

Guilherme J. M. Rosa

List of Publications by Year in descending order

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Version: 2024-02-01

234
papers

7,986
citations

53939

47
h-index

78623

77
g-index

243
all docs

243
docs citations

243
times ranked

7918
citing authors

#	ARTICLE	IF	CITATIONS
1	Economic values of reproductive, growth, feed efficiency and carcass traits in Nelore cattle. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 170-180.	0.8	5
2	Investigating potential causal relationships among carcass and meat quality traits using structural equation model in Nelore cattle. <i>Meat Science</i> , 2022, 187, 108771.	2.7	4
3	Predictive assessment of single-step BLUP with linear and non-linear similarity RKHS kernels: A case study in chickens. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 247-258.	0.8	3
4	Role of CSN2, CSN3, and BLG genes and the polygenic background in the cattle milk protein profile. <i>Journal of Dairy Science</i> , 2022, , .	1.4	4
5	A Random Forest-Based Genome-Wide Scan Reveals Fertility-Related Candidate Genes and Potential Inter-Chromosomal Epistatic Regions Associated With Age at First Calving in Nelore Cattle. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	1
6	Assessment of alternative models for genetic analysis of worm and tick infestation in nelore cattle. <i>Livestock Science</i> , 2021, 244, 104276.	0.6	1
7	Enviromics in breeding: applications and perspectives on envirotypic-assisted selection. <i>Theoretical and Applied Genetics</i> , 2021, 134, 95-112.	1.8	103
8	Grand Challenge in Precision Livestock Farming. <i>Frontiers in Animal Science</i> , 2021, 2, .	0.8	14
9	The economic cost of metritis in dairy herds. <i>Journal of Dairy Science</i> , 2021, 104, 3158-3168.	1.4	29
10	Structural equation modeling for unraveling the multivariate genomic architecture of milk proteins in dairy cattle. <i>Journal of Dairy Science</i> , 2021, 104, 5705-5718.	1.4	7
11	Beef production from cull dairy cows: a review from culling to consumption. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	9
12	Editorial: High-Throughput Phenotyping in the Genomic Improvement of Livestock. <i>Frontiers in Genetics</i> , 2021, 12, 707343.	1.1	7
13	Disentangling data dependency using cross-validation strategies to evaluate prediction quality of cattle grazing activities using machine learning algorithms and wearable sensor data. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	7
14	Effect of body condition change and health status during early lactation on performance and survival of Holstein cows. <i>Journal of Dairy Science</i> , 2021, 104, 12785-12799.	1.4	17
15	Nonlinear modeling to describe the pattern of 15 milk protein and nonprotein compounds over lactation in dairy cows. <i>Journal of Dairy Science</i> , 2021, 104, 10950-10969.	1.4	5
16	Genome-enabled prediction of meat and carcass traits using Bayesian regression, single-step genomic best linear unbiased prediction and blending methods in Nelore cattle. <i>Animal</i> , 2021, 15, 100006.	1.3	11
17	The effect of life history events on carcass merit and price of cull dairy cows. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	3
18	Automated computer vision system to predict body weight and average daily gain in beef cattle during growing and finishing phases. <i>Livestock Science</i> , 2020, 232, 103904.	0.6	75

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19	Network analysis of swine movements in a multi-site pig production system in Iowa, USA. <i>Preventive Veterinary Medicine</i> , 2020, 174, 104856.	0.7	30
20	Would large dataset sample size unveil the potential of deep neural networks for improved genome-enabled prediction of complex traits? The case for body weight in broilers. <i>BMC Genomics</i> , 2020, 21, 771.	1.2	4
21	Comparison of data analytics strategies in computer vision systems to predict pig body composition traits from 3D images. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	18
22	Genomic mating as sustainable breeding for Chinese indigenous Ningxiang pigs. <i>PLoS ONE</i> , 2020, 15, e0236629.	1.1	13
23	Native chicken farming: A tool for wealth creation and food security in Benin. <i>International Journal of Livestock Production</i> , 2020, 11, 146-162.	0.6	2
24	A Causality Perspective of Genomic Breed Composition for Composite Animals. <i>Frontiers in Genetics</i> , 2020, 11, 546052.	1.1	4
25	Image Analysis and Computer Vision Applications in Animal Sciences: An Overview. <i>Frontiers in Veterinary Science</i> , 2020, 7, 551269.	0.9	59
26	Structural equation modeling for investigating multi-trait genetic architecture of udder health in dairy cattle. <i>Scientific Reports</i> , 2020, 10, 7751.	1.6	18
27	Genome-wide scan highlights the role of candidate genes on phenotypic plasticity for age at first calving in Nellore heifers. <i>Scientific Reports</i> , 2020, 10, 6481.	1.6	30
28	Inferring phenotypic causal networks for tick infestation, <i>Babesia bovis</i> infection, and weight gain in Hereford and Braford cattle using structural equation models. <i>Livestock Science</i> , 2020, 238, 104032.	0.6	3
29	Estimation of Genomic Breed Composition for Purebred and Crossbred Animals Using Sparsely Regularized Admixture Models. <i>Frontiers in Genetics</i> , 2020, 11, 576.	1.1	8
30	Inferring phenotypic causal structure among farrowing and weaning traits in pigs. <i>Animal Science Journal</i> , 2020, 91, e13369.	0.6	7
31	Bayesian and Machine Learning Models for Genomic Prediction of Anterior Cruciate Ligament Rupture in the Canine Model. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2619-2628.	0.8	14
32	Associations of reproductive indices with fertility outcomes, milk yield, and survival in Holstein cows. <i>Journal of Dairy Science</i> , 2020, 103, 6647-6660.	1.4	26
33	Genome-wide association study of milk production traits in a crossbred dairy sheep population using three statistical models. <i>Animal Genetics</i> , 2020, 51, 624-628.	0.6	14
34	Estimation of genomic breed composition of individual animals in composite beef cattle. <i>Animal Genetics</i> , 2020, 51, 457-460.	0.6	5
35	Deep Learning image segmentation for extraction of fish body measurements and prediction of body weight and carcass traits in Nile tilapia. <i>Computers and Electronics in Agriculture</i> , 2020, 170, 105274.	3.7	79
36	Integration of single nucleotide variants and whole-genome DNA methylation profiles for classification of rheumatoid arthritis cases from controls. <i>Heredity</i> , 2020, 124, 658-674.	1.2	10

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37	Improving genomic prediction accuracy for meat tenderness in Nellore cattle using artificial neural networks. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 438-448.	0.8	15
38	Genome-enabled prediction for health traits using high-density SNP panel in US Holstein cattle. <i>Animal Genetics</i> , 2020, 51, 192-199.	0.6	11
39	Forecasting beef production and quality using large-scale integrated data from Brazil. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	6
40	248 Application of computer vision and data analytics strategies for prediction of carcass composition in live pigs. <i>Journal of Animal Science</i> , 2020, 98, 178-178.	0.2	9
41	Early-lactation diseases and fertility in 2 seasons of calving across US dairy herds. <i>Journal of Dairy Science</i> , 2020, 103, 10560-10576.	1.4	39
42	169 Investigating relationships between weather variables and dry matter intake of beef cattle in feedlot. <i>Journal of Animal Science</i> , 2020, 98, 124-125.	0.2	0
43	163 Investigating relationships between life history events, carcass quality and price of cull dairy cows sold through auction markets. <i>Journal of Animal Science</i> , 2020, 98, 135-135.	0.2	0
44	PSXI-5 Best production practices for improvement of Beef Cattle carcass quality. <i>Journal of Animal Science</i> , 2020, 98, 384-384.	0.2	0
45	PSXI-22 Prediction quality of cattle behavior traits evaluated through different cross-validation strategies using wearable sensor data and machine learning algorithms. <i>Journal of Animal Science</i> , 2020, 98, 383-383.	0.2	0
46	Record linkage for farm-level data analytics: Comparison of deterministic, stochastic and machine learning methods. <i>Computers and Electronics in Agriculture</i> , 2019, 163, 104857.	3.7	18
47	Genotype by environment interaction across time for Nile tilapia, from juvenile to finishing stages, reared in different production systems. <i>Aquaculture</i> , 2019, 513, 734429.	1.7	6
48	Causal phenotypic networks for egg traits in an F2 chicken population. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1455-1462.	1.0	15
49	Genomic prediction of bovine leukosis incidence in a US Holstein population. <i>Livestock Science</i> , 2019, 225, 73-77.	0.6	2
50	Generalized additive mixed model on the analysis of total transport losses of market-weight pigs ¹ . <i>Journal of Animal Science</i> , 2019, 97, 2025-2034.	0.2	11
51	Investigating causal biological relationships between reproductive performance traits in high-performing gilts and sows ¹ . <i>Journal of Animal Science</i> , 2019, 97, 2385-2401.	0.2	9
52	PSXI-41 Investigating the relationship between life history factors, live animal auction price, and carcass quality of cull dairy cows. <i>Journal of Animal Science</i> , 2019, 97, 184-184.	0.2	0
53	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. <i>Frontiers in Genetics</i> , 2019, 10, 1197.	1.1	64
54	227 Leveraging on high-throughput phenotyping technologies to optimize livestock genetic improvement and husbandry. <i>Journal of Animal Science</i> , 2019, 97, 55-55.	0.2	2

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55	151 Use of an automated computer vision system to predict body weight and average daily gain in beef cattle in different phases of growth development. <i>Journal of Animal Science</i> , 2019, 97, 150-151.	0.2	0
56	A novel automated system to acquire biometric and morphological measurements and predict body weight of pigs via 3D computer vision1. <i>Journal of Animal Science</i> , 2019, 97, 496-508.	0.2	54
57	Effect of quality control, density and allele frequency of markers on the accuracy of genomic prediction for complex traits in Nelore cattle. <i>Animal Production Science</i> , 2019, 59, 48.	0.6	1
58	Estimation of the variance due to parent-of-origin effects for productive and reproductive traits in Lori-Bakhtiari sheep. <i>Small Ruminant Research</i> , 2018, 160, 95-102.	0.6	42
59	Improving accuracy of genomic prediction in Brangus cattle by adding animals with imputed low-density SNP genotypes. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 14-27.	0.8	12
60	Mining data from milk infrared spectroscopy to improve feed intake predictions in lactating dairy cows. <i>Journal of Dairy Science</i> , 2018, 101, 5878-5889.	1.4	55
61	Technical note: an R package for fitting sparse neural networks with application in animal breeding1. <i>Journal of Animal Science</i> , 2018, 96, 2016-2026.	0.2	12
62	Estimation of genetic parameters for cow age at last calving under different censorship criteria. <i>Livestock Science</i> , 2018, 208, 40-43.	0.6	2
63	Including Phenotypic Causal Networks in Genome-Wide Association Studies Using Mixed Effects Structural Equation Models. <i>Frontiers in Genetics</i> , 2018, 9, 455.	1.1	26
64	Predictive ability of genome-assisted statistical models under various forms of gene action. <i>Scientific Reports</i> , 2018, 8, 12309.	1.6	38
65	Conceptual framework for investigating causal effects from observational data in livestock1. <i>Journal of Animal Science</i> , 2018, 96, 4045-4062.	0.2	22
66	Multivariate genome-wide association analysis identifies novel and relevant variants associated with anterior cruciate ligament rupture risk in the dog model. <i>BMC Genetics</i> , 2018, 19, 39.	2.7	16
67	A predictive assessment of genetic correlations between traits in chickens using markers. <i>Genetics Selection Evolution</i> , 2017, 49, 16.	1.2	30
68	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
69	Evaluation of longevity modeling censored records in Nelore. <i>Animal</i> , 2017, 11, 2113-2119.	1.3	3
70	Genome-wide association study for cheese yield and curd nutrient recovery in dairy cows. <i>Journal of Dairy Science</i> , 2017, 100, 1259-1271.	1.4	18
71	Pathway-based genome-wide association analysis of milk coagulation properties, curd firmness, cheese yield, and curd nutrient recovery in dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 1223-1231.	1.4	32
72	Causal effect of prolificacy on milk yield in dairy sheep using propensity score. <i>Journal of Dairy Science</i> , 2017, 100, 8443-8450.	1.4	3

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73	Genome-wide association and pathway-based analysis using latent variables related to milk protein composition and cheesemaking traits in dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 9085-9102.	1.4	18
74	Bayesian Networks Illustrate Genomic and Residual Trait Connections in Maize (<i>Zea mays</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2779-2789.	0.8	16
75	Estimation of genetic parameters for longevity considering the cow's age at last calving. <i>Journal of Applied Genetics</i> , 2017, 58, 103-109.	1.0	3
76	Research Article Bayesian analyses of genetic parameters for growth traits in Nellore cattle raised on pasture. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.3	9
77	Genome-wide association analysis in dogs implicates 99 loci as risk variants for anterior cruciate ligament rupture. <i>PLoS ONE</i> , 2017, 12, e0173810.	1.1	39
78	748 Mining farm- and animal-level data to optimize beef cattle production. <i>Journal of Animal Science</i> , 2017, 95, 363-363.	0.2	2
79	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
80	Accuracy of genomic breeding values for meat tenderness in Polled Nellore cattle. <i>Journal of Animal Science</i> , 2016, 94, 2752-2760.	0.2	17
81	Genome-wide association mapping and pathway analysis of leukosis incidence in a US Holstein cattle population. <i>Animal Genetics</i> , 2016, 47, 395-407.	0.6	25
82	Relationship between calving difficulty and fertility traits in first-parity Iranian Holsteins under standard and recursive models. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 513-522.	0.8	6
83	Comparison of models for the genetic evaluation of reproductive traits with censored data in Nellore cattle. <i>Journal of Animal Science</i> , 2016, 94, 2297-2306.	0.2	11
84	Applications of Graphical Models in Quantitative Genetics and Genomics. , 2016, , 95-116.		4
85	Genome scan for postmortem carcass traits in Nellore cattle. <i>Journal of Animal Science</i> , 2016, 94, 4087-4095.	0.2	31
86	Inferring phenotypic causal structures among meat quality traits and the application of a structural equation model in Japanese Black cattle. <i>Journal of Animal Science</i> , 2016, 94, 4133-4142.	0.2	19
87	1486 The use of artificial neural network to estimate feed intake in lactating cows through milk mid-infrared spectra of individual cow milk samples. <i>Journal of Animal Science</i> , 2016, 94, 721-722.	0.2	0
88	Bayesian Variable Selection in Multilevel Item Response Theory Models with Application in Genomics. <i>Genetic Epidemiology</i> , 2016, 40, 253-263.	0.6	2
89	Incorporating parent-of-origin effects in whole-genome prediction of complex traits. <i>Genetics Selection Evolution</i> , 2016, 48, 34.	1.2	8
90	Cluster analyses to explore the genetic curve pattern for milk yield of Holstein. <i>Livestock Science</i> , 2016, 183, 28-32.	0.6	10

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91	Differential contribution of genomic regions to marked genetic variation and prediction of quantitative traits in broiler chickens. <i>Genetics Selection Evolution</i> , 2016, 48, 10.	1.2	26
92	Genomic prediction of breeding values for carcass traits in Nellore cattle. <i>Genetics Selection Evolution</i> , 2016, 48, 7.	1.2	48
93	Short communication: Genetic correlation of bovine leukosis incidence with somatic cell score and milk yield in a US Holstein population. <i>Journal of Dairy Science</i> , 2016, 99, 2005-2009.	1.4	13
94	Survival in crossbred lambs: Breed and heterosis effects. <i>Journal of Animal Science</i> , 2015, 93, 912.	0.2	13
95	Exploring causal networks underlying fat deposition and muscularity in pigs through the integration of phenotypic, genotypic and transcriptomic data. <i>BMC Systems Biology</i> , 2015, 9, 58.	3.0	13
96	Searching for causal networks involving latent variables in complex traits: Application to growth, carcass, and meat quality traits in pigs. <i>Journal of Animal Science</i> , 2015, 93, 4617-4623.	0.2	27
97	Assessment of bagging <scp>GBLUP</scp> for whole-€genome prediction of broiler chicken traits. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 218-228.	0.8	13
98	Bootstrap study of genome-enabled prediction reliabilities using haplotype blocks across Nordic Red cattle breeds. <i>Journal of Dairy Science</i> , 2015, 98, 7351-7363.	1.4	11
99	The Causal Meaning of Genomic Predictors and How It Affects Construction and Comparison of Genome-Enabled Selection Models. <i>Genetics</i> , 2015, 200, 483-494.	1.2	24
100	Using multiple regression, Bayesian networks and artificial neural networks for prediction of total egg production in European quails based on earlier expressed phenotypes. <i>Poultry Science</i> , 2015, 94, 772-780.	1.5	35
101	Genotype-€environment interaction for weaning weight in Nellore cattle using reaction norm analysis. <i>Livestock Science</i> , 2015, 176, 40-46.	0.6	9
102	Defining window-boundaries for genomic analyses using smoothing spline techniques. <i>Genetics Selection Evolution</i> , 2015, 47, 30.	1.2	72
103	A GWAS assessment of the contribution of genomic imprinting to the variation of body mass index in mice. <i>BMC Genomics</i> , 2015, 16, 576.	1.2	8
104	Prediction of Plant Height in <i>Arabidopsis thaliana</i> Using DNA Methylation Data. <i>Genetics</i> , 2015, 201, 779-793.	1.2	61
105	One Hundred Years of Statistical Developments in Animal Breeding. <i>Annual Review of Animal Biosciences</i> , 2015, 3, 19-56.	3.6	81
106	Quantitative genetic study of age at subsequent rebreeding in Nellore cattle by using survival analysis. <i>Genetics and Molecular Research</i> , 2014, 13, 4071-4082.	0.3	1
107	Meta-Analysis of Candidate Gene Effects Using Bayesian Parametric and Non-Parametric Approaches. <i>Journal of Genomics</i> , 2014, 2, 1-19.	0.6	3
108	Liver functional genomics in beef cows on grazing systems: novel genes and pathways revealed. <i>Physiological Genomics</i> , 2014, 46, 138-147.	1.0	14

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109	Exploring causal networks of bovine milk fatty acids in a multivariate mixed model context. <i>Genetics Selection Evolution</i> , 2014, 46, 2.	1.2	23
110	Effect of genotype imputation on genome-enabled prediction of complex traits: an empirical study with mice data. <i>BMC Genetics</i> , 2014, 15, 149.	2.7	12
111	Effect of allele frequencies, effect sizes and number of markers on prediction of quantitative traits in chickens. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 123-133.	0.8	9
112	Dissection of additive genetic variability for quantitative traits in chickens using <scp>SNP</scp> markers. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 183-193.	0.8	27
113	Medidas repetidas no estudo de características de crescimento e carcaça avaliadas por ultrassom em novilhas de corte cruzadas. <i>Boletim De Indústria Animal</i> , 2014, 71, 200-210.	0.2	4
114	Is Structural Equation Modeling Advantageous for the Genetic Improvement of Multiple Traits?. <i>Genetics</i> , 2013, 194, 561-572.	1.2	56
115	Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. <i>Genetics Selection Evolution</i> , 2013, 45, 17.	1.2	33
116	Predicting expected progeny difference for marbling score in Angus cattle using artificial neural networks and Bayesian regression models. <i>Genetics Selection Evolution</i> , 2013, 45, 34.	1.2	50
117	Identification of a novel gene set in human cumulus cells predictive of an oocyte's pregnancy potential. <i>Fertility and Sterility</i> , 2013, 99, 745-752.e6.	0.5	56
118	Genetic analysis of leukosis incidence in United States Holstein and Jersey populations. <i>Journal of Dairy Science</i> , 2013, 96, 6022-6029.	1.4	13
119	Estimates of genetic parameters and eigenvector indices for milk production of Holstein cows. <i>Journal of Dairy Science</i> , 2013, 96, 7284-7293.	1.4	10
120	Mixed Effects Structural Equation Models and Phenotypic Causal Networks. <i>Methods in Molecular Biology</i> , 2013, 1019, 449-464.	0.4	10
121	Technical Note: An R package for fitting Bayesian regularized neural networks with applications in animal breeding1. <i>Journal of Animal Science</i> , 2013, 91, 3522-3531.	0.2	43
122	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. <i>Animal</i> , 2013, 7, 540-546.	1.3	9
123	Estradiol and Progesterone Exhibit Similar Patterns of Hepatic Gene Expression Regulation in the Bovine Model. <i>PLoS ONE</i> , 2013, 8, e73552.	1.1	4
124	BREEDING AND GENETICS SYMPOSIUM: Inferring causal effects from observational data in livestock1,2. <i>Journal of Animal Science</i> , 2013, 91, 553-564.	0.2	27
125	O Uso da Estatística Bayesiana no Melhoramento Genético Animal: Uma Breve Explicação. <i>Scientia Agraria Paranaensis</i> , 2013, 12, 247-257.	0.1	1
126	A Comprehensive Genetic Approach for Improving Prediction of Skin Cancer Risk in Humans. <i>Genetics</i> , 2012, 192, 1493-1502.	1.2	50

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127	An ensemble-based approach to imputation of moderate-density genotypes for genomic selection with application to Angus cattle. <i>Genetical Research</i> , 2012, 94, 133-150.	0.3	40
128	Características reprodutivas e suas associações com outras características de importância econômica na raça Nelore. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2012, 64, 91-100.	0.1	12
129	An assessment of linkage disequilibrium in Holstein cattle using a Bayesian network. <i>Journal of Animal Breeding and Genetics</i> , 2012, 129, 474-487.	0.8	14
130	Short communication: Principal components and factor analytic models for test-day milk yield in Brazilian Holstein cattle. <i>Journal of Dairy Science</i> , 2012, 95, 2157-2164.	1.4	16
131	Sampling strategies for total bacterial count of unpasteurized bulk milk. <i>Journal of Dairy Science</i> , 2012, 95, 2326-2335.	1.4	7
132	Comparative genomics between fly, mouse, and cattle identifies genes associated with sire conception rate. <i>Journal of Dairy Science</i> , 2012, 95, 6122-6129.	1.4	21
133	Accuracy of Genome-Enabled Prediction in a Dairy Cattle Population using Different Cross-Validation Layouts. <i>Frontiers in Genetics</i> , 2012, 3, 27.	1.1	33
134	Humble Thanks to a Gentle Giant (an Obituary for James F. Crow). <i>Frontiers in Genetics</i> , 2012, 3, 93.	1.1	1
135	Comparison of selective genotyping strategies for prediction of breeding values in a population undergoing selection. <i>Journal of Animal Science</i> , 2012, 90, 4716-4722.	0.2	32
136	Predictive ability of alternative models for genetic analysis of clinical mastitis. <i>Journal of Animal Breeding and Genetics</i> , 2012, 129, 120-128.	0.8	14
137	Inferring Quantitative Trait Pathways Associated with Bull Fertility from a Genome-Wide Association Study. <i>Frontiers in Genetics</i> , 2012, 3, 307.	1.1	45
138	Generalized linear mixed models for the genetic evaluation of binary reproductive traits: a simulation study. <i>Revista Brasileira De Zootecnia</i> , 2012, 41, 52-57.	0.3	2
139	Erratum to "Predictive ability of subsets of single nucleotide polymorphisms with and without parent average in US Holsteins" (<i>J. Dairy Sci.</i> 93:5942-5949). <i>Journal of Dairy Science</i> , 2011, 94, 537.	1.4	1
140	Bayesian analysis of autoregressive panel data model: application in genetic evaluation of beef cattle. <i>Scientia Agricola</i> , 2011, 68, 237-245.	0.6	11
141	Zero-inflated Poisson regression models for QTL mapping applied to tick-resistance in a Gyr x Holstein F2 population. <i>Genetics and Molecular Biology</i> , 2011, 34, 575-582.	0.6	6
142	A Primer on High-Throughput Computing for Genomic Selection. <i>Frontiers in Genetics</i> , 2011, 2, 4.	1.1	18
143	Grand Challenge in Livestock Genomics: For Food, for Medicine, for the Environment, for Knowledge. <i>Frontiers in Genetics</i> , 2011, 2, 34.	1.1	1
144	Genome-Wide Linkage Analysis of Global Gene Expression in Loin Muscle Tissue Identifies Candidate Genes in Pigs. <i>PLoS ONE</i> , 2011, 6, e16766.	1.1	45

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145	Dimension reduction and variable selection for genomic selection: application to predicting milk yield in Holsteins. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 247-257.	0.8	43
146	Marker-assisted prediction of non-additive genetic values. <i>Genetica</i> , 2011, 139, 843-854.	0.5	26
147	Application of support vector regression to genome-assisted prediction of quantitative traits. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1065-1074.	1.8	82
148	Long-term impacts of genome-enabled selection. <i>Journal of Applied Genetics</i> , 2011, 52, 467-480.	1.0	16
149	Searching for phenotypic causal networks involving complex traits: an application to European quail. <i>Genetics Selection Evolution</i> , 2011, 43, 37.	1.2	26
150	Inferring causal phenotype networks using structural equation models. <i>Genetics Selection Evolution</i> , 2011, 43, 6.	1.2	101
151	Prediction of body mass index in mice using dense molecular markers and a regularized neural network. <i>Genetical Research</i> , 2011, 93, 189-201.	0.3	67
152	Integrating biological information into the statistical analysis and design of microarray experiments. <i>Animal</i> , 2010, 4, 165-172.	1.3	3
153	Bayesian model averaging for evaluation of candidate gene effects. <i>Genetica</i> , 2010, 138, 395-407.	0.5	4
154	Modeling relationships between calving traits: a comparison between standard and recursive mixed models. <i>Genetics Selection Evolution</i> , 2010, 42, 1.	1.2	66
155	A genome-wide association study using selective DNA pooling identifies candidate markers for fertility in Holstein cattle. <i>Animal Genetics</i> , 2010, 41, 570-578.	0.6	58
156	Technical note: An R package for fitting generalized linear mixed models in animal breeding1. <i>Journal of Animal Science</i> , 2010, 88, 497-504.	0.2	128
157	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. <i>Genetical Research</i> , 2010, 92, 295-308.	0.3	319
158	Searching for Recursive Causal Structures in Multivariate Quantitative Genetics Mixed Models. <i>Genetics</i> , 2010, 185, 633-644.	1.2	96
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