Fabyano Silva

List of Publications by Year
in descending order

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	NIK1-mediated translation suppression functions as a plant antiviral immunity mechanism. Nature, 2015, 520, 679-682.	27.8	195
2	BIG DATA ANALYTICS AND PRECISION ANIMAL AGRICULTURE SYMPOSIUM: Machine learning and data mining advance predictive big data analysis in precision animal agriculture1. Journal of Animal Science, 2018, 96, 1540-1550.	0.5	136
3	Effects of equine chorionic gonadotropin and type of ovulatory stimulus in a timed-AI protocol on reproductive responses in dairy cows. Theriogenology, 2009, 72, 10-21.	2.1	119
4	The tomato RLK superfamily: phylogeny and functional predictions about the role of the LRRII-RLK subfamily in antiviral defense. BMC Plant Biology, 2012, 12, 229.	3.6	119
5	Enviromics in breeding: applications and perspectives on envirotypic-assisted selection. Theoretical and Applied Genetics, 2021, 134, 95-112.	3.6	103
6	Regional heritability mapping and genome‑wide association identify loci for complex growth, wood and disease resistance traits in *Eucalyptus*. New Phytologist, 2017, 213, 1287-1300.	7.3	95
7	The diversification of begomovirus populations is predominantly driven by mutational dynamics. Virus Evolution, 2017, 3, vex005.	4.9	92
8	Assessing the expected response to genomic selection of individuals and families in Eucalyptus breeding with an additive-dominant model. Heredity, 2017, 119, 245-255.	2.6	76
9	The contribution of dominance to phenotype prediction in a pine breeding and simulated population. Heredity, 2016, 117, 33-41.	2.6	72
10	Revealing new candidate genes for reproductive traits in pigs: combining Bayesian GWAS and functional pathways. Genetics Selection Evolution, 2016, 48, 9.	3.0	68
11	Multi-Trait GWAS and New Candidate Genes Annotation for Growth Curve Parameters in Brahman Cattle. PLoS ONE, 2015, 10, e0139906.	2.5	66
12	Machine learning approaches and their current application in plant molecular biology: A systematic review. Plant Science, 2019, 284, 37-47.	3.6	66
13	Performance of constructed wetlands in the treatment of aerated coffee processing wastewater: Removal of nutrients and phenolic compounds. Ecological Engineering, 2012, 49, 264-269.	3.6	58
14	Linkage disequilibrium and haplotype block structure in six commercial pig lines. Journal of Animal Science, 2013, 91, 3493-3501.	0.5	56
15	Ridge, Lasso and Bayesian additive-dominance genomic models. BMC Genetics, 2015, 16, 105.	2.7	53
16	Molecular Factors Underlying the Deposition of Intramuscular Fat and Collagen in Skeletal Muscle of Nellore and Angus Cattle. PLoS ONE, 2015, 10, e0139943.	2.5	52
17	Weighted single-step GWAS and gene network analysis reveal new candidate genes for semen traits in pigs. Genetics Selection Evolution, 2018, 50, 40.	3.0	49
18	Sire evaluation for total number born in pigs using a genomic reaction norms approach1. Journal of Animal Science, 2014, 92, 3825-3834.	0.5	46

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19	Invited review: Advances and applications of random regression models: From quantitative genetics to genomics. Journal of Dairy Science, 2019, 102, 7664-7683.	3.4	46
20	Application of single-step genomic evaluation using multiple-trait random regression test-day models in dairy cattle. Journal of Dairy Science, 2019, 102, 2365-2377.	3.4	45
21	Environmental uniformity, site quality and tree competition interact to determine stand productivity of clonal Eucalyptus. Forest Ecology and Management, 2018, 410, 76-83.	3.2	44
22	Sustained <scp>NIK</scp>â€mediated antiviral signalling confers broadâ€spectrum tolerance to begomoviruses in cultivated plants. Plant Biotechnology Journal, 2015, 13, 1300-1311.	8.3	43
23	Effect of influent aeration on removal of organic matter from coffee processing wastewater in constructed wetlands. Journal of Environmental Management, 2013, 128, 912-919.	7.8	42
24	Genomeâ€wide association study and annotating candidate gene networks affecting age at first calving in Nellore cattle. Journal of Animal Breeding and Genetics, 2017, 134, 484-492.	2.0	42
25	Genetic parameters for semen quality and quantity traits in five pig lines1. Journal of Animal Science, 2017, 95, 4251-4259.	0.5	42
26	Genome-wide association for milk production traits and somatic cell score in different lactation stages of Ayrshire, Holstein, and Jersey dairy cattle. Journal of Dairy Science, 2019, 102, 8159-8174.	3.4	42
27	Genome-Wide Association and Regional Heritability Mapping of Plant Architecture, Lodging and Productivity in<i>Phaseolus vulgaris</i>. G3: Genes, Genomes, Genetics, 2018, 8, 2841-2854.	1.8	41
28	Independent Component Analysis (ICA) based-clustering of temporal RNA-seq data. PLoS ONE, 2017, 12, e0181195.	2.5	39
29	Bayesian GWAS and network analysis revealed new candidate genes for number of teats in pigs. Journal of Applied Genetics, 2015, 56, 123-132.	1.9	35
30	Multi-trait multi-environment Bayesian model reveals G x E interaction for nitrogen use efficiency components in tropical maize. PLoS ONE, 2018, 13, e0199492.	2.5	35
31	Improved estimation of inbreeding and kinship in pigs using optimized SNP panels. BMC Genetics, 2013, 14, 92.	2.7	34
32	Linkage disequilibrium patterns and persistence of phase in purebred and crossbred pig (Sus scrofa) populations. BMC Genetics, 2014, 15, 126.	2.7	33
33	Novel lactic acid bacteria strains as inoculants on alfalfa silage fermentation. Scientific Reports, 2019, 9, 8007.	3.3	31
34	Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. Canadian Journal of Animal Science, 2020, 100, 587-604.	1.5	31
35	Genomeâ€wide association studies pathwayâ€based metaâ€analysis for residual feed intake in beef cattle. Animal Genetics, 2019, 50, 150-153.	1.7	30
36	Genetic parameters of body weight and egg traits in meat-type quail. Livestock Science, 2013, 153, 27-32.	1.6	29

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37	Single-step genome-wide association for longitudinal traits of Canadian Ayrshire, Holstein, and Jersey dairy cattle. Journal of Dairy Science, 2019, 102, 9995-10011.	3.4	29
38	A genome-wide association study reveals a novel candidate gene for sperm motility in pigs. Animal Reproduction Science, 2014, 151, 201-207.	1.5	28
39	Efficacy of population structure analysis with breeding populations and inbred lines. Genetica, 2013, 141, 389-399.	1.1	27
40	Genomic selection for boar taint compounds and carcass traits in a commercial pig population. Livestock Science, 2015, 174, 10-17.	1.6	27
41	Effect of maternal nutrition and days of gestation on pituitary gland and gonadal gene expression in cattle. Journal of Dairy Science, 2016, 99, 3056-3071.	3.4	27
42	Análise de medidas repetidas na avaliação de clones de café 'Conilon'. Pesquisa Agropecuaria Brasileira, 2008, 43, 1171-1176.	0.9	26
43	Geminivirus data warehouse: a database enriched with machine learning approaches. BMC Bioinformatics, 2017, 18, 240.	2.6	26
44	Genetic correlations between feed efficiency traits, and growth performance and carcass traits in purebred and crossbred pigs. Journal of Animal Science, 2018, 96, 817-829.	0.5	26
45	Bayesian inference of mixed models in quantitative genetics of crop species. Theoretical and Applied Genetics, 2013, 126, 1749-1761.	3.6	25
46	Análise da curva de crescimento de machos Hereford. Ciencia E Agrotecnologia, 2003, 27, 1105-1112.	1.5	24
47	Curva de crescimento de novilhos Hereford: heterocedasticidade e resíduos autorregressivos. Ciencia Rural, 2005, 35, 422-427.	0.5	24
48	Genomic Prediction of Additive and Non-additive Effects Using Genetic Markers and Pedigrees. G3: Genes, Genomes, Genetics, 2019, 9, 2739-2748.	1.8	24
49	Identidade de modelos não lineares para comparar curvas de crescimento de bovinos da raça Tabapuã. Pesquisa Agropecuaria Brasileira, 2014, 49, 57-62.	0.9	24
50	Avaliação de curvas de crescimento morfométrico de linhagens de tilápia do nilo (Oreochromis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.5	23
51	Short communication: Molecular characterization and antimicrobial resistance of pathogenic Escherichia coli isolated from raw milk and Minas Frescal cheeses in Brazil. Journal of Dairy Science, 2019, 102, 10850-10854.	3.4	23
52	Genomic Predictions Using Low-Density SNP Markers, Pedigree and GWAS Information: A Case Study with the Non-Model Species Eucalyptus cladocalyx. Plants, 2020, 9, 99.	3.5	23
53	Análise de agrupamento na seleção de modelos de regressão não-lineares para curvas de crescimento de ovinos cruzados. Ciencia Rural, 2011, 41, 692-698.	0.5	23
54	A raça Indubrasil no Nordeste brasileiro: melhoramento e estrutura populacional. Revista Brasileira De Zootecnia, 2009, 38, 2327-2334.	0.8	22

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55	Linear and <scp>P</scp>oisson models for genetic evaluation of tick resistance in crossâ€bred <scp>H</scp>ereford x <scp>N</scp>ellore cattle. Journal of Animal Breeding and Genetics, 2013, 130, 417-424.	2.0	22
56	Meta-analysis of genetic-parameter estimates for reproduction, growth and carcass traits in Nellore cattle by using a random-effects model. Animal Production Science, 2018, 58, 1575.	1.3	22
57	Differentially expressed mRNAs, proteins and miRNAs associated to energy metabolism in skeletal muscle of beef cattle identified for low and high residual feed intake. BMC Genomics, 2019, 20, 501.	2.8	22
58	Quantile regression for genome-wide association study of flowering time-related traits in common bean. PLoS ONE, 2018, 13, e0190303.	2.5	22
59	Modelo logÃstico difÃ¡sico no estudo do crescimento de fÃªmeas da raÃ§a Hereford. Ciencia Rural, 2008, 38, 1984-1990.	0.5	21
60	A time series analysis of brown eye spot progress in conventional and organic coffee production systems. Plant Pathology, 2015, 64, 157-166.	2.4	21
61	Nitrous oxide, methane, and ammonia emissions from cattle excreta on Brachiaria decumbens growing in monoculture or silvopasture with Acacia mangium and Eucalyptus grandis. Agriculture, Ecosystems and Environment, 2020, 295, 106896.	5.3	21
62	Genomic prediction of leaf rust resistance to Arabica coffee using machine learning algorithms. Scientia Agricola, 2021, 78, .	1.2	21
63	Quantitative genetics theory for genomic selection and efficiency of breeding value prediction in open-pollinated populations. Scientia Agricola, 2016, 73, 243-251.	1.2	20
64	Genomic prediction of lactation curves for milk, fat, protein, and somatic cell score in Holstein cattle. Journal of Dairy Science, 2019, 102, 452-463.	3.4	20
65	Curvas de crescimento e influÃªncia de fatores nÃ£o-genÃ©ticos sobre as taxas de crescimento de bovinos da raÃ§a Nelore. Ciencia E Agrotecnologia, 2004, 28, 647-654.	1.5	20
66	Genome-enabled prediction for tick resistance in Hereford and Braford beef cattle via reaction norm models1. Journal of Animal Science, 2016, 94, 1834-1843.	0.5	19
67	Effects of increasing palm kernel cake inclusion in supplements fed to grazing lambs on growth performance, carcass characteristics, and fatty acid profile. Animal Feed Science and Technology, 2017, 226, 71-80.	2.2	19
68	Use of molecular markers to improve relationship information in the genetic evaluation of beef cattle tick resistance under pedigreeâ€based models. Journal of Animal Breeding and Genetics, 2017, 134, 14-26.	2.0	19
69	Best Linear Unbiased Prediction and Family Selection in Crop Species. Crop Science, 2011, 51, 2371-2381.	1.8	18
70	Genotype by environment interaction for tick resistance of Hereford and Braford beef cattle using reaction norm models. Genetics Selection Evolution, 2016, 48, 3.	3.0	18
71	Combining different functions to describe milk, fat, and protein yield in goats using Bayesian multiple-trait random regression models1. Journal of Animal Science, 2016, 94, 1865-1874.	0.5	18
72	Comparing Alternative Single-Step GBLUP Approaches and Training Population Designs for Genomic Evaluation of Crossbred Animals. Frontiers in Genetics, 2020, 11, 263.	2.3	18

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73	Prediction of aboveground biomass and dry‑matter content in *Brachiaria* pastures by combining meteorological data and satellite imagery. Grass and Forage Science, 2021, 76, 340-352.	2.9	18
74	MÃ©todo de comparaÃ§Ã£o de modelos de regressÃ£o nÃ£o-lineares em bananeiras. Ciencia Rural, 2009, 39, 1380-1386.	0.5	18
75	Traditional and alternative nonlinear models for estimating the growth of Morada Nova sheep. Revista Brasileira De Zootecnia, 2013, 42, 651-655.	0.8	17
76	Effects of nutrient intake level on mammary parenchyma growth and gene expression in crossbred (Holstein Ã— Gyr) prepubertal heifers. Journal of Dairy Science, 2016, 99, 9962-9973.	3.4	17
77	Comparing deregression methods for genomic prediction of test‑day traits in dairy cattle. Journal of Animal Breeding and Genetics, 2018, 135, 97-106.	2.0	17
78	Efficiency of genomic prediction of non-assessed single crosses. Heredity, 2018, 120, 283-295.	2.6	17
79	Genetic analysis of morphological and functional traits in Campolina horses using Bayesian multi-trait model. Livestock Science, 2018, 216, 119-129.	1.6	17
80	Genomic analyses for predicted milk fatty acid composition throughout lactation in North American Holstein cattle. Journal of Dairy Science, 2020, 103, 6318-6331.	3.4	17
81	Abordagem Bayesiana das curvas de crescimento de duas cultivares de feijoeiro. Ciencia Rural, 2008, 38, 1516-1521.	0.5	16
82	MÃ©todos de agrupamento em estudo de divergÃªncia genÃ©tica de pimentas. Horticultura Brasileira, 2012, 30, 428-432.	0.5	16
83	Analyses of reaction norms reveal new chromosome regions associated with tick resistance in cattle. Animal, 2018, 12, 205-214.	3.3	16
84	Abordagem bayesiana para avaliaÃ§Ã£o da adaptabilidade e estabilidade de genÃ³tipos de alfafa. Pesquisa Agropecuaria Brasileira, 2011, 46, 26-32.	0.9	16
85	Estudo das curvas de crescimento de cordeiros das raÃ§as santa inÃªs e bergamÃ¡cia considerando heterogeneidade de variÃ¢ncias. Ciencia E Agrotecnologia, 2004, 28, 381-388.	1.5	16
86	Desempenho produtivo, caracterÃsticas de carcaÃ§a e avaliaÃ§Ã£o econÃ´mica de bovinos cruzados, castrados e nÃ£o-castrados, terminados em pastagens de Brachiaria decumbens. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2008, 60, 1157-1165.	0.4	15
87	Selection of models of lactation curves to use in milk production simulation systems. Revista Brasileira De Zootecnia, 2010, 39, 891-902.	0.8	15
88	Fracionamento de carboidratos e proteÃnas de gramÃneas tropicais cortadas em trÃªs idades. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2010, 62, 667-676.	0.4	15
89	Three-step Bayesian factor analysis applied to QTL detection in crosses between outbred pig populations. Livestock Science, 2011, 142, 210-215.	1.6	15
90	Efficiency of low heritability QTL mapping under high SNP density. Euphytica, 2017, 213, 1.	1.2	15

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91	Genotype by feed interaction for feed efficiency and growth performance traits in pigs1. Journal of Animal Science, 2018, 96, 4125-4135.	0.5	15
92	Linkage disequilibrium and haplotype block patterns in popcorn populations. PLoS ONE, 2019, 14, e0219417.	2.5	15
93	Genetic parameters for fertility traits in Nellore bulls. Reproduction in Domestic Animals, 2020, 55, 38-43.	1.4	15
94	Optimization of Eucalyptus breeding through random regression models allowing for reaction norms in response to environmental gradients. Tree Genetics and Genomes, 2020, 16, 1.	1.6	15
95	Genetic characterization of papaya plants (Carica papaya L.) derived from the first backcross generation. Genetics and Molecular Research, 2011, 10, 393-403.	0.2	14
96	Epidemiology, clinical signs, histopathology and molecular characterization of canine leproid granuloma: a retrospective study of cases from Brazil. Veterinary Dermatology, 2011, 22, 249-256.	1.2	14
97	Supervised independent component analysis as an alternative method for genomic selection in pigs. Journal of Animal Breeding and Genetics, 2014, 131, 452-461.	2.0	14
98	Eberhart and Russel's Bayesian Method in the Selection of Popcorn Cultivars. Crop Science, 2015, 55, 571-577.	1.8	14
99	Relevance of genetic relationship in GWAS and genomic prediction. Journal of Applied Genetics, 2018, 59, 1-8.	1.9	14
100	Genotypic variation and relationships among traits for root morphology in a panel of tropical maize inbred lines under contrasting nitrogen levels. Euphytica, 2019, 215, 1.	1.2	14
101	Multiple-trait model through Bayesian inference applied to Jatropha curcas breeding for bioenergy. PLoS ONE, 2021, 16, e0247775.	2.5	14
102	Genotype-environment interaction in common bean cultivars with carioca grain, recommended for cultivation in Brazil in the last 40 years. Crop Breeding and Applied Biotechnology, 2015, 15, 244-250.	0.4	14
103	Divergência genética entre genótipos de pimenta com base em caracteres morfo-agrônomicos. Horticultura Brasileira, 2011, 29, 354-358.	0.5	14
104	Genomic growth curves of an outbred pig population. Genetics and Molecular Biology, 2013, 36, 520-527.	1.3	13
105	Comparing multi-trait Poisson and Gaussian Bayesian models for genetic evaluation of litter traits in pigs. Livestock Science, 2015, 176, 47-53.	1.6	13
106	Bayesian Models combining Legendre and B-spline polynomials for genetic analysis of multiple lactations in Gyr cattle. Livestock Science, 2017, 201, 78-84.	1.6	13
107	Artificial neural network for prediction of the area under the disease progress curve of tomato late blight. Scientia Agricola, 2017, 74, 51-59.	1.2	13
108	Bayesian segmented regression model for adaptability and stability evaluation of cotton genotypes. Euphytica, 2020, 216, 1.	1.2	13

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109	Investigating pig survival in different production phases using genomic models. Journal of Animal Science, 2021, 99, .	0.5	13
110	Abordagem Bayesiana da curva de lactação de cabras Saanen de primeira e segunda ordem de parto. Pesquisa Agropecuaria Brasileira, 2005, 40, 27-33.	0.9	13
111	Modelos de regressão não linear aplicados a grupos de acessos de alho. Horticultura Brasileira, 2014, 32, 178-183.	0.5	13
112	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
113	BLUP for genetic evaluation of plants in non-inbred families of annual crops. Euphytica, 2010, 174, 31-39.	1.2	12
114	Seleção e classificação multivariada de modelos de crescimento não lineares para bovinos Nelore. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2011, 63, 364-371.	0.4	12
115	Regressão via componentes independentes aplicada à seleção genômica para características de carcaça em suínos. Pesquisa Agropecuaria Brasileira, 2013, 48, 619-626.	0.9	12
116	Wind dispersal of <i>Puccinia psidii</i> urediniospores and progress of eucalypt rust. Forest Pathology, 2015, 45, 102-110.	1.1	12
117	Accessing marker effects and heritability estimates from genome prediction by Bayesian regularized neural networks. Livestock Science, 2016, 191, 91-96.	1.6	12
118	Genome-wide association studies, meta-analyses and derived gene network for meat quality and carcass traits in pigs. Animal Production Science, 2018, 58, 1100.	1.3	12
119	Genome wide association study reveals new candidate genes for resistance to nematodes in Creole goat. Small Ruminant Research, 2018, 166, 109-114.	1.2	12
120	Evaluation of a long-established silvopastoral Brachiaria decumbens system: plant characteristics and feeding value for cattle. Crop and Pasture Science, 2019, 70, 814.	1.5	12
121	GWAS and gene networks for milk-related traits from test-day multiple lactations in Portuguese Holstein cattle. Journal of Applied Genetics, 2020, 61, 465-476.	1.9	12
122	Intramuscular collagen characteristics and expression of related genes in skeletal muscle of cull cows receiving a high-energy diet. Meat Science, 2021, 177, 108495.	5.5	12
123	Obtenção de corante natural azul extraído de frutos de jenipapo. Pesquisa Agropecuaria Brasileira, 2009, 44, 649-652.	0.9	12
124	Novel Vasopressin Type 2 (AVPR2) Gene Mutations in Brazilian Nephrogenic Diabetes Insipidus Patients. Genetic Testing and Molecular Biomarkers, 2006, 10, 157-162.	1.7	11
125	Agrupamento de curvas de progresso de requeima, em tomateiro originado de cruzamento interespecífico. Pesquisa Agropecuaria Brasileira, 2010, 45, 1095-1101.	0.9	11
126	Bayesian analysis of autoregressive panel data model: application in genetic evaluation of beef cattle. Scientia Agricola, 2011, 68, 237-245.	1.2	11

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127	Selection of sugar cane families by using BLUP and multi-diverse analyses for planting in the Brazilian savannah. Genetics and Molecular Research, 2014, 13, 1619-1626.	0.2	11
128	Caracterização de colágenos tipos I e III no estroma do carcinoma de células escamosas cutâneo em cães. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2016, 68, 147-154.	0.4	11
129	After genome-wide association studies: Gene networks elucidating candidate genes divergences for number of teats across two pig populations1. Journal of Animal Science, 2016, 94, 1446-1458.	0.5	11
130	Genomic selection for productive traits in biparental cassava breeding populations. PLoS ONE, 2019, 14, e0220245.	2.5	11
131	Proteomic analysis reveals changes in energy metabolism of skeletal muscle in beef cattle supplemented with vitamin A. Journal of the Science of Food and Agriculture, 2020, 100, 3536-3543.	3.5	11
132	Urea supplementation in rumen and post-rumen for cattle fed a low-quality tropical forage. British Journal of Nutrition, 2020, 124, 1166-1178.	2.3	11
133	Estimated genetic associations among reproductive traits in Nellore cattle using Bayesian analysis. Animal Reproduction Science, 2020, 214, 106305.	1.5	11
134	Multiple centroid method to evaluate the adaptability of alfalfa genotypes. Revista Ceres, 2015, 62, 30-36.	0.4	11
135	Quantitative genetics theory for genomic selection and efficiency of genotypic value prediction in open-pollinated populations. Scientia Agricola, 2017, 74, 41-50.	1.2	11
136	Population structure correction for genomic selection through eigenvector covariates. Crop Breeding and Applied Biotechnology, 2017, 17, 350-358.	0.4	11
137	Produção, composição e rendimento em queijo do leite de ovelhas Santa Inês tratadas com ocitocina. Revista Brasileira De Zootecnia, 2007, 36, 438-444.	0.8	11
138	Genetic progress resulting from forty-three years of breeding of the carioca common bean in Brazil. Genetics and Molecular Research, 2016, 15, .	0.2	11
139	Degradabilidade ruminal do feno de alguns alimentos volumosos para ruminantes. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2006, 58, 575-580.	0.4	10
140	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
141	Differentially transcribed genes in skeletal muscle of lambs. Livestock Science, 2012, 150, 31-41.	1.6	10
142	Bayesian model-based clustering of temporal gene expression using autoregressive panel data approach. Bioinformatics, 2012, 28, 2004-2007.	4.1	10
143	Follicular dynamics and gene expression in granulosa cells, corpora lutea and oocytes from gilts of breeds with low and high ovulation rates. Reproduction, Fertility and Development, 2014, 26, 316.	0.4	10
144	Effects of alleles in crossbred pigs estimated for genomic prediction depend on their breed-of-origin. BMC Genomics, 2018, 19, 740.	2.8	10

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145	Energy and protein requirements of Holstein Ã— Gyr crossbred heifers. Animal, 2020, 14, 1857-1866.	3.3	10
146	Genome-Wide Analyses Reveal the Genetic Architecture and Candidate Genes of Indicine, Taurine, Synthetic Crossbreds, and Locally Adapted Cattle in Brazil. Frontiers in Genetics, 2021, 12, 702822.	2.3	10
147	Five decades of black common bean genetic breeding in Brazil. Pesquisa Agropecuaria Tropical, 2016, 46, 259-266.	1.0	10
148	ClassificaÃ§Ã£o multivariada de modelos de crescimento para grupos genÃ©ticos de ovinos de corte. Revista Brasileira De Saude E Producao Animal, 2012, 13, 62-73.	0.3	10
149	Fine mapping and single nucleotide polymorphism effects estimation on pig chromosomes 1, 4, 7, 8, 17 and X. Genetics and Molecular Biology, 2013, 36, 511-519.	1.3	9
150	Effect of the dietary inclusion of dried oregano (Origanum vulgare L.) on the characteristics of milk from HolsteinÃ—Zebu cows. Animal Feed Science and Technology, 2014, 192, 101-105.	2.2	9
151	Comparison of dimensionality reduction methods to predict genomic breeding values for carcass traits in pigs. Genetics and Molecular Research, 2015, 14, 12217-12227.	0.2	9
152	Estimating additive and dominance variances for complex traits in pigs combining genomic and pedigree information. Genetics and Molecular Research, 2015, 14, 6303-6311.	0.2	9
153	Accuracy of genome-enabled prediction exploring purebred and crossbred pig populations1. Journal of Animal Science, 2015, 93, 4684-4691.	0.5	9
154	Bayesian estimation of genetic parameters for individual feed conversion and body weight gain in meat quail. Livestock Science, 2017, 200, 76-79.	1.6	9
155	Benchmarking Bayesian genome enabled-prediction models for age at first calving in Nellore cows. Livestock Science, 2018, 211, 75-79.	1.6	9
156	Oscillating and static dietary crude protein supply. I. Impacts on intake, digestibility, performance, and nitrogen balance in young Nellore bulls1. Translational Animal Science, 2019, 3, 1205-1215.	1.1	9
157	Applying the Metafounders Approach for Genomic Evaluation in a Multibreed Beef Cattle Population. Frontiers in Genetics, 2020, 11, 556399.	2.3	9
158	Factors affecting heterotic grouping with cross‐pollinating crops. Agronomy Journal, 2021, 113, 210-223.	1.8	9
159	Genetic evaluation of grain sorghum hybrids in Brazilian environments using the REML/BLUP procedure. Scientia Agricola, 2014, 71, 146-150.	1.2	9
160	CNV detection and their association with growth, efficiency and carcass traits in Santa InÃªs sheep. Journal of Animal Breeding and Genetics, 2022, 139, 476-487.	2.0	9
161	Linkage disequilibrium, SNP frequency change due to selection, and association mapping in popcorn chromosome regions containing QTLs for quality traits. Genetics and Molecular Biology, 2016, 39, 97-110.	1.3	8
162	Expression of myogenes in longissimus dorsi muscle during prenatal development in commercial and local Piau pigs. Genetics and Molecular Biology, 2016, 39, 589-599.	1.3	8

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163	Regularized quantile regression for SNP marker estimation of pig growth curves. Journal of Animal Science and Biotechnology, 2017, 8, 59.	5.3	8
164	Transgenerational epigenetic variance for body weight in meat quails. Journal of Animal Breeding and Genetics, 2018, 135, 178-185.	2.0	8
165	Can scrotal circumference-based selection discard bulls with good productive and reproductive potential?. PLoS ONE, 2018, 13, e0193103.	2.5	8
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167	Associations between morphometric variables and weight and yields carcass in Pirapitinga<i>Piaractus brachypomus</i>. Aquaculture Research, 2019, 50, 2004-2011.	1.8	8
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