90.	0.8	7
129	Metafounders May Reduce Bias in Composite Cattle Genomic Predictions. Frontiers in Genetics, 2021, 12, 678587.	1.1	7
130	Breeding value accuracy estimates for growth traits using random regression and multi-trait models in Nelore cattle. Genetics and Molecular Research, 2011, 10, 1227-1236.	0.3	7
131	Multi-trait and random regression mature weight heritability and breeding value estimates in Nelore cattle. South African Journal of Animal Sciences, 2010, 39, .	0.2	6
132	AplicaÃ§Ã£o de modelos nÃ£o-lineares para descrever a evoluÃ§Ã£o de caracterÃsticas de crescimento e carcaÃ§a em bovinos da raÃ§a Hereford. Ciencia Rural, 2013, 43, 513-519.	0.3	6
133	Reducing supplementation frequency for Nellore beef steers grazing tropical pastures. Scientia Agricola, 2014, 71, 105-113.	0.6	6
134	Estimates of genetic parameters for total milk yield over multiple ages in Brazilian Murrah buffaloes using different models. Genetics and Molecular Research, 2014, 13, 2784-2795.	0.3	6
135	Estimates of genetic parameters for growth traits in Brahman cattle using random regression and multitrait models1. Journal of Animal Science, 2015, 93, 3814-3819.	0.2	6
136	Genetic parameter estimates for prenatal and postnatal mortality in Nellore cattle. Journal of Animal Breeding and Genetics, 2017, 134, 27-33.	0.8	6
137	Ovulation and ovulation rate in ewes under grazing conditions: factors affecting the response to short-term supplementation. Animal, 2021, 15, 100100.	1.3	6
138	Genomic prediction ability for carcass composition indicator traits in Nellore cattle. Livestock Science, 2021, 245, 104421.	0.6	6
139	Genome-Wide Association Study Provides Insights into Important Genes for Reproductive Traits in Nelore Cattle. Animals, 2021, 11, 1386.	1.0	6
140	CorrelaÃ§Ãµes genÃ©ticas de caracterÃsticas de tamanho corporal e condiÃ§Ã£o corporal com caracterÃsticas de eficiÃªncia produtiva de fÃªmeas da raÃ§a Canchim. Revista Brasileira De Zootecnia, 2008, 37, 420-426.	0.3	6
141	Genetic correlations between heifer subsequent rebreeding and age at first calving and growth traits in Nellore cattle by Bayesian inference. Genetics and Molecular Research, 2012, 11, 4516-4524.	0.3	6
142	Identification of genomic regions related to tenderness in Nellore beef cattle. Advances in Animal Biosciences, 2017, 8, s42-s44.	1.0	5
143	Effect of early shearing during gestation on the productive and reproductive behavior of female sheep offspring in their first 18 months of age. Animal, 2020, 14, 807-813.	1.3	5
144	Genome-wide association study and predictive ability for growth traits in Nellore cattle. Livestock Science, 2020, 231, 103861.	0.6	5

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145	Effect of growth path on carcass and meat-quality traits of Hereford steers finished on pasture or in feedlot. Animal Production Science, 2020, 60, 323.	0.6	5
146	Genomic integration to identify molecular biomarkers associated with indicator traits of gastrointestinal nematode resistance in sheep. Journal of Animal Breeding and Genetics, 2022, 139, 502-516.	0.8	5
147	204 Genomic study for beef tenderness in a polled Nelore cattle population. Journal of Animal Science, 2017, 95, 101-101.	0.2	4
148	Genetic-quantitative analysis for reproductive traits in Nellor cattle selected for sexual precocity. Animal Production Science, 2020, 60, 896.	0.6	4
149	Integrating genome-wide association study and pathway analysis reveals physiological aspects affecting heifer early calving defined at different ages in Nelore cattle. Genomics, 2022, 114, 110395.	1.3	4
150	Current applications and perspectives of genomic selection in Bos indicus (Nellore) cattle. Livestock Science, 2022, 263, 105001.	0.6	4
151	Genetic parameters for milk yield ofBubalus bubalisusing unadjusted and adjusted milk production for days in milk.^{1,2}. Italian Journal of Animal Science, 2007, 6, 310-313.	0.8	3
152	Genetic Factors that Determine the Meat Fatty Acids Composition. , 0, , .		3
153	Genetic parameters and genomic regions associated with calving ease in primiparous Nellore heifers. Livestock Science, 2020, 240, 104183.	0.6	3
154	Effect of Different Selection Criteria on Performance, Carcass and Meat Quality of Nellore Young Bulls. Agriculture (Switzerland), 2021, 11, 294.	1.4	3
155	Integration analyses of structural variations and differential gene expression associated with beef fatty acid profile in Nellore cattle. Animal Genetics, 2022, 53, 570-582.	0.6	3
156	Genomic prediction ability for beef fatty acid profile in Nelore cattle using different pseudo-phenotypes. Journal of Applied Genetics, 2018, 59, 493-501.	1.0	2
157	Shearing ewes in the first third of gestation improves offspring performance. Animal Production Science, 2018, 58, 1908.	0.6	2
158	An assessment of genomic connectedness measures in Nellore cattle. Journal of Animal Science, 2020, 98, .	0.2	2
159	Genome-wide association study between copy number variation regions and carcass- and meat-quality traits in Nellore cattle. Animal Production Science, 2021, 61, 731.	0.6	2
160	Probability of pregnancy to artificial insemination either after detected oestrus or at a fixed time in dairy cows: Influence of intrinsic and extrinsic factors in a largeâ€scale, onâ€farm study. Reproduction in Domestic Animals, 2021, 56, 783-791.	0.6	2
161	Genomeâ€wide interaction study reveals epistatic interactions for beef lipidâ€related traits in Nellore cattle. Animal Genetics, 2022, 53, 35-48.	0.6	2
162	Multivariate analysis of test-day and total milk yield in goats. Genetics and Molecular Research, 2015, 14, 13719-13727.	0.3	2

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163	Transcriptome Profile Reveals Genetic and Metabolic Mechanisms Related to Essential Fatty Acid Content of Intramuscular Longissimus thoracis in Nellore Cattle. Metabolites, 2022, 12, 471.	1.3	2
164	Desempenho de bovinos em pastejo submetidos a duas frequÃªncias de suplementaÃ§Ã£o no perÃodo da seca. Acta Scientiarum - Animal Sciences, 2009, 31, .	0.3	1
165	Plane of nutrition of Corriedale ewe lambs from foetal life to the onset of breeding affects weight at service and reproductive outcome. Animal Production Science, 2015, 55, 1011.	0.6	1
166	Genetic correlations between visual slaughter conformation scores and growth and reproductive traits in Canchim cattle. Genetics and Molecular Research, 2016, 15, .	0.3	1
167	Desempenho, caracterÃsticas da carcaÃ§a e qualidade da carne de novilhos cruzados Hereford-Angus alimentados com silagem de grÃ£o Ãºmido de sorgo. Revista Brasileira De Saude E Producao Animal, 2016, 17, 685-695.	0.3	1
168	Inclusion of genomic information in estimation of genetic parameters for body weights and visual scores in Nelore cattle. Revista Brasileira De Zootecnia, 2021, 50, .	0.3	1
169	Comparison of methods for predicting genomic breeding values for growth traits in Nellore cattle. Tropical Animal Health and Production, 2021, 53, 349.	0.5	1
170	Accuracy of genomic breeding values and predictive ability for postweaning liveweight and age at first calving in a Nellore cattle population with missing sire information. Tropical Animal Health and Production, 2021, 53, 432.	0.5	1
171	Effect of quality control, density and allele frequency of markers on the accuracy of genomic prediction for complex traits in Nellore cattle. Animal Production Science, 2019, 59, 48.	0.6	1
172	Inclusion of cytoplasmic lineage effect and direct-maternal genetic covariance for genetic evaluation of growth traits in Nellore cattle. Genetics and Molecular Research, 2016, 15, .	0.3	1
173	EvaluaciÃ³n de panel SNP en genes candidatos de vÃas metabÃ³licas para carne en Hereford. Archivos De Zootecnia, 2014, 63, 73-84.	0.2	1
174	PSIII-10 Economic impact from the use of genetically evaluated registered animals-PO and with special certificate of identification and production-PODIUM in brazilian savannah. Journal of Animal Science, 2020, 98, 233-234.	0.2	1
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