Guilherme J. M. Rosa

List of Publications by Year
in descending order

234 papers	7,986 citations	47006 47 h-index	69250 77 g-index
243 all docs	243 docs citations	243 times ranked	7262 citing authors

#	Article	IF	Citations
1	Synchronization rate, size of the ovulatory follicle, and pregnancy rate after synchronization of ovulation beginning on different days of the estrous cycle in lactating dairy cows. Theriogenology, 1999, 52, 1067-1078.	2.1	715
2	Comparison of Ovarian Function and Circulating Steroids in Estrous Cycles of Holstein Heifers and Lactating Cows. Journal of Dairy Science, 2004, 87, 905-920.	3.4	322
3	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. Genetical Research, 2010, 92, 295-308.	0.9	319
4	A powerful and flexible linear mixed model framework for the analysis of relative quantification RT-PCR data. Genomics, 2009, 94, 146-152.	2.9	210
5	The transcriptome of human oocytes. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14027-14032.	7.1	177
6	Reproducing kernel Hilbert spaces regression: A general framework for genetic evaluation1. Journal of Animal Science, 2009, 87, 1883-1887.	0.5	156
7	Glucosamine and chondroitin sulfate regulate gene expression and synthesis of nitric oxide and prostaglandin E2 in articular cartilage explants. Osteoarthritis and Cartilage, 2005, 13, 387-394.	1.3	155
8	Ovarian Structures and Circulating Steroids in Heifers and Lactating Cows in Summer and Lactating and Dry Cows in Winter. Journal of Dairy Science, 2002, 85, 2813-2822.	3.4	145
9	Technical note: An R package for fitting generalized linear mixed models in animal breeding1. Journal of Animal Science, 2010, 88, 497-504.	0.5	128
10	Robust Linear Mixed Models with Normal/Independent Distributions and Bayesian MCMC Implementation. Biometrical Journal, 2003, 45, 573-590.	1.0	115
11	Mutations in the STAT5A Gene Are Associated with Embryonic Survival and Milk Composition in Cattle. Journal of Dairy Science, 2008, 91, 784-793.	3.4	111
12	Nonparametric Methods for Incorporating Genomic Information Into Genetic Evaluations: An Application to Mortality in Broilers. Genetics, 2008, 178, 2305-2313.	2.9	110
13	Predictive ability of direct genomic values for lifetime net merit of Holstein sires using selected subsets of single nucleotide polymorphism markers. Journal of Dairy Science, 2009, 92, 5248-5257.	3.4	108
14	Enviromics in breeding: applications and perspectives on envirotypic-assisted selection. Theoretical and Applied Genetics, 2021, 134, 95-112.	3.6	103
15	Inferring causal phenotype networks using structural equation models. Genetics Selection Evolution, 2011, 43, 6.	3.0	101
16	Searching for Recursive Causal Structures in Multivariate Quantitative Genetics Mixed Models. Genetics, 2010, 185, 633-644.	2.9	96
17	The Association of Bovine PPARGC1A and OPN Genes with Milk Composition in Two Independent Holstein Cattle Populations. Journal of Dairy Science, 2007, 90, 2966-2970.	3.4	95
18	Machine learning classification procedure for selecting SNPs in genomic selection: application to early mortality in broilers. Journal of Animal Breeding and Genetics, 2007, 124, 377-389.	2.0	95

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19	Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. Journal of Dairy Science, 2010, 93, 5423-5435.	3.4	85
20	Application of support vector regression to genome-assisted prediction of quantitative traits. Theoretical and Applied Genetics, 2011, 123, 1065-1074.	3.6	82
21	One Hundred Years of Statistical Developments in Animal Breeding. Annual Review of Animal Biosciences, 2015, 3, 19-56.	7.4	81
22	Deep Learning image segmentation for extraction of fish body measurements and prediction of body weight and carcass traits in Nile tilapia. Computers and Electronics in Agriculture, 2020, 170, 105274.	7.7	79
23	Identification of Small Molecules from Human Embryonic Stem Cells Using Metabolomics. Stem Cells and Development, 2007, 16, 869-882.	2.1	75
24	Automated computer vision system to predict body weight and average daily gain in beef cattle during growing and finishing phases. Livestock Science, 2020, 232, 103904.	1.6	75
25	Defining window-boundaries for genomic analyses using smoothing spline techniques. Genetics Selection Evolution, 2015, 47, 30.	3.0	72
26	Predictive ability of subsets of single nucleotide polymorphisms with and without parent average in US Holsteins. Journal of Dairy Science, 2010, 93, 5942-5949.	3.4	71
27	Prediction of body mass index in mice using dense molecular markers and a regularized neural network. Genetical Research, 2011, 93, 189-201.	0.9	67
28	Modeling relationships between calving traits: a comparison between standard and recursive mixed models. Genetics Selection Evolution, 2010, 42, 1.	3.0	66
29	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. Frontiers in Genetics, 2019, 10, 1197.	2.3	64
30	Prediction of Plant Height in *Arabidopsis thaliana* Using DNA Methylation Data. Genetics, 2015, 201, 779-793.	2.9	61
31	Evidence for a Novel Gene Expression Program in Peripheral Blood Mononuclear Cells from *Mycobacterium avium* subsp. *paratuberculosis* -Infected Cattle. Infection and Immunity, 2003, 71, 6487-6498.	2.2	60
32	Quantitative trait loci mapping in an F2 Duroc Ã— Pietrain resource population: I. Growth traits1. Journal of Animal Science, 2008, 86, 241-253.	0.5	59
33	Image Analysis and Computer Vision Applications in Animal Sciences: An Overview. Frontiers in Veterinary Science, 2020, 7, 551269.	2.2	59
34	Microarray analysis of gene expression in blood neutrophils of parturient cows. Physiological Genomics, 2004, 16, 212-221.	2.3	58
35	Reassessing Design and Analysis of two-Colour Microarray Experiments Using Mixed Effects Models. Comparative and Functional Genomics, 2005, 6, 123-131.	2.0	58
36	A genomeâ€wide association study using selective DNA pooling identifies candidate markers for fertility in Holstein cattle. Animal Genetics, 2010, 41, 570-578.	1.7	58

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37	Antioxidant defense in rat brain regions after developmental lead exposure. Toxicology, 2001, 169, 145-151.	4.2	57
38	Is Structural Equation Modeling Advantageous for the Genetic Improvement of Multiple Traits?. Genetics, 2013, 194, 561-572.	2.9	56
39	Identification of a novel gene set in human cumulus cells predictive of an oocyte's pregnancy potential. Fertility and Sterility, 2013, 99, 745-752.e6.	1.0	56
40	Additive genetic relationships between scrotal circumference, heifer pregnancy, and stayability in Nellore cattle. Journal of Animal Science, 2010, 88, 3809-3813.	0.5	55
41	Mining data from milk infrared spectroscopy to improve feed intake predictions in lactating dairy cows. Journal of Dairy Science, 2018, 101, 5878-5889.	3.4	55
42	Genome-assisted prediction of a quantitative trait measured in parents and progeny: application to food conversion rate in chickens. Genetics Selection Evolution, 2009, 41, 3.	3.0	54
43	A novel automated system to acquire biometric and morphological measurements and predict body weight of pigs via 3D computer vision1. Journal of Animal Science, 2019, 97, 496-508.	0.5	54
44	Transcriptome of Local Innate and Adaptive Immunity during Early Phase of Infectious Bronchitis Viral Infection. Viral Immunology, 2006, 19, 768-774.	1.3	53
45	Noninvasive Estimation of Black Bear Abundance Incorporating Genotyping Errors and Harvested Bear. Journal of Wildlife Management, 2007, 71, 2684-2693.	1.8	53
46	Exploring Biological Relationships Between Calving Traits in Primiparous Cattle with a Bayesian Recursive Model. Genetics, 2009, 181, 277-287.	2.9	50
47	A Comprehensive Genetic Approach for Improving Prediction of Skin Cancer Risk in Humans. Genetics, 2012, 192, 1493-1502.	2.9	50
48	Predicting expected progeny difference for marbling score in Angus cattle using artificial neural networks and Bayesian regression models. Genetics Selection Evolution, 2013, 45, 34.	3.0	50
49	Genomic prediction of breeding values for carcass traits in Nellore cattle. Genetics Selection Evolution, 2016, 48, 7.	3.0	48
50	Transcriptional reprogramming of somatic cell nuclei during preimplantation development of cloned bovine embryos. Developmental Biology, 2007, 305, 637-649.	2.0	47
51	Study of stayability in Nellore cows using a threshold model1. Journal of Animal Science, 2007, 85, 1780-1786.	0.5	46
52	Bayesian Longitudinal Data Analysis with Mixed Models and Thick-tailed Distributions using MCMC. Journal of Applied Statistics, 2004, 31, 855-873.	1.3	45
53	Genome-Wide Linkage Analysis of Global Gene Expression in Loin Muscle Tissue Identifies Candidate Genes in Pigs. PLoS ONE, 2011, 6, e16766.	2.5	45
54	Inferring Quantitative Trait Pathways Associated with Bull Fertility from a Genome-Wide Association Study. Frontiers in Genetics, 2012, 3, 307.	2.3	45

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55	Radial basis function regression methods for predicting quantitative traits using SNP markers. Genetical Research, 2010, 92, 209-225.	0.9	43
56	Dimension reduction and variable selection for genomic selection: application to predicting milk yield in Holsteins. Journal of Animal Breeding and Genetics, 2011, 128, 247-257.	2.0	43
57	Technical Note: An R package for fitting Bayesian regularized neural networks with applications in animal breeding1. Journal of Animal Science, 2013, 91, 3522-3531.	0.5	43
58	Estimation of the variance due to parent-of-origin effects for productive and reproductive traits in Lori-Bakhtiari sheep. Small Ruminant Research, 2018, 160, 95-102.	1.2	42
59	Glucocorticoid Modulation of Bcl-2 Family Members A1 and Bak during Delayed Spontaneous Apoptosis of Bovine Blood Neutrophils. Endocrinology, 2006, 147, 3826-3834.	2.8	40
60	An ensemble-based approach to imputation of moderate-density genotypes for genomic selection with application to Angus cattle. Genetical Research, 2012, 94, 133-150.	0.9	40
61	Analysis of the bovine neutrophil transcriptome during glucocorticoid treatment. Physiological Genomics, 2006, 28, 97-112.	2.3	39
62	Genome-wide association analysis in dogs implicates 99 loci as risk variants for anterior cruciate ligament rupture. PLoS ONE, 2017, 12, e0173810.	2.5	39
63	Early-lactation diseases and fertility in 2 seasons of calving across US dairy herds. Journal of Dairy Science, 2020, 103, 10560-10576.	3.4	39
64	Predictive ability of genome-assisted statistical models under various forms of gene action. Scientific Reports, 2018, 8, 12309.	3.3	38
65	Genetic evaluation of susceptibility to clinical mastitis in Spanish Holstein cows. Journal of Dairy Science, 2009, 92, 3472-3480.	3.4	37
66	Review of microarray experimental design strategies for genetical genomics studies. Physiological Genomics, 2006, 28, 15-23.	2.3	35
67	Using multiple regression, Bayesian networks and artificial neural networks for prediction of total egg production in European quails based on earlier expressed phenotypes. Poultry Science, 2015, 94, 772-780.	3.4	35
68	Medidas objetivas e composição tecidual da carcaça de cordeiros alimentados com diferentes níveis de energia em creep feeding. Revista Brasileira De Zootecnia, 2003, 32, 1380-1390.	0.8	34
69	Accuracy of Genome-Enabled Prediction in a Dairy Cattle Population using Different Cross-Validation Layouts. Frontiers in Genetics, 2012, 3, 27.	2.3	33
70	Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. Genetics Selection Evolution, 2013, 45, 17.	3.0	33
71	Design of Microarray Experiments for Genetical Genomics Studies. Genetics, 2006, 174, 945-957.	2.9	32
72	Comparison of selective genotyping strategies for prediction of breeding values in a population undergoing selection. Journal of Animal Science, 2012, 90, 4716-4722.	0.5	32

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73	Pathway-based genome-wide association analysis of milk coagulation properties, curd firmness, cheese yield, and curd nutrient recovery in dairy cattle. Journal of Dairy Science, 2017, 100, 1223-1231.	3.4	32
74	A Zero-Inflated Poisson Model for Genetic Analysis of the Number of Mastitis Cases in Norwegian Red Cows. Journal of Dairy Science, 2007, 90, 5306-5315.	3.4	31
75	Genome scan for postmortem carcass traits in Nellore cattle1. Journal of Animal Science, 2016, 94, 4087-4095.	0.5	31
76	Gene expression profiling of peripheral blood mononuclear cells (PBMC) from Mycobacterium bovis infected cattle after in vitro antigenic stimulation with purified protein derivative of tuberculin (PPD). Veterinary Immunology and Immunopathology, 2006, 113, 73-89.	1.2	30
77	Upregulation of imprinted genes in mice: An insight into the intensity of gene expression and the evolution of genomic imprinting. Epigenetics, 2010, 5, 149-158.	2.7	30
78	A predictive assessment of genetic correlations between traits in chickens using markers. Genetics Selection Evolution, 2017, 49, 16.	3.0	30
79	Network analysis of swine movements in a multi-site pig production system in Iowa, USA. Preventive Veterinary Medicine, 2020, 174, 104856.	1.9	30
80	Genome-wide scan highlights the role of candidate genes on phenotypic plasticity for age at first calving in Nellore heifers. Scientific Reports, 2020, 10, 6481.	3.3	30
81	The economic cost of metritis in dairy herds. Journal of Dairy Science, 2021, 104, 3158-3168.	3.4	29
82	Pattern of Expression of the Uterine Milk Protein Gene and its Association with Productive Life in Dairy Cattle. Journal of Dairy Science, 2007, 90, 2427-2433.	3.4	27
83	L_2-Boosting algorithm applied to high-dimensional problems in genomic selection. Genetical Research, 2010, 92, 227-237.	0.9	27
84	BREEDING AND GENETICS SYMPOSIUM: Inferring causal effects from observational data in livestock1,2. Journal of Animal Science, 2013, 91, 553-564.	0.5	27
85	Dissection of additive genetic variability for quantitative traits in chickens using SNP markers. Journal of Animal Breeding and Genetics, 2014, 131, 183-193.	2.0	27
86	Searching for causal networks involving latent variables in complex traits: Application to growth, carcass, and meat quality traits in pigs1. Journal of Animal Science, 2015, 93, 4617-4623.	0.5	27
87	Marker-assisted prediction of non-additive genetic values. Genetica, 2011, 139, 843-854.	1.1	26
88	Searching for phenotypic causal networks involving complex traits: an application to European quail. Genetics Selection Evolution, 2011, 43, 37.	3.0	26
89	Differential contribution of genomic regions to marked genetic variation and prediction of quantitative traits in broiler chickens. Genetics Selection Evolution, 2016, 48, 10.	3.0	26
90	Including Phenotypic Causal Networks in Genome-Wide Association Studies Using Mixed Effects Structural Equation Models. Frontiers in Genetics, 2018, 9, 455.	2.3	26

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91	Associations of reproductive indices with fertility outcomes, milk yield, and survival in Holstein cows. Journal of Dairy Science, 2020, 103, 6647-6660.	3.4	26
92	Forma fÃsica da raÃ§Ã£o e pesos de abate nas caracterÃsticas de carcaÃ§a de cordeiros em creep feeding. Revista Brasileira De Zootecnia, 2001, 30, 948-954.	0.8	26
93	Gene expression profile of mechanically impacted bovine articular cartilage explants. Journal of Orthopaedic Research, 2005, 23, 1146-1151.	2.3	25
94	Genome-wide association mapping and pathway analysis of leukosis incidence in a US Holstein cattle population. Animal Genetics, 2016, 47, 395-407.	1.7	25
95	NÃveis de vitamina C e ferro para tilÃ¡pia do nilo (Oreochromis niloticus). Revista Brasileira De Zootecnia, 2002, 31, 2149-2156.	0.8	25
96	Improvement in recovery of embryos/ova using a shallow uterine horn flushing technique in superovulated Holstein heifers. Theriogenology, 2003, 60, 1319-1330.	2.1	24
97	The Causal Meaning of Genomic Predictors and How It Affects Construction and Comparison of Genome-Enabled Selection Models. Genetics, 2015, 200, 483-494.	2.9	24
98	Exploring causal networks of bovine milk fatty acids in a multivariate mixed model context. Genetics Selection Evolution, 2014, 46, 2.	3.0	23
99	Conceptual framework for investigating causal effects from observational data in livestock1. Journal of Animal Science, 2018, 96, 4045-4062.	0.5	22
100	Interpretation of microarray data: Trudging out of the abyss towards elucidation of biological significance1. Journal of Animal Science, 2007, 85, E20-E23.	0.5	21
101	Comparative genomics between fly, mouse, and cattle identifies genes associated with sire conception rate. Journal of Dairy Science, 2012, 95, 6122-6129.	3.4	21
102	Anxiolytic effect of Rubus brasilensis in rats and mice. Journal of Ethnopharmacology, 1998, 61, 111-117.	4.1	19
103	Poisson versus threshold models for genetic analysis of clinical mastitis in US Holsteins. Journal of Dairy Science, 2009, 92, 5239-5247.	3.4	19
104	Inferring phenotypic causal structures among meat quality traits and the application of a structural equation model in Japanese Black cattle1. Journal of Animal Science, 2016, 94, 4133-4142.	0.5	19
105	Genomewide association mapping and pathway analysis of meat tenderness in Polled Nellore cattle. Journal of Animal Science, 2017, 95, 1945.	0.5	19
106	Involvement of GABAA-benzodiazepine receptor in the anxiolytic effect induced by hexanic fraction of Rubus brasiliensis. Journal of Ethnopharmacology, 1998, 61, 119-126.	4.1	18
107	Short communication: Effects of the progesterone receptor variants on fertility traits in cattle. Journal of Dairy Science, 2009, 92, 4082-4085.	3.4	18
108	A Primer on High-Throughput Computing for Genomic Selection. Frontiers in Genetics, 2011, 2, 4.	2.3	18

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109	Genome-wide association study for cheese yield and curd nutrient recovery in dairy cows. Journal of Dairy Science, 2017, 100, 1259-1271.	3.4	18
110	Genome-wide association and pathway-based analysis using latent variables related to milk protein composition and cheesemaking traits in dairy cattle. Journal of Dairy Science, 2017, 100, 9085-9102.	3.4	18
111	Record linkage for farm-level data analytics: Comparison of deterministic, stochastic and machine learning methods. Computers and Electronics in Agriculture, 2019, 163, 104857.	7.7	18
112	Comparison of data analytics strategies in computer vision systems to predict pig body composition traits from 3D images. Journal of Animal Science, 2020, 98, .	0.5	18
113	Structural equation modeling for investigating multi-trait genetic architecture of udder health in dairy cattle. Scientific Reports, 2020, 10, 7751.	3.3	18
114	On Reference Designs For Microarray Experiments. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article36.	0.6	17
115	Comparison of classification methods for detecting associations between SNPs and chick mortality. Genetics Selection Evolution, 2009, 41, 18.	3.0	17
116	Accuracy of genomic breeding values for meat tenderness in Polled Nellore cattle1. Journal of Animal Science, 2016, 94, 2752-2760.	0.5	17
117	Effect of body condition change and health status during early lactation on performance and survival of Holstein cows. Journal of Dairy Science, 2021, 104, 12785-12799.	3.4	17
118	Long-term impacts of genome-enabled selection. Journal of Applied Genetics, 2011, 52, 467-480.	1.9	16
119	Short communication: Principal components and factor analytic models for test-day milk yield in Brazilian Holstein cattle. Journal of Dairy Science, 2012, 95, 2157-2164.	3.4	16
120	Bayesian Networks Illustrate Genomic and Residual Trait Connections in Maize (*Zea mays* L.). G3: Genes, Genomes, Genetics, 2017, 7, 2779-2789.	1.8	16
121	Multivariate genome-wide association analysis identifies novel and relevant variants associated with anterior cruciate ligament rupture risk in the dog model. BMC Genetics, 2018, 19, 39.	2.7	16
122	NÃveis de energia no desempenho e caracterÃsticas da carcaÃ§a de cordeiros alimentados em creep feeding. Revista Brasileira De Zootecnia, 2003, 32, 1371-1379.	0.8	16
123	NÃveis de feno de alfafa e forma fÃsica da raÃ§Ã£o no desempenho de cordeiros em creep feeding. Revista Brasileira De Zootecnia, 2001, 30, 941-947.	0.8	15
124	Additional support for an association between OLR1 and milk fat traits in cattle. Animal Genetics, 2007, 38, 308-310.	1.7	15
125	Causal phenotypic networks for egg traits in an F2 chicken population. Molecular Genetics and Genomics, 2019, 294, 1455-1462.	2.1	15
126	Improving genomic prediction accuracy for meat tenderness in Nellore cattle using artificial neural networks. Journal of Animal Breeding and Genetics, 2020, 137, 438-448.	2.0	15

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127	Accounting for outliers and heteroskedasticity in multibreed genetic evaluations of postweaning gain of Nelore-Hereford cattle. Journal of Animal Science, 2007, 85, 909.	0.5	15
128	An assessment of linkage disequilibrium in <scp>H</scp>olstein cattle using a <scp>B</scp>ayesian network. Journal of Animal Breeding and Genetics, 2012, 129, 474-487.	2.0	14
129	Predictive ability of alternative models for genetic analysis of clinical mastitis. Journal of Animal Breeding and Genetics, 2012, 129, 120-128.	2.0	14
130	Liver functional genomics in beef cows on grazing systems: novel genes and pathways revealed. Physiological Genomics, 2014, 46, 138-147.	2.3	14
131	Bayesian and Machine Learning Models for Genomic Prediction of Anterior Cruciate Ligament Rupture in the Canine Model. G3: Genes, Genomes, Genetics, 2020, 10, 2619-2628.	1.8	14
132	Genome‐wide association study of milk production traits in a crossbred dairy sheep population using three statistical models. Animal Genetics, 2020, 51, 624-628.	1.7	14
133	Grand Challenge in Precision Livestock Farming. Frontiers in Animal Science, 2021, 2, .	1.9	14
134	Genetic analysis of leukosis incidence in United States Holstein and Jersey populations. Journal of Dairy Science, 2013, 96, 6022-6029.	3.4	13
135	Survival in crossbred lambs: Breed and heterosis effects. Journal of Animal Science, 2015, 93, 912.	0.5	13
136	Exploring causal networks underlying fat deposition and muscularity in pigs through the integration of phenotypic, genotypic and transcriptomic data. BMC Systems Biology, 2015, 9, 58.	3.0	13
137	Assessment of bagging <scp>GBLUP</scp> for whole‐genome prediction of broiler chicken traits. Journal of Animal Breeding and Genetics, 2015, 132, 218-228.	2.0	13
138	Short communication: Genetic correlation of bovine leukosis incidence with somatic cell score and milk yield in a US Holstein population. Journal of Dairy Science, 2016, 99, 2005-2009.	3.4	13
139	Genomic mating as sustainable breeding for Chinese indigenous Ningxiang pigs. PLoS ONE, 2020, 15, e0236629.	2.5	13
140	Marker-assisted assessment of genotype by environment interaction: A case study of single nucleotide polymorphism-mortality association in broilers in two hygiene environments1. Journal of Animal Science, 2008, 86, 3358-3366.	0.5	12
141	Características reprodutivas e suas associações com outras características de importância econômica na raça Nelore. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2012, 64, 91-100.	0.4	12
142	Effect of genotype imputation on genome-enabled prediction of complex traits: an empirical study with mice data. BMC Genetics, 2014, 15, 149.	2.7	12
143	Improving accuracy of genomic prediction in Brangus cattle by adding animals with imputed low‐density <scp>SNP</scp> genotypes. Journal of Animal Breeding and Genetics, 2018, 135, 14-27.	2.0	12
144	Technical note: an R package for fitting sparse neural networks with application in animal breeding1. Journal of Animal Science, 2018, 96, 2016-2026.	0.5	12

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145	Selective Transcriptional Profiling and Data Analysis Strategies for Expression Quantitative Trait Loci Mapping in Outbred F2 Populations. Genetics, 2008, 180, 1679-1690.	2.9	11
146	Analysis of segregation distortion and association of the bovine *FGF2* with fertilization rate and early embryonic survival. Animal Genetics, 2009, 40, 722-728.	1.7	11
147	Bayesian analysis of autoregressive panel data model: application in genetic evaluation of beef cattle. Scientia Agricola, 2011, 68, 237-245.	1.2	11
148	Bootstrap study of genome-enabled prediction reliabilities using haplotype blocks across Nordic Red cattle breeds. Journal of Dairy Science, 2015, 98, 7351-7363.	3.4	11
149	Comparison of models for the genetic evaluation of reproductive traits with censored data in Nellore cattle1. Journal of Animal Science, 2016, 94, 2297-2306.	0.5	11
150	Generalized additive mixed model on the analysis of total transport losses of market-weight pigs1. Journal of Animal Science, 2019, 97, 2025-2034.	0.5	11
151	Genome‐enable prediction for health traits using high‐density SNP panel in US Holstein cattle. Animal Genetics, 2020, 51, 192-199.	1.7	11
152	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.	3.3	11
153	Genetic Control of Prolificacy and Related Traits in the Golden Glow Maize Population: I. Phenotypic Evaluation. Crop Science, 2005, 45, 1361-1369.	1.8	10
154	Estimates of genetic parameters and eigenvector indices for milk production of Holstein cows. Journal of Dairy Science, 2013, 96, 7284-7293.	3.4	10
155	Mixed Effects Structural Equation Models and Phenotypic Causal Networks. Methods in Molecular Biology, 2013, 1019, 449-464.	0.9	10
156	Cluster analyses to explore the genetic curve pattern for milk yield of Holstein. Livestock Science, 2016, 183, 28-32.	1.6	10
157	Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. Heredity, 2020, 124, 658-674.	2.6	10
158	A Bayesian approach for constructing genetic maps when markers are miscoded. Genetics Selection Evolution, 2002, 34, 353-69.	3.0	9
159	Characterization of the variable cow's age at last calving as a measurement of longevity by using the Kaplan–Meier estimator and the Cox model. Animal, 2013, 7, 540-546.	3.3	9
160	Effect of allele frequencies, effect sizes and number of markers on prediction of quantitative traits in chickens. Journal of Animal Breeding and Genetics, 2014, 131, 123-133.	2.0	9
161	Genotype×—environment interaction for weaning weight in Nellore cattle using reaction norm analysis. Livestock Science, 2015, 176, 40-46.	1.6	9
162	Research Article Bayesian analyses of genetic parameters for growth traits in Nellore cattle raised on pasture.. Genetics and Molecular Research, 2017, 16, .	0.2	9

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163	Investigating causal biological relationships between reproductive performance traits in high-performing gilts and sows1. Journal of Animal Science, 2019, 97, 2385-2401.	0.5	9
164	Beef production from cull dairy cows: a review from culling to consumption. Journal of Animal Science, 2021, 99, .	0.5	9
165	248 Application of computer vision and data analytics strategies for prediction of carcass composition in live pigs. Journal of Animal Science, 2020, 98, 178-178.	0.5	9
166	Subsampling Hair Samples Affects Accuracy and Precision of DNA-Based Population Estimates. Journal of Wildlife Management, 2009, 73, 1184-1188.	1.8	8
167	A GWAS assessment of the contribution of genomic imprinting to the variation of body mass index in mice. BMC Genomics, 2015, 16, 576.	2.8	8
168	Incorporating parent-of-origin effects in whole-genome prediction of complex traits. Genetics Selection Evolution, 2016, 48, 34.	3.0	8
169	Estimation of Genomic Breed Composition for Purebred and Crossbred Animals Using Sparsely Regularized Admixture Models. Frontiers in Genetics, 2020, 11, 576.	2.3	8
170	Sampling strategies for total bacterial count of unpasteurized bulk milk. Journal of Dairy Science, 2012, 95, 2326-2335.	3.4	7
171	Inferring phenotypic causal structure among farrowing and weaning traits in pigs. Animal Science Journal, 2020, 91, e13369.	1.4	7
172	Structural equation modeling for unraveling the multivariate genomic architecture of milk proteins in dairy cattle. Journal of Dairy Science, 2021, 104, 5705-5718.	3.4	7
173	Editorial: High-Throughput Phenotyping in the Genomic Improvement of Livestock. Frontiers in Genetics, 2021, 12, 707343.	2.3	7
174	Disentangling data dependency using cross-validation strategies to evaluate prediction quality of cattle grazing activities using machine learning algorithms and wearable sensor data. Journal of Animal Science, 2021, 99, .	0.5	7
175	Delineamento de experimentos em genÃ©tica genÃ´mica. Revista Brasileira De Zootecnia, 2007, 36, 211-218.	0.8	6
176	Predictive ability of models for calving difficulty in US Holsteins. Journal of Animal Breeding and Genetics, 2009, 126, 179-188.	2.0	6
177	Zero-inflated Poisson regression models for QTL mapping applied to tick-resistance in a Gyr x Holstein F2 population. Genetics and Molecular Biology, 2011, 34, 575-582.	1.3	6
178	Relationship between calving difficulty and fertility traits in firstâ€parity Iranian Holsteins under standard and recursive models. Journal of Animal Breeding and Genetics, 2016, 133, 513-522.	2.0	6
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