

Fabyano Silva

List of Publications by Year in descending order

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Version: 2024-02-01

331
papers

4,759
citations

159585
30
h-index

206112
48
g-index

338
all docs

338
docs citations

338
times ranked

4976
citing authors

#	ARTICLE	IF	CITATIONS
1	Rowâ€“Col and Bayesian approach seeking to improve the predictive capacity and selection of passion fruit. <i>Scientia Agricola</i> , 2022, 79, .	1.2	1
2	Evaluation of Bayesian methods of genomic association via chromosomal regions using simulated data. <i>Scientia Agricola</i> , 2022, 79, .	1.2	2
3	Evaluation of a new additive-dominance genomic model and implications for quantitative genetics and genomic selection. <i>Scientia Agricola</i> , 2022, 79, .	1.2	0
4	Determination of optimal number of independent components in yield traits in rice. <i>Scientia Agricola</i> , 2022, 79, .	1.2	0
5	Searching for causal relationships among latent variables concerning performance, carcass, and meat quality traits in broilers. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 181-192.	2.0	2
6	Genetic study of quantitative traits supports the use of GuzerÃ¡ as dual-purpose cattle. <i>Animal Bioscience</i> , 2022, 35, 955-963.	2.0	5
7	Weighted genome-wide association study reveals new candidate genes related to boar taint compounds 1. <i>Livestock Science</i> , 2022, 257, 104845.	1.6	2
8	Exploring the Removal of Organic Matter in Constructed Wetlands Using First Order Kinetic Models. <i>Water (Switzerland)</i> , 2022, 14, 472.	2.7	3
9	CNV detection and their association with growth, efficiency and carcass traits in Santa InÃ³s sheep. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 476-487.	2.0	9
10	Random regression testâ€day models to describe milk production and fatty acid traits in first lactation Walloon Holstein cows. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 398-413.	2.0	7
11	Is single-step genomic REML with the algorithm for proven and young more computationally efficient when less generations of data are present?. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	5
12	Genetic Modeling and Genomic Analyses of Yearling Temperament in American Angus Cattle and Its Relationship With Productive Efficiency and Resilience Traits. <i>Frontiers in Genetics</i> , 2022, 13, 794625.	2.3	2
13	Preliminary study on tick ectoparasites of horses: effects on tick development and on the haematological parameters of hosts. <i>International Journal of Acarology</i> , 2022, 48, 43-49.	0.7	0
14	Alternative bayesian models for genetic evaluation of biometrical, physical, and morphological reproductive traits in nelore bulls. <i>Livestock Science</i> , 2021, 244, 104313.	1.6	6
15	Autoregressive singleâ€step model for genomic evaluation of longitudinal reproductive traits in portuguese holstein cattle. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 349-359.	2.0	0
16	Applying an association weight matrix in weighted genomic prediction of boar taint compounds. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 442-453.	2.0	4
17	Autoregressive model for genetic evaluation of longitudinal reproductive traits in Brazilian Holstein cattle. <i>Reproduction in Domestic Animals</i> , 2021, 56, 391-399.	1.4	0
18	Factors affecting heterotic grouping with crossâ€pollinating crops. <i>Agronomy Journal</i> , 2021, 113, 210-223.	1.8	9

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19	Enviromics in breeding: applications and perspectives on envirotypic-assisted selection. <i>Theoretical and Applied Genetics</i> , 2021, 134, 95-112.	3.6	103
20	Genomic prediction of leaf rust resistance to Arabica coffee using machine learning algorithms. <i>Scientia Agricola</i> , 2021, 78, .	1.2	21
21	Prediction of aboveground biomass and dry matter content in <i>< i>Brachiaria</i></i> pastures by combining meteorological data and satellite imagery. <i>Grass and Forage Science</i> , 2021, 76, 340-352.	2.9	18
22	Genotype by environment interaction for Holstein cattle populations using autoregressive and within- and across-country multi-trait reaction norms test-day models. <i>Animal</i> , 2021, 15, 100084.	3.3	3
23	Multiple-trait model through Bayesian inference applied to <i>Jatropha curcas</i> breeding for bioenergy. <i>PLoS ONE</i> , 2021, 16, e0247775.	2.5	14
24	Estimation of genetic parameters for body areas in Nile tilapia measured by digital image analysis. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 731-738.	2.0	7
25	Exploring the use of residual variance for uniformity of body weight in meat quail lines using Bayesian inference. <i>British Poultry Science</i> , 2021, 62, 474-484.	1.7	1
26	Proteomic Analysis of Liver from Finishing Beef Cattle Supplemented with a Rumen-Protected B-Vitamin Blend and Hydroxy Trace Minerals. <i>Animals</i> , 2021, 11, 1934.	2.3	0
27	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.	2.3	10
28	Intramuscular collagen characteristics and expression of related genes in skeletal muscle of cull cows receiving a high-energy diet. <i>Meat Science</i> , 2021, 177, 108495.	5.5	12
29	Investigating pig survival in different production phases using genomic models. <i>Journal of Animal Science</i> , 2021, 99, .	0.5	13
30	Choice of non-linear models to determine the growth curve of meat-type quail. <i>Ciencia Rural</i> , 2021, 51, .	0.5	1
31	Assessment of digestible lysine requirements in lipopolysaccharide-challenged pigs. <i>Journal of Animal Science</i> , 2021, 99, .	0.5	0
32	Reduced rank analysis of morphometric and functional traits in Campolina horses. <i>Journal of Animal Breeding and Genetics</i> , 2021, .	2.0	2
33	Mixed model-based Jinks and Pooni method to predict segregating populations in wheat breeding. <i>Crop Breeding and Applied Biotechnology</i> , 2021, 21, .	0.4	3
34	Análise genética de curvas de crescimento de suínos: um estudo de simulação. <i>Archivos De Zootecnia</i> , 2021, 70, 224-228.	0.1	0
35	Genetic evaluation for latent variables derived from factor analysis in broilers. <i>British Poultry Science</i> , 2020, 61, 3-9.	1.7	7
36	Genetic parameters for fertility traits in Nellore bulls. <i>Reproduction in Domestic Animals</i> , 2020, 55, 38-43.	1.4	15

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37	Autoregressive and random regression test-day models for multiple lactations in genetic evaluation of Brazilian Holstein cattle. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 305-315.	2.0	5
38	Genetic parameters, genome-wide association and gene networks for milk and reproductive traits in Guzerá cattle. <i>Livestock Science</i> , 2020, 242, 104273.	1.6	6
39	Applying the Metafounders Approach for Genomic Evaluation in a Multibreed Beef Cattle Population. <i>Frontiers in Genetics</i> , 2020, 11, 556399.	2.3	9
40	GWAS and gene networks for milk-related traits from test-day multiple lactations in Portuguese Holstein cattle. <i>Journal of Applied Genetics</i> , 2020, 61, 465-476.	1.9	12
41	Short communication: Time-dependent genetic parameters and single-step genome-wide association analyses for predicted milk fatty acid composition in Ayrshire and Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2020, 103, 5263-5269.	3.4	7
42	Short communication: Genetic parameter estimates for caprine arthritis encephalitis in dairy goats. <i>Journal of Dairy Science</i> , 2020, 103, 6407-6411.	3.4	5
43	Feeding behavior, water intake, and energy and protein requirements of young Nellore bulls with different residual feed intakes. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	8
44	Efficiency of Bayesian quantitative trait loci mapping with full-sib progeny. <i>Agronomy Journal</i> , 2020, 112, 2759-2767.	1.8	3
45	Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. <i>Canadian Journal of Animal Science</i> , 2020, 100, 587-604.	1.5	31
46	Nitrous oxide, methane, and ammonia emissions from cattle excreta on Brachiaria decumbens growing in monoculture or silvopasture with Acacia mangium and Eucalyptus grandis. <i>Agriculture, Ecosystems and Environment</i> , 2020, 295, 106896.	5.3	21
47	Proteomic analysis reveals changes in energy metabolism of skeletal muscle in beef cattle supplemented with vitamin A. <i>Journal of the Science of Food and Agriculture</i> , 2020, 100, 3536-3543.	3.5	11
48	Optimization of Eucalyptus breeding through random regression models allowing for reaction norms in response to environmental gradients. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	15
49	Genetic parameters for milk, growth, and reproductive traits in Guzerá cattle under tropical conditions. <i>Tropical Animal Health and Production</i> , 2020, 52, 2251-2257.	1.4	5
50	Genomic analyses for predicted milk fatty acid composition throughout lactation in North American Holstein cattle. <i>Journal of Dairy Science</i> , 2020, 103, 6318-6331.	3.4	17
51	Urea supplementation in rumen and post-rumen for cattle fed a low-quality tropical forage. <i>British Journal of Nutrition</i> , 2020, 124, 1166-1178.	2.3	11
52	Estimated genetic associations among reproductive traits in Nellore cattle using Bayesian analysis. <i>Animal Reproduction Science</i> , 2020, 214, 106305.	1.5	11
53	Effect of duration of restricted-feeding on nutrient excretion, animal performance, and carcass characteristics of Holstein – Zebu finishing steers. <i>Animal Production Science</i> , 2020, 60, 535.	1.3	3
54	Genomic Predictions Using Low-Density SNP Markers, Pedigree and GWAS Information: A Case Study with the Non-Model Species Eucalyptus cladocalyx. <i>Plants</i> , 2020, 9, 99.	3.5	23

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55	Bayesian segmented regression model for adaptability and stability evaluation of cotton genotypes. <i>Euphytica</i> , 2020, 216, 1.	1.2	13
56	Autoregressive repeatability model for genetic evaluation of longitudinal reproductive traits in dairy cattle. <i>Journal of Dairy Research</i> , 2020, 87, 37-44.	1.4	3
57	Energy and protein requirements of Holstein × Gyr crossbred heifers. <i>Animal</i> , 2020, 14, 1857-1866.	3.3	10
58	Comparing Alternative Single-Step GBLUP Approaches and Training Population Designs for Genomic Evaluation of Crossbred Animals. <i>Frontiers in Genetics</i> , 2020, 11, 263.	2.3	18
59	Multivariate diallel analysis by factor analysis for establish mega-trait. <i>Anais Da Academia Brasileira De Ciencias</i> , 2020, 92, e20180874.	0.8	6
60	Progesterone and estrogen receptor expression by canine cutaneous soft tissue sarcomas. <i>Pesquisa Veterinaria Brasileira</i> , 2020, 40, 284-288.	0.5	2
61	Genetic study of litter size and litter uniformity in Landrace pigs. <i>Revista Brasileira De Zootecnia</i> , 2020, 49, .	0.8	8
62	Nonlinear quantile regression to describe the dry matter accumulation of garlic plants. <i>Ciencia Rural</i> , 2020, 50, .	0.5	3
63	Effects of dietary nucleotide supplementation on growth performance and physiology of broiler chickens under pre- and post-inflammatory challenge. <i>Revista Brasileira De Zootecnia</i> , 2020, 49, .	0.8	2
64	Quantifying individual variation in reaction norms using random regression models fitted through Legendre polynomials: application in eucalyptus breeding. <i>Bragantia</i> , 2020, 79, 485-501.	1.3	3
65	Quail growth curve model identity. <i>Research, Society and Development</i> , 2020, 9, e9439109328.	0.1	2
66	Effects of nutritional plans and genetic groups on performance, carcass and meat quality traits of finishing pigs. <i>Food Science and Technology</i> , 2019, 39, 538-545.	1.7	3
67	Genetic correlations between growth performance and carcass traits of purebred and crossbred pigs raised in tropical and temperate climates. <i>Journal of Animal Science</i> , 2019, 97, 3648-3657.	0.5	4
68	Genomic selection for productive traits in biparental cassava breeding populations. <i>PLoS ONE</i> , 2019, 14, e0220245.	2.5	11
69	Efficiency of Genomic Prediction of Nonassessed Testcrosses. <i>Crop Science</i> , 2019, 59, 2020-2027.	1.8	8
70	Invited review: Advances and applications of random regression models: From quantitative genetics to genomics. <i>Journal of Dairy Science</i> , 2019, 102, 7664-7683.	3.4	46
71	Genetic evaluation for days to calving in Nellore heifers using Exponential and Gaussian Censored Bayesian models. <i>Livestock Science</i> , 2019, 230, 103828.	1.6	0
72	Short communication: Molecular characterization and antimicrobial resistance of pathogenic <i>Escherichia coli</i> isolated from raw milk and Minas Frescal cheeses in Brazil. <i>Journal of Dairy Science</i> , 2019, 102, 10850-10854.	3.4	23

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73	Oscillating and static dietary crude protein supply. I. Impacts on intake, digestibility, performance, and nitrogen balance in young Nellore bulls1. <i>Translational Animal Science</i> , 2019, 3, 1205-1215.	1.1	9
74	61 The impact of selective phenotyping and genotyping over generations in beef cattle. <i>Journal of Animal Science</i> , 2019, 97, 37-39.	0.5	0
75	Combined index of genomic prediction methods applied to productivity. <i>Ciencia Rural</i> , 2019, 49, .	0.5	4
76	Genome-wide association for milk production traits and somatic cell score in different lactation stages of Ayrshire, Holstein, and Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 8159-8174.	3.4	42
77	Single-step genome-wide association for longitudinal traits of Canadian Ayrshire, Holstein, and Jersey dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 9995-10011.	3.4	29
78	Linkage disequilibrium and haplotype block patterns in popcorn populations. <i>PLoS ONE</i> , 2019, 14, e0219417.	2.5	15
79	Application of single-step genomic evaluation using multiple-trait random regression test-day models in dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 2365-2377.	3.4	45
80	Differentially expressed mRNAs, proteins and miRNAs associated to energy metabolism in skeletal muscle of beef cattle identified for low and high residual feed intake. <i>BMC Genomics</i> , 2019, 20, 501.	2.8	22
81	Genes expression and phenotypic differences in corpus luteum and cumulus cells of commercial line and piau breed gilts. <i>Theriogenology</i> , 2019, 136, 111-117.	2.1	1
82	Novel lactic acid bacteria strains as inoculants on alfalfa silage fermentation. <i>Scientific Reports</i> , 2019, 9, 8007.	3.3	31
83	Impact of including information from bulls and their daughters in the training population of multiple-step genomic evaluations in dairy cattle: A simulation study. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 441-452.	2.0	5
84	Autoregressive single-step test-day model for genomic evaluations of Portuguese Holstein cattle. <i>Journal of Dairy Science</i> , 2019, 102, 6330-6339.	3.4	7
85	Triple categorical regression for genomic selection: application to cassava breeding. <i>Scientia Agricola</i> , 2019, 76, 368-375.	1.2	5
86	Associations between morphometric variables and weight and yields carcass in Pirapitinga< i>Piaractus brachypomus</i>. <i>Aquaculture Research</i> , 2019, 50, 2004-2011.	1.8	8
87	Alternative count Bayesian models for genetic evaluation of litter traits in pigs. <i>Livestock Science</i> , 2019, 225, 140-143.	1.6	3
88	Use of nonlinear mixed models for describing testicular volume growth curve in Nellore bulls. <i>Theriogenology</i> , 2019, 133, 65-70.	2.1	1
89	Analysis of the adaptability of black bean cultivars by means of quantile regression. <i>Ciencia Rural</i> , 2019, 49, .	0.5	1
90	Evaluation of Bayesian models for analysis of crude protein requirement for pigs of Brazilian Piau breed. <i>Scientia Agricola</i> , 2019, 76, 208-213.	1.2	4

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91	New insights into genomic selection through population-based non-parametric prediction methods. <i>Scientia Agricola</i> , 2019, 76, 290-298.	1.2	3
92	Machine learning approaches and their current application in plant molecular biology: A systematic review. <i>Plant Science</i> , 2019, 284, 37-47.	3.6	66
93	Genotypic variation and relationships among traits for root morphology in a panel of tropical maize inbred lines under contrasting nitrogen levels. <i>Euphytica</i> , 2019, 215, 1.	1.2	14
94	Genotype imputation strategies for Portuguese Holstein cattle using different SNP panels. <i>Czech Journal of Animal Science</i> , 2019, 64, 377-386.	1.3	2
95	Evaluation of a long-established silvopastoral Brachiaria decumbens system: plant characteristics and feeding value for cattle. <i>Crop and Pasture Science</i> , 2019, 70, 814.	1.5	12
96	Quantile Regression Applied to Genome-Enabled Prediction of Traits Related to Flowering Time in the Common Bean. <i>Agronomy</i> , 2019, 9, 796.	3.0	7
97	Genomic Prediction of Additive and Non-additive Effects Using Genetic Markers and Pedigrees. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2739-2748.	1.8	24
98	Censored Bayesian models for genetic evaluation of age at first calving in Brazilian Brahman cattle. <i>Livestock Science</i> , 2019, 221, 177-180.	1.6	3
99	Unknown parent and contemporary groups for genetic evaluation of Brazilian Holstein using autoregressive test-day models. <i>Livestock Science</i> , 2019, 220, 1-7.	1.6	5
100	Genomic prediction of lactation curves for milk, fat, protein, and somatic cell score in Holstein cattle. <i>Journal of Dairy Science</i> , 2019, 102, 452-463.	3.4	20
101	Genome-wide association studies pathway-based meta-analysis for residual feed intake in beef cattle. <i>Animal Genetics</i> , 2019, 50, 150-153.	1.7	30
102	Epigenética: mecanismos, herança e implicações no melhoramento animal. <i>Archivos De Zootecnia</i> , 2019, 68, 304-311.	0.1	6
103	Comparing deregression methods for genomic prediction of test-day traits in dairy cattle. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 97-106.	2.0	17
104	Genetic correlations between feed efficiency traits, and growth performance and carcass traits in purebred and crossbred pigs. <i>Journal of Animal Science</i> , 2018, 96, 817-829.	0.5	26
105	Bayesian model combining linkage and linkage disequilibrium analysis for low density-based genomic selection in animal breeding. <i>Journal of Applied Animal Research</i> , 2018, 46, 873-878.	1.2	4
106	BIG DATA ANALYTICS AND PRECISION ANIMAL AGRICULTURE SYMPOSIUM: Machine learning and data mining advance predictive big data analysis in precision animal agriculture1. <i>Journal of Animal Science</i> , 2018, 96, 1540-1550.	0.5	136
107	Environmental uniformity, site quality and tree competition interact to determine stand productivity of clonal Eucalyptus. <i>Forest Ecology and Management</i> , 2018, 410, 76-83.	3.2	44
108	Benchmarking Bayesian genome enabled-prediction models for age at first calving in Nellore cows. <i>Livestock Science</i> , 2018, 211, 75-79.	1.6	9

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109	Genome-wide association studies, meta-analyses and derived gene network for meat quality and carcass traits in pigs. <i>Animal Production Science</i> , 2018, 58, 1100.	1.3	12
110	Meta-analysis of genetic-parameter estimates for reproduction, growth and carcass traits in Nellore cattle by using a random-effects model. <i>Animal Production Science</i> , 2018, 58, 1575.	1.3	22
111	Analyses of reaction norms reveal new chromosome regions associated with tick resistance in cattle. <i>Animal</i> , 2018, 12, 205-214.	3.3	16
112	A model-based site selection approach associated with regional frequency analysis for modeling extreme rainfall depths in Minas Gerais state, Southeast Brazil. <i>Stochastic Environmental Research and Risk Assessment</i> , 2018, 32, 469-484.	4.0	4
113	Efficiency of genomic prediction of non-assessed single crosses. <i>Heredity</i> , 2018, 120, 283-295.	2.6	17
114	Relevance of genetic relationship in GWAS and genomic prediction. <i>Journal of Applied Genetics</i> , 2018, 59, 1-8.	1.9	14
115	GenomicLand: Software for genome-wide association studies and genomic prediction. <i>Acta Scientiarum - Agronomy</i> , 2018, 41, 45361.	0.6	7
116	Genome prediction accuracy of common bean via Bayesian models. <i>Ciencia Rural</i> , 2018, 48, .	0.5	6
117	Isotonic regression analysis of Guzerá cattle growth curves. <i>Revista Ceres</i> , 2018, 65, 24-27.	0.4	1
118	Use of regularized quantile regression to predict the genetic merit of pigs for asymmetric carcass traits. <i>Pesquisa Agropecuaria Brasileira</i> , 2018, 53, 1011-1017.	0.9	2
119	Ingestive behavior of dairy goats fed diets containing increasing levels of neutral detergent fiber and particle size using multivariate analysis. <i>Acta Scientiarum - Animal Sciences</i> , 2018, 41, 45870.	0.3	3
120	Linkage fine-mapping and QTLs affecting morpho-agronomic traits of a Mesoamerican–Andean RIL common bean population. <i>Euphytica</i> , 2018, 214, 1.	1.2	7
121	Impact of embryo transfer phenotypic records on large-scale beef cattle genetic evaluations. <i>Revista Brasileira De Zootecnia</i> , 2018, 47, .	0.8	1
122	Research Article Support vector machines applied to the genetic classification problem of hybrid populations with high degrees of similarity. <i>Genetics and Molecular Research</i> , 2018, 17, .	0.2	1
123	Quantile regression of nonlinear models to describe different levels of dry matter accumulation in garlic plants. <i>Ciencia Rural</i> , 2018, 48, .	0.5	6
124	Effects of alleles in crossbred pigs estimated for genomic prediction depend on their breed-of-origin. <i>BMC Genomics</i> , 2018, 19, 740.	2.8	10
125	Avaliação da imobilidade tática em codornas de corte via análise de sobrevivência. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2018, 70, 1009-1012.	0.4	0
126	Exigência de proteína bruta para juvenis de curimatá-pacu. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2018, 70, 921-930.	0.4	2

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127	Genetic evaluation of growth traits in Nellore cattle through multi-trait and random regression models. <i>Czech Journal of Animal Science</i> , 2018, 63, 212-221.	1.3	3
128	Multi-trait multi-environment Bayesian model reveals G x E interaction for nitrogen use efficiency components in tropical maize. <i>PLoS ONE</i> , 2018, 13, e0199492.	2.5	35
129	Genotype by feed interaction for feed efficiency and growth performance traits in pigs1. <i>Journal of Animal Science</i> , 2018, 96, 4125-4135.	0.5	15
130	Research Article Expression of lipid metabolism and myosin heavy chain genes in pigs is affected by genotype and dietary lysine. <i>Genetics and Molecular Research</i> , 2018, 17, .	0.2	3
131	Relationship of testicular biometry with semen variables in breeding soundness evaluation of Nellore bulls. <i>Animal Reproduction Science</i> , 2018, 196, 168-175.	1.5	6
132	Genome-Wide Association and Regional Heritability Mapping of Plant Architecture, Lodging and Productivity in <i>Phaseolus vulgaris</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2841-2854.	1.8	41
133	Weighted single-step GWAS and gene network analysis reveal new candidate genes for semen traits in pigs. <i>Genetics Selection Evolution</i> , 2018, 50, 40.	3.0	49
134	A note on transgenerational epigenetics affecting egg quality traits in meat-type quail. <i>British Poultry Science</i> , 2018, 59, 624-628.	1.7	5
135	Genetic analysis of morphological and functional traits in Campolina horses using Bayesian multi-trait model. <i>Livestock Science</i> , 2018, 216, 119-129.	1.6	17
136	Genetic evaluation of age at first calving for Guzerá beef cattle using linear, threshold, and survival Bayesian models. <i>Journal of Animal Science</i> , 2018, 96, 2517-2524.	0.5	5
137	Transgenerational epigenetic variance for body weight in meat quails. <i>Journal of Animal Breeding and Genetics</i> , 2018, 135, 178-185.	2.0	8
138	Genome wide association study reveals new candidate genes for resistance to nematodes in Creole goat. <i>Small Ruminant Research</i> , 2018, 166, 109-114.	1.2	12
139	Can scrotal circumference-based selection discard bulls with good productive and reproductive potential?. <i>PLoS ONE</i> , 2018, 13, e0193103.	2.5	8
140	Quantile regression for genome-wide association study of flowering time-related traits in common bean. <i>PLoS ONE</i> , 2018, 13, e0190303.	2.5	22
141	Effects of increasing palm kernel cake inclusion in supplements fed to grazing lambs on growth performance, carcass characteristics, and fatty acid profile. <i>Animal Feed Science and Technology</i> , 2017, 226, 71-80.	2.2	19
142	Count Bayesian models for genetic analysis of in vitro embryo production traits in Guzerá cattle. <i>Animal</i> , 2017, 11, 1440-1448.	3.3	6
143	Bayesian estimation of genetic parameters for individual feed conversion and body weight gain in meat quail. <i>Livestock Science</i> , 2017, 200, 76-79.	1.6	9
144	Bayesian random regression threshold models for genetic evaluation of pregnancy probability in Red Sindhi heifers. <i>Livestock Science</i> , 2017, 202, 166-170.	1.6	3

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145	Geminivirus data warehouse: a database enriched with machine learning approaches. <i>BMC Bioinformatics</i> , 2017, 18, 240.	2.6	26
146	Bayesian Models combining Legendre and B-spline polynomials for genetic analysis of multiple lactations in Gyr cattle. <i>Livestock Science</i> , 2017, 201, 78-84.	1.6	13
147	Gene networks for total number born in pigs across divergent environments. <i>Mammalian Genome</i> , 2017, 28, 426-435.	2.2	3
148	Bayesian analysis of pig growth curves combining pedigree and genomic information. <i>Livestock Science</i> , 2017, 201, 34-40.	1.6	7
149	Efficiency of low heritability QTL mapping under high SNP density. <i>Euphytica</i> , 2017, 213, 1.	1.2	15
150	Genome-wide association study and annotating candidate gene networks affecting age at first calving in Nellore cattle. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 484-492.	2.0	42
151	Efficiency of genome-wide association studies in random cross populations. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	6
152	Assessing the expected response to genomic selection of individuals and families in Eucalyptus breeding with an additive-dominant model. <i>Heredity</i> , 2017, 119, 245-255.	2.6	76
153	Regional heritability mapping and genome-wide association identify loci for complex growth, wood and disease resistance traits in <i>Eucalyptus</i> . <i>New Phytologist</i> , 2017, 213, 1287-1300.	7.3	95
154	Use of molecular markers to improve relationship information in the genetic evaluation of beef cattle tick resistance under pedigree-based models. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 14-26.	2.0	19
155	The diversification of begomovirus populations is predominantly driven by mutational dynamics. <i>Virus Evolution</i> , 2017, 3, vex005.	4.9	92
156	Genetic parameters for semen quality and quantity traits in five pig lines1. <i>Journal of Animal Science</i> , 2017, 95, 4251-4259.	0.5	42
157	Contemporary groups in the genetic evaluation of Nellore cattle using Bayesian inference. <i>Pesquisa Agropecuaria Brasileira</i> , 2017, 52, 643-651.	0.9	3
158	Genome association study through nonlinear mixed models revealed new candidate genes for pig growth curves. <i>Scientia Agricola</i> , 2017, 74, 1-7.	1.2	4
159	Independent Component Analysis (ICA) based-clustering of temporal RNA-seq data. <i>PLoS ONE</i> , 2017, 12, e0181195.	2.5	39
160	Regularized quantile regression for SNP marker estimation of pig growth curves. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 59.	5.3	8
161	The optimal number of partial least squares components in genomic selection for pork pH. <i>Ciencia Rural</i> , 2017, 47, .	0.5	2
162	Artificial neural network for prediction of the area under the disease progress curve of tomato late blight. <i>Scientia Agricola</i> , 2017, 74, 51-59.	1.2	13

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164	Population structure correction for genomic selection through eigenvector covariates. <i>Crop Breeding and Applied Biotechnology</i> , 2017, 17, 350-358.	0.4	11
165	Bayesian inference for the fitting of dry matter accumulation curves in garlic plants. <i>Pesquisa Agropecuaria Brasileira</i> , 2017, 52, 572-581.	0.9	6
166	TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: Dedifferentiated fat cells: Potential and perspectives for their use in clinical and animal science purpose. <i>Journal of Animal Science</i> , 2017, 95, 2255.	0.5	4
167	Bayesian random regression for genetic evaluation of South American leaf blight in rubber trees. <i>Revista Ciencia Agronomica</i> , 2017, 48, .	0.3	2
168	Parâmetros e ganhos genéticos em características de crescimento de bovinos Tabapuá da Bahia. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2016, 68, 1043-1052.	0.4	2
169	Composição centesimal e de ácidos graxos do músculo Longissimus de cordeiros confinados, alimentados com dietas contendo casca de mandioca. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2016, 68, 1325-1333.	0.4	3
170	Linkage disequilibrium, SNP frequency change due to selection, and association mapping in popcorn chromosome regions containing QTLs for quality traits. <i>Genetics and Molecular Biology</i> , 2016, 39, 97-110.	1.3	8
171	Expression of myogenes in longissimus dorsi muscle during prenatal development in commercial and local Piau pigs. <i>Genetics and Molecular Biology</i> , 2016, 39, 589-599.	1.3	8
172	Genomic prediction for additive and dominance effects of censored traits in pigs. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	4
173	Caracterização de colágenos tipos I e III no estroma do carcinoma de células escamosas cutâneo em cães. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2016, 68, 147-154.	0.4	11
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175	Quantitative genetics theory for genomic selection and efficiency of breeding value prediction in open-pollinated populations. <i>Scientia Agricola</i> , 2016, 73, 243-251.	1.2	20
176	Multi-trait and repeatability models for genetic evaluation of litter traits in pigs considering different farrowings. <i>Revista Brasileira De Saude E Produção Animal</i> , 2016, 17, 666-676.	0.3	5
177	Genotype by environment interaction for tick resistance of Hereford and Braford beef cattle using reaction norm models. <i>Genetics Selection Evolution</i> , 2016, 48, 3.	3.0	18
178	New accuracy estimators for genomic selection with application in a cassava (<i>Manihot esculenta</i>) breeding program. <i>Genetics and Molecular Research</i> , 2016, 15, .	0.2	6
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182	Combining different functions to describe milk, fat, and protein yield in goats using Bayesian multiple-trait random regression models. <i>Journal of Animal Science</i> , 2016, 94, 1865-1874.	0.5	18
183	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations. <i>Journal of Animal Science</i> , 2016, 94, 1446-1458.	0.5	11
184	Revealing new candidate genes for reproductive traits in pigs: combining Bayesian GWAS and functional pathways. <i>Genetics Selection Evolution</i> , 2016, 48, 9.	3.0	68
185	Accessing marker effects and heritability estimates from genome prediction by Bayesian regularized neural networks. <i>Livestock Science</i> , 2016, 191, 91-96.	1.6	12
186	Effects of nutrient intake level on mammary parenchyma growth and gene expression in crossbred (Holstein × Gyr) prepubertal heifers. <i>Journal of Dairy Science</i> , 2016, 99, 9962-9973.	3.4	17
187	Genome-enabled prediction for tick resistance in Hereford and Braford beef cattle via reaction norm models. <i>Journal of Animal Science</i> , 2016, 94, 1834-1843.	0.5	19
188	Effect of maternal nutrition and days of gestation on pituitary gland and gonadal gene expression in cattle. <i>Journal of Dairy Science</i> , 2016, 99, 3056-3071.	3.4	27
189	Weight gain potential affects pregnancy rates in bovine embryo recipients raised under pasture conditions. <i>Tropical Animal Health and Production</i> , 2016, 48, 103-107.	1.4	5
190	Inferência bayesiana da conversão alimentar em diferentes experimentos animais. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2016, 68, 466-474.	0.4	2
191	Five decades of black common bean genetic breeding in Brazil. <i>Pesquisa Agropecuaria Tropical</i> , 2016, 46, 259-266.	1.0	10
192	Seleção genética para melhoramento vegetal com diferentes estruturas populacionais. <i>Pesquisa Agropecuaria Brasileira</i> , 2016, 51, 1857-1867.	0.9	4
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195	Multi-Trait analysis of growth traits: fitting reduced rank models using principal components for Simmental beef cattle. <i>Ciencia Rural</i> , 2016, 46, 1656-1661.	0.5	0
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198	Multi-Trait GWAS and New Candidate Genes Annotation for Growth Curve Parameters in Brahman Cattle. <i>PLoS ONE</i> , 2015, 10, e0139906.	2.5	66

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200	Accuracy of genome-enabled prediction exploring purebred and crossbred pig populations1. <i>Journal of Animal Science</i> , 2015, 93, 4684-4691.	0.5	9
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202	Sustained <scp>NIK</scp>-mediated antiviral signalling confers broad-spectrum tolerance to begomoviruses in cultivated plants. <i>Plant Biotechnology Journal</i> , 2015, 13, 1300-1311.	8.3	43
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205	Genomic selection for boar taint compounds and carcass traits in a commercial pig population. <i>Livestock Science</i> , 2015, 174, 10-17.	1.6	27
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207	Ridge, Lasso and Bayesian additive-dominance genomic models. <i>BMC Genetics</i> , 2015, 16, 105.	2.7	53
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218	Genome-Wide Association Studies (GWAS). , 2014, , 83-104.		1
219	Genome-Wide Selection (GWS). , 2014, , 105-133.		3
220	Modelagem hierárquica Bayesiana na avaliação de curvas de crescimento de suínos genotipados para o gene halotano. <i>Ciencia Rural</i> , 2014, 44, 1853-1859.	0.5	1
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223	Supervised independent component analysis as an alternative method for genomic selection in pigs. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 452-461.	2.0	14
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225	Sire evaluation for total number born in pigs using a genomic reaction norms approach1. <i>Journal of Animal Science</i> , 2014, 92, 3825-3834.	0.5	46
226	Effect of the dietary inclusion of dried oregano (<i>Origanum vulgare L.</i>) on the characteristics of milk from Holstein-Zebu cows. <i>Animal Feed Science and Technology</i> , 2014, 192, 101-105.	2.2	9
227	Best linear unbiased prediction for genetic evaluation in reciprocal recurrent selection with popcorn populations. <i>Journal of Agricultural Science</i> , 2014, 152, 428-438.	1.3	3
228	Identidade de modelos não lineares para comparar curvas de crescimento de bovinos da raça Tabapuã. <i>Pesquisa Agropecuária Brasileira</i> , 2014, 49, 57-62.	0.9	24
229	Modelos de regressão não linear aplicados a grupos de acessos de alho. <i>Horticultura Brasileira</i> , 2014, 32, 178-183.	0.5	13
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232	Interação ordenhador-vaca e as respostas comportamentais, produtivas e econômica dos animais. <i>Archivos De Zootecnia</i> , 2014, 63, 381-384.	0.1	2
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239	Identification and expression levels of pig miRNAs in skeletal muscle. <i>Livestock Science</i> , 2013, 154, 45-54.	1.6	6
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244	Genomic growth curves of an outbred pig population. <i>Genetics and Molecular Biology</i> , 2013, 36, 520-527.	1.3	13
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246	Viabilidade econômica do uso de fontes lipídicas na dieta de vacas em lactação. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2013, 65, 1454-1462.	0.4	2
247	Fine mapping and single nucleotide polymorphism effects estimation on pig chromosomes 1, 4, 7, 8, 17 and X. <i>Genetics and Molecular Biology</i> , 2013, 36, 511-519.	1.3	9
248	Traditional and alternative nonlinear models for estimating the growth of Morada Nova sheep. <i>Revista Brasileira De Zootecnia</i> , 2013, 42, 651-655.	0.8	17
249	Micropropagação da bananeira 'Mãe-De-Suá', cultivada in vitro em diferentes volumes de meio líquido. <i>Revista Ceres</i> , 2013, 60, 745-751.	0.4	3
250	Quadrados mínimos parciais uni e multivariado aplicados na seleção genética para características de carcaça em suínos. <i>Ciencia Rural</i> , 2013, 43, 1642-1649.	0.5	4
251	Seleção genética ampla para curvas de crescimento. <i>Arquivo Brasileiro De Medicina Veterinaria E Zootecnia</i> , 2013, 65, 1519-1526.	0.4	1
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273	Epidemiology, clinical signs, histopathology and molecular characterization of canine leproid granuloma: a retrospective study of cases from Brazil. <i>Veterinary Dermatology</i> , 2011, 22, 249-256.	1.2	14
274	Three-step Bayesian factor analysis applied to QTL detection in crosses between outbred pig populations. <i>Livestock Science</i> , 2011, 142, 210-215.	1.6	15
275	A note on accuracy of Bayesian LASSO regression in GWS. <i>Livestock Science</i> , 2011, 142, 310-314.	1.6	7
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278	Métodos de análise de dados longitudinais para o melhoramento genético da pinha. <i>Pesquisa Agropecuaria Brasileira</i> , 2011, 46, 1657-1664.	0.9	7
279	Divergência genética entre genótipos de pimenta com base em caracteres morfo-agrónomos. <i>Horticultura Brasileira</i> , 2011, 29, 354-358.	0.5	14
280	Análise de agrupamento na seleção de modelos de regressão não-lineares para curvas de crescimento de ovinos cruzados. <i>Ciencia Rural</i> , 2011, 41, 692-698.	0.5	23
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282	Modelos não-lineares generalizados aplicados na predição da área basal e volume de Eucalyptus clonal. <i>Cerne</i> , 2011, 17, 541-548.	0.9	8
283	Comportamento ingestivo de vacas alimentadas com cana-de-açúcar e diferentes níveis de concentrado.. <i>Archivos De Zootecnia</i> , 2011, 60, 265-273.	0.1	0
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290	Modelo hierárquico bayesiano aplicado na avaliação genética de curvas de crescimento de bovinos de corte. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2010, 62, 409-418.	0.4	6
291	Digestibilidade aparente da dieta com capim-elefante ensilado com diferentes aditivos. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2010, 62, 889-897.	0.4	7
292	Novilhos nelore suplementados em pastagens: consumo, desempenho e digestibilidade. Archivos De Zootecnia, 2010, 59,	0.1	4
293	A raça Indubrasil no Nordeste brasileiro: melhoramento e estrutura populacional. Revista Brasileira De Zootecnia, 2009, 38, 2327-2334.	0.8	22
294	Abordagem bayesiana da sensitividade de modelos para o coeficiente de endogamia. Ciencia Rural, 2009, 39, 1752-1759.	0.5	2
295	Análise bayesiana para modelos de degradabilidade ruminal. Ciencia Rural, 2009, 39, 2169-2177.	0.5	3
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304	Comparação bayesiana de modelos de previsão de diferenças esperadas nas produtividades no melhoramento genético de gado Nelore. Pesquisa Agropecuaria Brasileira, 2008, 43, 37-45.	0.9	6
305	Desempenho produtivo, características de carcaça e avaliação econômica de bovinos cruzados, castrados e não-castrados, terminados em pastagens de Brachiaria decumbens. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2008, 60, 1157-1165.	0.4	15
306	Perdas na ensilagem de capim-elefante aditivado com farelo de cacau e cana-de-açúcar. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2008, 60, 227-233.	0.4	10

#	ARTICLE	IF	CITATIONS
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308	Consumo, desempenho e parâmetros econômicos de novilhos Nelore e F1 Brangus x Nelore terminados em pastagens, suplementados com mistura mineral e sal nitrogenado com uréia ou amiréia. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2008, 60, 419-427.	0.4	12
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314	Avaliação da produção de bezerros em confinamento ou em suplementação exclusiva. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2007, 59, 948-954.	0.4	4
315	Avaliação de curvas de crescimento morfométrico de linhagens de tilápia do nilo (<i>Oreochromis</i>) Tj ETQq1 1 0,784314 rgBT /Overline{23}	0.4	1
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