Luis Varona

List of Publications by Year in descending order

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109321 155660 4,321 156 35 55 h-index citations g-index papers 156 156 156 3295 citing authors docs citations times ranked all docs

#	Article	IF	CITATIONS
1	On the Additive and Dominant Variance and Covariance of Individuals Within the Genomic Selection Scope. Genetics, 2013, 195, 1223-1230.	2.9	253
2	Detecting inbreeding depression for reproductive traits in Iberian pigs using genome-wide data. Genetics Selection Evolution, 2015, 47, 1.	3.0	191
3	Non-additive Effects in Genomic Selection. Frontiers in Genetics, 2018, 9, 78.	2.3	157
4	Fine mapping of porcine chromosome 6 QTL and LEPR effects on body composition in multiple generations of an Iberian by Landrace intercross. Genetical Research, 2005, 85, 57-67.	0.9	127
5	Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. Genetics, 2017, 206, 1297-1307.	2.9	125
6	A note on mate allocation for dominance handling in genomic selection. Genetics Selection Evolution, 2010, 42, 33.	3.0	118
7	Quantitative trait locus mapping for meat quality traits in an Iberian × Landrace F2 pig population1. Journal of Animal Science, 2002, 80, 2801-2808.	0.5	104
8	A Bayesian analysis of the effect of selection for growth rate on growth curves in rabbits. Genetics Selection Evolution, 2003, 35, 21-41.	3.0	82
9	Detection of QTL affecting fatty acid composition in the pig. Mammalian Genome, 2003, 14, 650-656.	2.2	74
10	QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects. Genetical Research, 2002, 80, 145-154.	0.9	68
11	Revealing new candidate genes for reproductive traits in pigs: combining Bayesian GWAS and functional pathways. Genetics Selection Evolution, 2016, 48, 9.	3.0	68
12	Genetic analysis of growth curve parameters for male and female chickens resulting from selection on shape of growth curve Journal of Animal Science, 2000, 78, 2515.	0.5	66
13	Analysis of Fertility and Dystocia in Holsteins Using Recursive Models to Handle Censored and Categorical Data. Journal of Dairy Science, 2007, 90, 2012-2024.	3.4	64
14	Analysis of founder-specific inbreeding depression on birth weight in Ripollesa lambs1. Journal of Animal Science, 2009, 87, 72-79.	0.5	61
15	Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. Genetics Selection Evolution, 2014, 46, 40.	3.0	59
16	Analysis of Litter Size and Average Litter Weight in Pigs Using a Recursive Model. Genetics, 2007, 177, 1791-1799.	2.9	58
17	Threshold-linear versus linear-linear analysis of birth weight and calving ease using an animal model: I. Variance component estimation Journal of Animal Science, 1999, 77, 1994.	0.5	56
18	Genomic selection models for directional dominance: an example for litter size in pigs. Genetics Selection Evolution, 2018, 50, 1.	3.0	56

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19	Polymorphism of the pig <i>acetylâ€eoenzyme A carboxylase α</i> gene is associated with fatty acid composition in a Duroc commercial line. Animal Genetics, 2009, 40, 410-417.	1.7	54
20	Multiple trait genetic analysis of underlying biological variables of production functions. Livestock Science, 1997, 47, 201-209.	1.2	53
21	Quantitative Trait Loci Mapping in F2 Crosses Between Outbred Lines. Genetics, 2000, 155, 391-405.	2.9	53
22	Comparison of different nonlinear functions to describe Nelore cattle growth1. Journal of Animal Science, 2009, 87, 496-506.	0.5	52
23	Comparative study of equine bone marrow and adipose tissueâ€derived mesenchymal stromal cells. Equine Veterinary Journal, 2012, 44, 33-42.	1.7	52
24	Multivariate analysis of litter size for multiple parities with production traits in pigs: I. Bayesian variance component estimation. Journal of Animal Science, 2002, 80, 2540.	0.5	52
25	Mapping of quantitative trait loci for cholesterol, LDL, HDL, and triglyceride serum concentrations in pigs. Physiological Genomics, 2008, 35, 199-209.	2.3	51
26	A study of heterogeneity of environmental variance for slaughter weight in pigs. Animal, 2008, 2, 19-26.	3.3	49
27	Hypothalamic expression of porcine leptin receptor (LEPR), neuropeptide Y (NPY), and cocaine- and amphetamine-regulated transcript (CART) genes is influenced by LEPR genotype. Mammalian Genome, 2010, 21, 583-591.	2.2	42
28	Bayesian analysis of parent-specific transmission ratio distortion in seven Spanish beef cattle breeds. Animal Genetics, 2017, 48, 93-96.	1.7	42
29	Bayes factors for detection of Quantitative Trait Loci. Genetics Selection Evolution, 2001, 33, 133-52.	3.0	40
30	QTL mapping for teat number in an Iberian-by-Meishan pig intercross. Animal Genetics, 2005, 36, 050823030348002-???.	1.7	40
31	A bi-dimensional genome scan for prolificacy traits in pigs shows the existence of multiple epistatic QTL. BMC Genomics, 2009, 10, 636.	2.8	40
32	Genetic diversity and divergence among Spanish beef cattle breeds assessed by a bovine high-density SNP chip1. Journal of Animal Science, 2015, 93, 5164-5174.	0.5	40
33	Bayesian Analysis of Wood's Lactation Curve for Spanish Dairy Cows. Journal of Dairy Science, 1998, 81, 1469-1478.	3.4	39
34	Estrogen receptor polymorphism in Landrace pigs and its association with litter size performance. Livestock Science, 2003, 82, 53-59.	1.2	39
35	Genomic BLUP including additive and dominant variation in purebreds and F1 crossbreds, with an application in pigs. Genetics Selection Evolution, 2016, 48, 6.	3.0	39
36	Estimation of dominance variance in purebred Yorkshire swine Journal of Animal Science, 1998, 76, 448.	0.5	37

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37	<i>Malic enzyme $1 < li>genotype$ is associated with backfat thickness and meat quality traits in pigs. Animal Genetics, 2006, 37, 28-32.</i>	1.7	37
38	Expression profiling of functional genes in prenatal skeletal muscle tissue in Duroc and Pietrain pigs. Journal of Animal Breeding and Genetics, 2011, 128, 15-27.	2.0	36
39	Characterization of the porcine acyl-CoA synthetase long-chain 4 gene and its association with growth and meat quality traits. Animal Genetics, 2006, 37, 219-224.	1.7	35
40	Olive oil quality and ripening in superâ€highâ€density Arbequina orchard. Journal of the Science of Food and Agriculture, 2013, 93, 2207-2220.	3.5	35
41	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
42	GWAS by GBLUP: Single and Multimarker EMMAX and Bayes Factors, with an Example in Detection of a Major Gene for Horse Gait. G3: Genes, Genomes, Genetics, 2018, 8, 2301-2308.	1.8	35
43	On growth, fatness, and form: A further look at porcine Chromosome 4 in an Iberian \tilde{A} — Landrace cross. Mammalian Genome, 2005, 16, 374-382.	2.2	33
44	Characterization of the porcine FABP5 gene and its association with the FAT1 QTL in an Iberian by Landrace cross. Animal Genetics, 2006, 37, 589-591.	1.7	33
45	Hypothesis testing for the genetic background of quantitative traits. Genetics Selection Evolution, 2001, 33, 3-16.	3.0	32
46	Genetic evaluation including intermediate omics features. Genetics, 2021, 219, .	2.9	32
47	Accuracy of genome-wide evaluation for disease resistance in aquaculture breeding programs1. Journal of Animal Science, 2011, 89, 3433-3442.	0.5	31
48	Genome Scans for Transmission Ratio Distortion Regions in Mice. Genetics, 2012, 191, 247-259.	2.9	31
49	Method R Estimates of Additive Genetic, Dominance Genetic, and Permanent Environmental Fraction of Variance for Yield and Health Traits of Holsteins. Journal of Dairy Science, 2000, 83, 1873-1877.	3.4	30
50	Additive genetic relationship of longevity with fertility and production traits in Nellore cattle based on bivariate models. Genetics and Molecular Research, 2010, 9, 176-187.	0.2	30
51	Bayesian inference of variance components for litter size in Rasa Aragonesa sheep Journal of Animal Science, 1998, 76, 23.	0.5	29
52	Genetic parameters of fertility in two lines of rabbits with different reproductive potential. Journal of Animal Science, 2005, 83, 340-343.	0.5	29
53	Genomic information in pig breeding: Science meets industry needs. Livestock Science, 2014, 166, 94-100.	1.6	29
54	Allelic frequencies of NR6A1 and VRTN, two genes that affect vertebrae number in diverse pig breeds: A study of the effects of the VRTN insertion on phenotypic traits of a Duroc×Landrace–Large White cross. Meat Science, 2015, 100, 150-155.	5 . 5	29

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55	Multivariate analysis of litter size for multiple parities with production traits in pigs: II. Response to selection for litter size and correlated response to production traits. Journal of Animal Science, 2002, 80, 2548.	0.5	29
56	Maternal animal model with correlation between maternal environmental effects of related dams Journal of Animal Science, 1999, 77, 2904.	0.5	28
57	Computation of identity by descent probabilities conditional on DNA markers via a Monte Carlo Markov Chain method. Genetics Selection Evolution, 2000, 32, 467-82.	3.0	27
58	Analysis of beef cattle longitudinal data applying a nonlinear model1. Journal of Animal Science, 2007, 85, 3189-3197.	0.5	27
59	Gene expression profiling of mesenteric lymph nodes from sheep with natural scrapie. BMC Genomics, 2014, 15, 59.	2.8	27
60	Epigenetics modifications and Subclinical Atherosclerosis in Obstructive Sleep Apnea: The EPIOSA study. BMC Pulmonary Medicine, 2014, 14, 114.	2.0	27
61	Adipocyte fatty-acid binding protein is closely associated to the porcine FAT1 locus on chromosome 41. Journal of Animal Science, 2006, 84, 2907-2913.	0.5	26
62	Variance component estimation by resampling. Journal of Animal Breeding and Genetics, 1992, 109, 358-363.	2.0	24
63	Prediction of Parental Dominance Combinations for Planned Matings, Methodology, and Simulation Results. Journal of Dairy Science, 1999, 82, 2186-2191.	3.4	24
64	On the performance of tests for the detection of signatures of selection: a case study with the Spanish autochthonous beef cattle populations. Genetics Selection Evolution, 2016, 48, 81.	3.0	24
65	Bayesian threshold analysis of direct and maternal genetic parameters for piglet mortality at farrowing in Large White, Landrace, and Pietrain populations1. Journal of Animal Science, 2009, 87, 80-87.	0.5	23
66	Monitoring changes in the demographic and genealogical structure of the main Spanish local beef breeds1. Journal of Animal Science, 2014, 92, 4364-4374.	0.5	23
67	Exploring Alternative Models for Sex-Linked Quantitative Trait Loci in Outbred Populations: Application to an Iberian $ ilde{A}$ — Landrace Pig Intercross. Genetics, 2002, 161, 1625-1632.	2.9	23
68	A Bayesian Model for the Analysis of Transgenerational Epigenetic Variation. G3: Genes, Genomes, Genetics, 2015, 5, 477-485.	1.8	21
69	c.A2456C-substitution in Pck1 changes the enzyme kinetic and functional properties modifying fat distribution in pigs. Scientific Reports, 2016, 6, 19617.	3.3	21
70	Effect of Full Sibs on Additive Breeding Values Under the Dominance Model for Stature in United States Holsteins. Journal of Dairy Science, 1998, 81, 1126-1135.	3.4	20
71	Genetic determination of fatty acid composition in Spanish Churra sheep milk. Journal of Dairy Science, 2010, 93, 330-339.	3.4	19
72	The effects of leptin receptor (LEPR) and melanocortin-4 receptor (MC4R) polymorphisms on fat content, fat distribution and fat composition in a Duroc×Landrace/Large White cross. Livestock Science, 2012, 145, 145-152.	1.6	19

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73	Gene Expression Profiling and Association with Prion-Related Lesions in the Medulla Oblongata of Symptomatic Natural Scrapie Animals. PLoS ONE, 2011, 6, e19909.	2.5	19
74	A Genetic Analysis of Mortality in Pigs. Genetics, 2010, 184, 277-284.	2.9	18
75	Estimation of the additive and dominance variances in SA Duroc pigs. Livestock Science, 2010, 131, 144-147.	1.6	18
76	Genetic parameters for growth of fiber diameter in alpacas1. Journal of Animal Science, 2011, 89, 2310-2315.	0.5	18
77	Genetic inbreeding depression load for morphological traits and defects in the Pura Raza Española horse. Genetics Selection Evolution, 2020, 52, 62.	3.0	18
78	Two-step versus joint analysis of Von Bertalanffy function. Journal of Animal Breeding and Genetics, 1999, 116, 331-338.	2.0	17
79	Pig melatonin receptor 1a (MTNR1A) genotype is associated with seasonal variation of sow litter size. Animal Reproduction Science, 2009, 115, 317-322.	1.5	17
80	<i><scp>DECR</scp>1</i> and <i><scp>ME</scp>1</i> genotypes are associated with lipid composition traits in <scp>D</scp> uroc pigs. Journal of Animal Breeding and Genetics, 2014, 131, 46-52.	2.0	16
81	Estimation of predictionâ€error variances by resampling. Journal of Animal Breeding and Genetics, 1995, 112, 176-182.	2.0	15
82	Variance components of fertility in Spanish Landrace pigs. Livestock Science, 2001, 67, 217-221.	1.2	15
83	A whole-genome analysis using robust asymmetric distributions. Genetical Research, 2006, 88, 143.	0.9	15
84	Skew distribution of founder-specific inbreeding depression effects on the longevity of Landrace sows. Genetical Research, 2008, 90, 499-508.	0.9	15
85	Genetic parameters and direct, maternal and heterosis effects on litter size in a diallel cross among three commercial varieties of Iberian pig. Animal, 2019, 13, 2765-2772.	3.3	15
86	Consequences of selection for growth on carcass and meat quality in Pirenaica cattle. Livestock Science, 2005, 95, 103-114.	1.2	14
87	Genetic evaluation of racing performance in trotter horses by competitive models. Livestock Science, 2011, 140, 155-160.	1.6	14
88	Changes in HSP gene and protein expression in natural scrapie with brain damage. Veterinary Research, 2011, 42, 13.	3.0	14
89	Identification of resilient sows in porcine reproductive and respiratory syndrome virus–infected farms1. Journal of Animal Science, 2019, 97, 3228-3236.	0.5	14
90	Parametric bootstrap for testing model fitting in the proportional hazards framework: An application to the survival analysis of Bruna dels Pirineus beef calves1. Journal of Animal Science, 2006, 84, 2609-2616.	0.5	13

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91	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
92	Linkage disequilibrium, persistence of phase, and effective population size in Spanish local beef cattle breeds assessed through a high-density single nucleotide polymorphism chip1. Journal of Animal Science, 2016, 94, 2779-2788.	0.5	13
93	Distinct spatial activation of intrinsic and extrinsic apoptosis pathways in natural scrapie: association with prion-related lesions. Veterinary Research, 2009, 40, 42.	3.0	13
94	A simulation study on the detection of causal mutations from F2 experiments. Journal of Animal Breeding and Genetics, 2005, 122, 30-36.	2.0	12
95	Medulla oblongata transcriptome changes during presymptomatic natural scrapie and their association with prion-related lesions. BMC Genomics, 2012, 13, 399.	2.8	12
96	Joint analysis of additive, dominant and firstâ€order epistatic effects of four genes (<scp><i>IGF2</i></scp> <ii>(Scp><i>IGF2</i><ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2<ii>IGF2</ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii></ii>	O rgBT /C	verlock 10 Tf
97	Genetics, 2014, 45, 133-137. Joint Analysis of Binomial and Continuous Traits with a Recursive Model: A Case Study Using Mortality and Litter Size of Pigs. Genetics, 2014, 196, 643-651.	2.9	12
98	A comparison of nonlinear mixed models and response to selection of tick-infestation on lambs. PLoS ONE, 2017, 12, e0172711.	2.5	12
99	Usefulness of running animal models in absence of pedigrees: Estimation of genetic parameters for gastrointestinal parasite resistance traits in Djallonké sheep of Burkina Faso. Small Ruminant Research, 2018, 160, 81-88.	1.2	12
100	Cross-validation analysis for genetic evaluation models for ranking in endurance horses. Animal, 2018, 12, 20-27.	3.3	12
101	Genetic inbreeding depression load for fertility traits in Pura Raza Espa $\tilde{A}\pm$ ola mares. Journal of Animal Science, 2021, 99, .	0.5	12
102	Testing genetic determinism in rate of hoof growth in pigs using Bayes Factors. Livestock Science, 2006, 105, 50-56.	1.6	11
103	Inbreeding depression load for litter size in Entrepelado and Retinto Iberian pig varieties1. Journal of Animal Science, 2019, 97, 1979-1986.	0.5	11
104	The effect of divergent selection for intramuscular fat on the domestic rabbit genome. Animal, 2020, 14, 2225-2235.	3.3	11
105	Assignment of the 2,4-dienoyl-CoA reductase (DECR) gene to porcine chromosome 4. Animal Genetics, 2002, 33, 164-165.	1.7	10
106	A multivariate analysis with direct additive and inbreeding depression load effects. Genetics Selection Evolution, 2019, 51, 78.	3.0	10
107	A dimensional reduction approach to modulate the core ruminal microbiome associated with methane emissions via selective breeding. Journal of Dairy Science, 2021, 104, 8135-8151.	3.4	10
108	A model with heterogeneous thresholds for subjective traits: Fat cover and conformation score in the Pirenaica beef cattle1. Journal of Animal Science, 2009, 87, 1210-1217.	0.5	9

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109	Nucleotide Sequence and Association Analysis of Pig Apolipoprotein-B and LDL-Receptor Genes. Animal Biotechnology, 2009, 20, 110-123.	1.5	9
110	Exploring the possibilities of genetic improvement from traceability data. Livestock Science, 2009, 125, 115-120.	1.6	9
111	Genetic correlation of longevity with growth, post-mortem, docility and some morphological traits in the Pirenaica beef cattle breed. Animal, 2012, 6, 873-879.	3.3	9
112	An assessor-specific Bayesian multi-threshold mixed model for analyzing ordered categorical traits in tree breeding. Tree Genetics and Genomes, 2013, 9, 1423-1434.	1.6	9
113	Bayes factor for testing between different structures of random genetic groups: A case study using weaning weight in Bruna dels Pirineus beef cattle. Genetics Selection Evolution, 2007, 39, 39.	3.0	8
114	Genomic differentiation between Asturiana de los Valles, Avileña-Negra Ibérica, Bruna dels Pirineus, Morucha, Pirenaica, Retinta and Rubia Gallega cattle breeds. Animal, 2017, 11, 1667-1679.	3.3	8
115	Mapping Recombination Rate on the Autosomal Chromosomes Based on the Persistency of Linkage Disequilibrium Phase Among Autochthonous Beef Cattle Populations in Spain. Frontiers in Genetics, 2019, 10, 1170.	2.3	8
116	Additive and Dominance Genomic Analysis for Litter Size in Purebred and Crossbred Iberian Pigs. Genes, 2022, 13, 12.	2.4	8
117	A note on accuracy of Bayesian LASSO regression in GWS. Livestock Science, 2011, 142, 310-314.	1.6	7
118	Crossbreeding effects on pig growth and carcass traits from two Iberian strains. Animal, 2014, 8, 1569-1576.	3.3	7
119	Consequences of paternally inherited effects on the genetic evaluation of maternal effects. Genetics Selection Evolution, 2015, 47, 63.	3.0	7
120	On the haplotype diversity along the genome in Spanish beef cattle populations. Livestock Science, 2017, 201, 30-33.	1.6	7
121	Bayesian analysis of pig growth curves combining pedigree and genomic information. Livestock Science, 2017, 201, 34-40.	1.6	7
122	Modeling Skewness in Human Transcriptomes. PLoS ONE, 2012, 7, e38919.	2.5	7
123	Empirical Bayes factor analyses of quantitative trait loci for gestation length in Iberian × Meishan F2 sows. Animal, 2008, 2, 177-183.	3.3	6
124	Forkhead Box P3 Methylation and Expression in Men with Obstructive Sleep Apnea. International Journal of Molecular Sciences, 2020, 21, 2233.	4.1	6
125	Genetic parameters for postweaning traits in Braunvieh cattle. Genetics and Molecular Research, 2010, 9, 545-553.	0.2	6
126	Genomic differentiation among varieties of Iberian pig. Spanish Journal of Agricultural Research, 2020, 18, e0401.	0.6	6

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127	Meat production using four terminal pig lines. Journal of the Science of Food and Agriculture, 2003, 83, 1504-1510.	3.5	5
128	A Multithreshold Model for Sensory Analysis. Journal of Food Science, 2006, 71, S333-S336.	3.1	5
129	O-GlcNAcylation mediates the control of cytosolic phosphoenolpyruvate carboxykinase activity via Pgc1 $\hat{1}$ ±. PLoS ONE, 2017, 12, e0179988.	2.5	5
130	Genetic evaluation of age at first calving for Guzer \tilde{A}_i beef cattle using linear, threshold, and survival Bayesian models. Journal of Animal Science, 2018, 96, 2517-2524.	0.5	5
131	Effect of growth selection on morphology in Pirenaica cattle. Animal Research, 2006, 55, 55-63.	0.6	5
132	Performance of genomic selection under a singleâ€step approach in autochthonous Spanish beef cattle populations. Journal of Animal Breeding and Genetics, 2017, 134, 289-299.	2.0	4
133	The influence of natural selection in breeding programs: A simulation study. Livestock Science, 2017, 204, 98-103.	1.6	4
134	Genome association study through nonlinear mixed models revealed new candidate genes for pig growth curves. Scientia Agricola, 2017, 74, 1-7.	1.2	4
135	Combining Threshold, Thurstonian and Classical Linear Models in Horse Genetic Evaluations for Endurance Competitions. Animals, 2020, 10, 1075.	2.3	4
136	Between-groups within-gene heterogeneity of residual variances in microarray gene expression data. BMC Genomics, 2008, 9, 319.	2.8	3
137	Carcass conformation and fat cover scores in beef cattle: A comparison of threshold linear models vs grouped data models. Genetics Selection Evolution, 2011, 43, 16.	3.0	3
138	Non-linear recursive models for growth traits in the Pirenaica beef cattle breed. Animal, 2014, 8, 904-911.	3.3	3
139	Censored Bayesian models for genetic evaluation of age at first calving in Brazilian Brahman cattle. Livestock Science, 2019, 221, 177-180.	1.6	3
140	Maternal Transmission Ratio Distortion in Two Iberian Pig Varieties. Genes, 2020, 11, 1050.	2.4	3
141	A cross-specific multiplicative binomial recursive model for the analysis of perinatal mortality in a diallel cross among three varieties of Iberian pig. Scientific Reports, 2020, 10, 21190.	3.3	3
142	Genomic Prediction Methods Accounting for Nonadditive Genetic Effects. Methods in Molecular Biology, 2022, 2467, 219-243.	0.9	3
143	Bayes factor between Student t and Gaussian mixed models within an animal breeding context. Genetics Selection Evolution, 2008, 40, 395.	3.0	2
144	Sources of sire-specific genetic variance for birth and weaning weight in Bruna dels Pirineus beef calves. Animal, 2012, 6, 1931-1938.	3.3	2

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145	A practical approach to detect ancestral haplotypes in livestock populations. BMC Genetics, 2016, 17, 91.	2.7	2
146	Evaluation of the potential use of a meta-population for genomic selection in autochthonous beef cattle populations. Animal, 2018, 12, 1350-1357.	3.3	2
147	GIBBSTHUR: Software for Estimating Variance Components and Predicting Breeding Values for Ranking Traits Based on a Thurstonian Model. Animals, 2020, 10, 1001.	2.3	2
148	Detection of Genomic Regions with Pleiotropic Effects for Growth and Carcass Quality Traits in the Rubia Gallega Cattle Breed. Animals, 2021, 11, 1682.	2.3	2
149	Bayesian inference of the inbreeding load variance for fertility traits in Brown Swiss cattle. Journal of Dairy Science, 2021, 104, 10040-10048.	3.4	2
150	Use of Bayes factors to evaluate the effects of host genetics, litter and cage on the rabbit cecal microbiota. Genetics Selection Evolution, 2022, 54, .	3.0	2
151	Understanding the use of Bayes factor for testing candidate genes. Journal of Animal Breeding and Genetics, 2010, 127, 16-25.	2.0	1
152	Genome-wide methylation profile and gene expression in Obstructive Sleep Apnoea., 2017,,.		1
153	Bayes factor for testing between different structures of random genetic groups: A case study using weaning weight inBruna dels Pirineusbeef cattle. Genetics Selection Evolution, 2007, 39, 39-53.	3.0	1
154	Decision support in attribute selection with machine learning approach. , 2014, , .		0
155	Analysis of reproductive seasonality in Entrepelado and Retinto Iberian pig varieties under intensive management. Livestock Science, 2021, 245, 104441.	1.6	0
156	Genetic parameters for growth of fibre diameter in alpacas. , 2011, , 107-110.		0