

Luis Varona

List of Publications by Year in descending order

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156
papers

4,321
citations

125106

35
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175968

55
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all docs

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156
times ranked

3529
citing authors

#	ARTICLE	IF	CITATIONS
1	Additive and Dominance Genomic Analysis for Litter Size in Purebred and Crossbred Iberian Pigs. <i>Genes</i> , 2022, 13, 12.	1.0	8
2	Genomic Prediction Methods Accounting for Nonadditive Genetic Effects. <i>Methods in Molecular Biology</i> , 2022, 2467, 219-243.	0.4	3
3	Use of Bayes factors to evaluate the effects of host genetics, litter and cage on the rabbit cecal microbiota. <i>Genetics Selection Evolution</i> , 2022, 54, .	1.2	2
4	Analysis of reproductive seasonality in Entrepelado and Retinto Iberian pig varieties under intensive management. <i>Livestock Science</i> , 2021, 245, 104441.	0.6	0
5	Detection of Genomic Regions with Pleiotropic Effects for Growth and Carcass Quality Traits in the Rubia Gallega Cattle Breed. <i>Animals</i> , 2021, 11, 1682.	1.0	2
6	A dimensional reduction approach to modulate the core ruminal microbiome associated with methane emissions via selective breeding. <i>Journal of Dairy Science</i> , 2021, 104, 8135-8151.	1.4	10
7	Genetic evaluation including intermediate omics features. <i>Genetics</i> , 2021, 219, .	1.2	32
8	Bayesian inference of the inbreeding load variance for fertility traits in Brown Swiss cattle. <i>Journal of Dairy Science</i> , 2021, 104, 10040-10048.	1.4	2
9	Genetic inbreeding depression load for fertility traits in Pura Raza Española mares. <i>Journal of Animal Science</i> , 2021, 99, .	0.2	12
10	Maternal Transmission Ratio Distortion in Two Iberian Pig Varieties. <i>Genes</i> , 2020, 11, 1050.	1.0	3
11	A cross-specific multiplicative binomial recursive model for the analysis of perinatal mortality in a diallel cross among three varieties of Iberian pig. <i>Scientific Reports</i> , 2020, 10, 21190.	1.6	3
12	Genetic inbreeding depression load for morphological traits and defects in the Pura Raza Española horse. <i>Genetics Selection Evolution</i> , 2020, 52, 62.	1.2	18
13	The effect of divergent selection for intramuscular fat on the domestic rabbit genome. <i>Animal</i> , 2020, 14, 2225-2235.	1.3	11
14	Forkhead Box P3 Methylation and Expression in Men with Obstructive Sleep Apnea. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2233.	1.8	6
15	Combining Threshold, Thurstonian and Classical Linear Models in Horse Genetic Evaluations for Endurance Competitions. <i>Animals</i> , 2020, 10, 1075.	1.0	4
16	GIBBSTHUR: Software for Estimating Variance Components and Predicting Breeding Values for Ranking Traits Based on a Thurstonian Model. <i>Animals</i> , 2020, 10, 1001.	1.0	2
17	Genomic differentiation among varieties of Iberian pig. <i>Spanish Journal of Agricultural Research</i> , 2020, 18, e0401.	0.3	6
18	Genetic parameters and direct, maternal and heterosis effects on litter size in a diallel cross among three commercial varieties of Iberian pig. <i>Animal</i> , 2019, 13, 2765-2772.	1.3	15

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19	Identification of resilient sows in porcine reproductive and respiratory syndrome virus-infected farms. <i>Journal of Animal Science</i> , 2019, 97, 3228-3236.	0.2	14
20	Inbreeding depression load for litter size in Entrepelado and Retinto Iberian pig varieties. <i>Journal of Animal Science</i> , 2019, 97, 1979-1986.	0.2	11
21	A multivariate analysis with direct additive and inbreeding depression load effects. <i>Genetics Selection Evolution</i> , 2019, 51, 78.	1.2	10
22	Mapping Recombination Rate on the Autosomal Chromosomes Based on the Persistency of Linkage Disequilibrium Phase Among Autochthonous Beef Cattle Populations in Spain. <i>Frontiers in Genetics</i> , 2019, 10, 1170.	1.1	8
23	Censored Bayesian models for genetic evaluation of age at first calving in Brazilian Brahman cattle. <i>Livestock Science</i> , 2019, 221, 177-180.	0.6	3
24	Usefulness of running animal models in absence of pedigrees: Estimation of genetic parameters for gastrointestinal parasite resistance traits in Djallonké sheep of Burkina Faso. <i>Small Ruminant Research</i> , 2018, 160, 81-88.	0.6	12
25	Cross-validation analysis for genetic evaluation models for ranking in endurance horses. <i>Animal</i> , 2018, 12, 20-27.	1.3	12
26	Evaluation of the potential use of a meta-population for genomic selection in autochthonous beef cattle populations. <i>Animal</i> , 2018, 12, 1350-1357.	1.3	2
27	GWAS by GBLUP: Single and Multimarker EMMAX and Bayes Factors, with an Example in Detection of a Major Gene for Horse Gait. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2301-2308.	0.8	35
28	Non-additive Effects in Genomic Selection. <i>Frontiers in Genetics</i> , 2018, 9, 78.	1.1	157
29	Genomic selection models for directional dominance: an example for litter size in pigs. <i>Genetics Selection Evolution</i> , 2018, 50, 1.	1.2	56
30	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.	0.2	5
31	Performance of genomic selection under a single-step approach in autochthonous Spanish beef cattle populations. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 289-299.	0.8	4
32	On the haplotype diversity along the genome in Spanish beef cattle populations. <i>Livestock Science</i> , 2017, 201, 30-33.	0.6	7
33	Orthogonal Estimates of Variances for Additive, Dominance, and Epistatic Effects in Populations. <i>Genetics</i> , 2017, 206, 1297-1307.	1.2	125
34	Bayesian analysis of pig growth curves combining pedigree and genomic information. <i>Livestock Science</i> , 2017, 201, 34-40.	0.6	7
35	Genomic differentiation between Asturiana de los Valles, Avileña-Negra Ibérica, Bruna dels Pirineus, Morucha, Pirenaica, Retinta and Rubia Gallega cattle breeds. <i>Animal</i> , 2017, 11, 1667-1679.	1.3	8
36	The influence of natural selection in breeding programs: A simulation study. <i>Livestock Science</i> , 2017, 204, 98-103.	0.6	4

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37	Bayesian analysis of parent-specific transmission ratio distortion in seven Spanish beef cattle breeds. <i>Animal Genetics</i> , 2017, 48, 93-96.	0.6	42
38	Genome association study through nonlinear mixed models revealed new candidate genes for pig growth curves. <i>Scientia Agricola</i> , 2017, 74, 1-7.	0.6	4
39	A comparison of nonlinear mixed models and response to selection of tick-infestation on lambs. <i>PLoS ONE</i> , 2017, 12, e0172711.	1.1	12
40	O-GlcNAcylation mediates the control of cytosolic phosphoenolpyruvate carboxykinase activity via Pgc1 β . <i>PLoS ONE</i> , 2017, 12, e0179988.	1.1	5
41	Genome-wide methylation profile and gene expression in Obstructive Sleep Apnoea. , 2017, , .		1
42	A practical approach to detect ancestral haplotypes in livestock populations. <i>BMC Genetics</i> , 2016, 17, 91.	2.7	2
43	Linkage disequilibrium, persistence of phase, and effective population size in Spanish local beef cattle breeds assessed through a high-density single nucleotide polymorphism chip1. <i>Journal of Animal Science</i> , 2016, 94, 2779-2788.	0.2	13
44	Revealing new candidate genes for reproductive traits in pigs: combining Bayesian GWAS and functional pathways. <i>Genetics Selection Evolution</i> , 2016, 48, 9.	1.2	68
45	c.A2456C-substitution in Pck1 changes the enzyme kinetic and functional properties modifying fat distribution in pigs. <i>Scientific Reports</i> , 2016, 6, 19617.	1.6	21
46	On the performance of tests for the detection of signatures of selection: a case study with the Spanish autochthonous beef cattle populations. <i>Genetics Selection Evolution</i> , 2016, 48, 81.	1.2	24
47	Genomic BLUP including additive and dominant variation in purebreds and F1 crossbreds, with an application in pigs. <i>Genetics Selection Evolution</i> , 2016, 48, 6.	1.2	39
48	Genetic diversity and divergence among Spanish beef cattle breeds assessed by a bovine high-density SNP chip1. <i>Journal of Animal Science</i> , 2015, 93, 5164-5174.	0.2	40
49	Consequences of paternally inherited effects on the genetic evaluation of maternal effects. <i>Genetics Selection Evolution</i> , 2015, 47, 63.	1.2	7
50	Comparing multi-trait Poisson and Gaussian Bayesian models for genetic evaluation of litter traits in pigs. <i>Livestock Science</i> , 2015, 176, 47-53.	0.6	13
51	Detecting inbreeding depression for reproductive traits in Iberian pigs using genome-wide data. <i>Genetics Selection Evolution</i> , 2015, 47, 1.	1.2	191
52	A Bayesian Model for the Analysis of Transgenerational Epigenetic Variation. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 477-485.	0.8	21
53	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 \times Landrace \times Large White cross. <i>Meat Science</i> , 2015, 100, 150-155.	2.7	29
54	Bayesian GWAS and network analysis revealed new candidate genes for number of teats in pigs. <i>Journal of Applied Genetics</i> , 2015, 56, 123-132.	1.0	35

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55	Monitoring changes in the demographic and genealogical structure of the main Spanish local beef breeds. <i>Journal of Animal Science</i> , 2014, 92, 4364-4374.	0.2	23
56	Decision support in attribute selection with machine learning approach. , 2014, , .		0
57	Non-linear recursive models for growth traits in the Pirenaica beef cattle breed. <i>Animal</i> , 2014, 8, 904-911.	1.3	3
58	Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 40.	1.2	59
59	Crossbreeding effects on pig growth and carcass traits from two Iberian strains. <i>Animal</i> , 2014, 8, 1569-1576.	1.3	7
60	Gene expression profiling of mesenteric lymph nodes from sheep with natural scrapie. <i>BMC Genomics</i> , 2014, 15, 59.	1.2	27
61	<i>DEC1</i> and <i>ME1</i> genotypes are associated with lipid composition traits in <i>Duroc</i> pigs. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 46-52.	0.8	16
62	Joint analysis of additive, dominant and first-order epistatic effects of four genes (<i>IGF2</i> , <i>MC4R</i> , <i>PRKAG3</i> and <i>TERT</i>) in <i>BT/Overlock 10</i> pigs. <i>Genetics</i> , 2014, 45, 133-137.	0.6	12
63	Joint Analysis of Binomial and Continuous Traits with a Recursive Model: A Case Study Using Mortality and Litter Size of Pigs. <i>Genetics</i> , 2014, 196, 643-651.	1.2	12
64	Epigenetics modifications and Subclinical Atherosclerosis in Obstructive Sleep Apnea: The EPIOSA study. <i>BMC Pulmonary Medicine</i> , 2014, 14, 114.	0.8	27
65	Genomic information in pig breeding: Science meets industry needs. <i>Livestock Science</i> , 2014, 166, 94-100.	0.6	29
66	On the Additive and Dominant Variance and Covariance of Individuals Within the Genomic Selection Scope. <i>Genetics</i> , 2013, 195, 1223-1230.	1.2	253
67	An assessor-specific Bayesian multi-threshold mixed model for analyzing ordered categorical traits in tree breeding. <i>Tree Genetics and Genomes</i> , 2013, 9, 1423-1434.	0.6	9
68	Olive oil quality and ripening in super-high-density Arbequina orchard. <i>Journal of the Science of Food and Agriculture</i> , 2013, 93, 2207-2220.	1.7	35
69	Genetic correlation of longevity with growth, post-mortem, docility and some morphological traits in the Pirenaica beef cattle breed. <i>Animal</i> , 2012, 6, 873-879.	1.3	9
70	Sources of sire-specific genetic variance for birth and weaning weight in Bruna dels Pirineus beef calves. <i>Animal</i> , 2012, 6, 1931-1938.	1.3	2
71	Comparative study of equine bone marrow and adipose tissue-derived mesenchymal stromal cells. <i>Equine Veterinary Journal</i> , 2012, 44, 33-42.	0.9	52
72	Genome Scans for Transmission Ratio Distortion Regions in Mice. <i>Genetics</i> , 2012, 191, 247-259.	1.2	31

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73	Medulla oblongata transcriptome changes during presymptomatic natural scrapie and their association with prion-related lesions. <i>BMC Genomics</i> , 2012, 13, 399.	1.2	12
74	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. <i>Livestock Science</i> , 2012, 145, 145-152.	0.6	19
75	Modeling Skewness in Human Transcriptomes. <i>PLoS ONE</i> , 2012, 7, e38919.	1.1	7
76	Expression profiling of functional genes in prenatal skeletal muscle tissue in Duroc and Pietrain pigs. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 15-27.	0.8	36
77	Genetic evaluation of racing performance in trotter horses by competitive models. <i>Livestock Science</i> , 2011, 140, 155-160.	0.6	14
78	A note on accuracy of Bayesian LASSO regression in GWS. <i>Livestock Science</i> , 2011, 142, 310-314.	0.6	7
79	Changes in HSP gene and protein expression in natural scrapie with brain damage. <i>Veterinary Research</i> , 2011, 42, 13.	1.1	14
80	Carcass conformation and fat cover scores in beef cattle: A comparison of threshold linear models vs grouped data models. <i>Genetics Selection Evolution</i> , 2011, 43, 16.	1.2	3
81	Genetic parameters for growth of fiber diameter in alpacas1. <i>Journal of Animal Science</i> , 2011, 89, 2310-2315.	0.2	18
82	Accuracy of genome-wide evaluation for disease resistance in aquaculture breeding programs1. <i>Journal of Animal Science</i> , 2011, 89, 3433-3442.	0.2	31
83	Gene Expression Profiling and Association with Prion-Related Lesions in the Medulla Oblongata of Symptomatic Natural Scrapie Animals. <i>PLoS ONE</i> , 2011, 6, e19909.	1.1	19
84	Genetic parameters for growth of fibre diameter in alpacas. , 2011, , 107-110.		0
85	Hypothalamic expression of porcine leptin receptor (LEPR), neuropeptide Y (NPY), and cocaine- and amphetamine-regulated transcript (CART) genes is influenced by LEPR genotype. <i>Mammalian Genome</i> , 2010, 21, 583-591.	1.0	42
86	A note on mate allocation for dominance handling in genomic selection. <i>Genetics Selection Evolution</i> , 2010, 42, 33.	1.2	118
87	Understanding the use of Bayes factor for testing candidate genes. <i>Journal of Animal Breeding and Genetics</i> , 2010, 127, 16-25.	0.8	1
88	A Genetic Analysis of Mortality in Pigs. <i>Genetics</i> , 2010, 184, 277-284.	1.2	18
89	Estimation of the additive and dominance variances in SA Duroc pigs. <i>Livestock Science</i> , 2010, 131, 144-147.	0.6	18
90	Genetic determination of fatty acid composition in Spanish Churra sheep milk. <i>Journal of Dairy Science</i> , 2010, 93, 330-339.	1.4	19

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91	Additive genetic relationship of longevity with fertility and production traits in Nelore cattle based on bivariate models. <i>Genetics and Molecular Research</i> , 2010, 9, 176-187.	0.3	30
92	Genetic parameters for postweaning traits in Braunvieh cattle. <i>Genetics and Molecular Research</i> , 2010, 9, 545-553.	0.3	6
93	Analysis of founder-specific inbreeding depression on birth weight in Ripollesa lambs ¹ . <i>Journal of Animal Science</i> , 2009, 87, 72-79.	0.2	61
94	A model with heterogeneous thresholds for subjective traits: Fat cover and conformation score in the Pirenaica beef cattle ¹ . <i>Journal of Animal Science</i> , 2009, 87, 1210-1217.	0.2	9
95	Bayesian threshold analysis of direct and maternal genetic parameters for piglet mortality at farrowing in Large White, Landrace, and Pietrain populations ¹ . <i>Journal of Animal Science</i> , 2009, 87, 80-87.	0.2	23
96	Nucleotide Sequence and Association Analysis of Pig Apolipoprotein-B and LDL-Receptor Genes. <i>Animal Biotechnology</i> , 2009, 20, 110-123.	0.7	9
97	A bi-dimensional genome scan for prolificacy traits in pigs shows the existence of multiple epistatic QTL. <i>BMC Genomics</i> , 2009, 10, 636.	1.2	40
98	Polymorphism of the pig <i>acetyl-coenzyme A carboxylase 1</i> gene is associated with fatty acid composition in a Duroc commercial line. <i>Animal Genetics</i> , 2009, 40, 410-417.	0.6	54
99	Exploring the possibilities of genetic improvement from traceability data. <i>Livestock Science</i> , 2009, 125, 115-120.	0.6	9
100	Pig melatonin receptor 1a (MTNR1A) genotype is associated with seasonal variation of sow litter size. <i>Animal Reproduction Science</i> , 2009, 115, 317-322.	0.5	17
101	Comparison of different nonlinear functions to describe Nelore cattle growth ¹ . <i>Journal of Animal Science</i> , 2009, 87, 496-506.	0.2	52
102	Distinct spatial activation of intrinsic and extrinsic apoptosis pathways in natural scrapie: association with prion-related lesions. <i>Veterinary Research</i> , 2009, 40, 42.	1.1	13
103	Bayes factor between Student t and Gaussian mixed models within an animal breeding context. <i>Genetics Selection Evolution</i> , 2008, 40, 395.	1.2	2
104	Between-groups within-gene heterogeneity of residual variances in microarray gene expression data. <i>BMC Genomics</i> , 2008, 9, 319.	1.2	3
105	Skew distribution of founder-specific inbreeding depression effects on the longevity of Landrace sows. <i>Genetical Research</i> , 2008, 90, 499-508.	0.3	15
106	Mapping of quantitative trait loci for cholesterol, LDL, HDL, and triglyceride serum concentrations in pigs. <i>Physiological Genomics</i> , 2008, 35, 199-209.	1.0	51
107	A study of heterogeneity of environmental variance for slaughter weight in pigs. <i>Animal</i> , 2008, 2, 19-26.	1.3	49
108	Empirical Bayes factor analyses of quantitative trait loci for gestation length in Iberian \times Meishan F2 sows. <i>Animal</i> , 2008, 2, 177-183.	1.3	6

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109	Analysis of Litter Size and Average Litter Weight in Pigs Using a Recursive Model. <i>Genetics</i> , 2007, 177, 1791-1799.	1.2	58
110	Analysis of Fertility and Dystocia in Holsteins Using Recursive Models to Handle Censored and Categorical Data. <i>Journal of Dairy Science</i> , 2007, 90, 2012-2024.	1.4	64
111	Analysis of beef cattle longitudinal data applying a nonlinear model1. <i>Journal of Animal Science</i> , 2007, 85, 3189-3197.	0.2	27
112	Bayes factor for testing between different structures of random genetic groups: A case study using weaning weight in Bruna dels Pirineus beef cattle. <i>Genetics Selection Evolution</i> , 2007, 39, 39.	1.2	8
113	Bayes factor for testing between different structures of random genetic groups: A case study using weaning weight in Bruna dels Pirineus beef cattle. <i>Genetics Selection Evolution</i> , 2007, 39, 39-53.	1.2	1
114	Testing genetic determinism in rate of hoof growth in pigs using Bayes Factors. <i>Livestock Science</i> , 2006, 105, 50-56.	0.6	11
115	Parametric bootstrap for testing model fitting in the proportional hazards framework: An application to the survival analysis of Bruna dels Pirineus beef calves1. <i>Journal of Animal Science</i> , 2006, 84, 2609-2616.	0.2	13
116	Adipocyte fatty-acid binding protein is closely associated to the porcine FAT1 locus on chromosome 41. <i>Journal of Animal Science</i> , 2006, 84, 2907-2913.	0.2	26
117	A Multithreshold Model for Sensory Analysis. <i>Journal of Food Science</i> , 2006, 71, S333-S336.	1.5	5
118	Malic enzyme 1 genotype is associated with backfat thickness and meat quality traits in pigs. <i>Animal Genetics</i> , 2006, 37, 28-32.	0.6	37
119	Characterization of the porcine acyl-CoA synthetase long-chain 4 gene and its association with growth and meat quality traits. <i>Animal Genetics</i> , 2006, 37, 219-224.	0.6	35
120	Characterization of the porcine FABP5 gene and its association with the FAT1 QTL in an Iberian by Landrace cross. <i>Animal Genetics</i> , 2006, 37, 589-591.	0.6	33
121	A whole-genome analysis using robust asymmetric distributions. <i>Genetical Research</i> , 2006, 88, 143.	0.3	15
122	Effect of growth selection on morphology in Pirenaica cattle. <i>Animal Research</i> , 2006, 55, 55-63.	0.6	5
123	A simulation study on the detection of causal mutations from F2 experiments. <i>Journal of Animal Breeding and Genetics</i> , 2005, 122, 30-36.	0.8	12
124	QTL mapping for teat number in an Iberian-by-Meishan pig intercross. <i>Animal Genetics</i> , 2005, 36, 050823030348002-???	0.6	40
125	Consequences of selection for growth on carcass and meat quality in Pirenaica cattle. <i>Livestock Science</i> , 2005, 95, 103-114.	1.2	14
126	On growth, fatness, and form: A further look at porcine Chromosome 4 in an Iberian \bar{A} – Landrace cross. <i>Mammalian Genome</i> , 2005, 16, 374-382.	1.0	33

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127	Genetic parameters of fertility in two lines of rabbits with different reproductive potential. <i>Journal of Animal Science</i> , 2005, 83, 340-343.	0.2	29
128	Fine mapping of porcine chromosome 6 QTL and LEPR effects on body composition in multiple generations of an Iberian by Landrace intercross. <i>Genetical Research</i> , 2005, 85, 57-67.	0.3	127
129	Detection of QTL affecting fatty acid composition in the pig. <i>Mammalian Genome</i> , 2003, 14, 650-656.	1.0	74
130	Estrogen receptor polymorphism in Landrace pigs and its association with litter size performance. <i>Livestock Science</i> , 2003, 82, 53-59.	1.2	39
131	A Bayesian analysis of the effect of selection for growth rate on growth curves in rabbits. <i>Genetics Selection Evolution</i> , 2003, 35, 21-41.	1.2	82
132	Meat production using four terminal pig lines. <i>Journal of the Science of Food and Agriculture</i> , 2003, 83, 1504-1510.	1.7	5
133	QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects. <i>Genetical Research</i> , 2002, 80, 145-154.	0.3	68
134	Quantitative trait locus mapping for meat quality traits in an Iberian \times Landrace F2 pig population1. <i>Journal of Animal Science</i> , 2002, 80, 2801-2808.	0.2	104
135	Assignment of the 2,4-dienoyl-CoA reductase (DECR) gene to porcine chromosome 4. <i>Animal Genetics</i> , 2002, 33, 164-165.	0.6	10
136	Exploring Alternative Models for Sex-Linked Quantitative Trait Loci in Outbred Populations: Application to an Iberian \times Landrace Pig Intercross. <i>Genetics</i> , 2002, 161, 1625-1632.	1.2	23
137	Multivariate analysis of litter size for multiple parities with production traits in pigs: I. Bayesian variance component estimation. <i>Journal of Animal Science</i> , 2002, 80, 2540.	0.2	52
138	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. <i>Journal of Animal Science</i> , 2002, 80, 2548.	0.2	29
139	Variance components of fertility in Spanish Landrace pigs. <i>Livestock Science</i> , 2001, 67, 217-221.	1.2	15
140	Hypothesis testing for the genetic background of quantitative traits. <i>Genetics Selection Evolution</i> , 2001, 33, 3-16.	1.2	32
141	Bayes factors for detection of Quantitative Trait Loci. <i>Genetics Selection Evolution</i> , 2001, 33, 133-52.	1.2	40
142	Computation of identity by descent probabilities conditional on DNA markers via a Monte Carlo Markov Chain method. <i>Genetics Selection Evolution</i> , 2000, 32, 467-82.	1.2	27
143	Genetic analysis of growth curve parameters for male and female chickens resulting from selection on shape of growth curve.. <i>Journal of Animal Science</i> , 2000, 78, 2515.	0.2	66
144	Method R Estimates of Additive Genetic, Dominance Genetic, and Permanent Environmental Fraction of Variance for Yield and Health Traits of Holsteins. <i>Journal of Dairy Science</i> , 2000, 83, 1873-1877.	1.4	30

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145	Quantitative Trait Loci Mapping in F2 Crosses Between Outbred Lines. <i>Genetics</i> , 2000, 155, 391-405.	1.2	53
146	Threshold-linear versus linear-linear analysis of birth weight and calving ease using an animal model: I. Variance component estimation.. <i>Journal of Animal Science</i> , 1999, 77, 1994.	0.2	56
147	Maternal animal model with correlation between maternal environmental effects of related dams.. <i>Journal of Animal Science</i> , 1999, 77, 2904.	0.2	28
148	Two-step versus joint analysis of Von Bertalanffy function. <i>Journal of Animal Breeding and Genetics</i> , 1999, 116, 331-338.	0.8	17
149	Prediction of Parental Dominance Combinations for Planned Matings, Methodology, and Simulation Results. <i>Journal of Dairy Science</i> , 1999, 82, 2186-2191.	1.4	24
150	Effect of Full Sibs on Additive Breeding Values Under the Dominance Model for Stature in United States Holsteins. <i>Journal of Dairy Science</i> , 1998, 81, 1126-1135.	1.4	20
151	Bayesian Analysis of Wood's Lactation Curve for Spanish Dairy Cows. <i>Journal of Dairy Science</i> , 1998, 81, 1469-1478.	1.4	39
152	Estimation of dominance variance in purebred Yorkshire swine.. <i>Journal of Animal Science</i> , 1998, 76, 448.	0.2	37
153	Bayesian inference of variance components for litter size in Rasa Aragonesa sheep.. <i>Journal of Animal Science</i> , 1998, 76, 23.	0.2	29
154	Multiple trait genetic analysis of underlying biological variables of production functions. <i>Livestock Science</i> , 1997, 47, 201-209.	1.2	53
155	Estimation of predictionâ€error variances by resampling. <i>Journal of Animal Breeding and Genetics</i> , 1995, 112, 176-182.	0.8	15
156	Variance component estimation by resampling. <i>Journal of Animal Breeding and Genetics</i> , 1992, 109, 358-363.	0.8	24