Dorian Garrick

List of Publications by Year
in descending order

258 papers	10,295 citations	50566 48 h-index	54771 88 g-index
271 all docs	271 docs citations	271 times ranked	7667 citing authors

#	Article	IF	Citations
1	Live weight and body condition score of mixed-aged beef breeding cows on commercial hill country farms in New Zealand. New Zealand Journal of Agricultural Research, 2022, 65, 172-187.	0.9	4
2	Non-additive QTL mapping of lactation traits in 124,000 cattle reveals novel recessive loci. Genetics Selection Evolution, 2022, 54, 5.	1.2	7
3	An inherited night blindness in Wiltshire sheep. Veterinary Pathology, 2022, , 030098582110674.	0.8	0
4	Genetic approaches for increasing fitness in endangered species. Trends in Ecology and Evolution, 2022, 37, 332-345.	4.2	14
5	Erratum to "Cumulative dairy cow genetic change from selection and crossbreeding over the last 2 decades in New Zealand closely aligns to model-based predictions published in 2000" (JDS Commun.) Tj ETQq1 1 0.784314 rgBT /Over	0.5	0
6	Pathology of the peripheral neuropathy Charcot-Marie-Tooth disease type 4H in Holstein Friesian cattle with a splice site mutation in <i>FGD4</i>. Veterinary Pathology, 2022, 59, 442-450.	0.8	2
7	XSim version 2: simulation of modern breeding programs. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	6
8	Pregnancy status predicted using milk mid-infrared spectra from dairy cattle. Journal of Dairy Science, 2022, 105, 3615-3632.	1.4	3
9	Genetic Parameters for Growth, Ultrasound and Carcass Traits in New Zealand Beef Cattle and Their Correlations with Maternal Performance. Animals, 2022, 12, 25.	1.0	5
10	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. Animals, 2022, 12, 1632.	1.0	5
11	Variance parameter estimation for age at puberty phenotypes under 2 levels of phenotype censorship. JDS Communications, 2022, 3, 339-342.	0.5	3
12	Genetic parameters for efficiency of crude protein utilisation and its relationship with production traits across lactations in grazing dairy cows. New Zealand Journal of Agricultural Research, 2021, 64, 62-82.	0.9	4
13	Reduced Animal Models Fitting Only Equations for Phenotyped Animals. Frontiers in Genetics, 2021, 12, 637626.	1.1	3
14	Cumulative dairy cow genetic change from selection and crossbreeding over the last 2 decades in New Zealand closely aligns to model-based predictions published in 2000. JDS Communications, 2021, 2, 51-54.	0.5	3
15	Mining the 99 Lives Cat Genome Sequencing Consortium database implicates genes and variants for the <i>Ticked</i> locus in domestic cats (<i>FelisÂcatus</i>). Animal Genetics, 2021, 52, 321-332.	0.6	9
16	Identification of Genomic Regions Associated with Concentrations of Milk Fat, Protein, Urea and Efficiency of Crude Protein Utilization in Grazing Dairy Cows. Genes, 2021, 12, 456.	1.0	12
17	Can Nitrogen Excretion of Dairy Cows Be Reduced by Genetic Selection for Low Milk Urea Nitrogen Concentration?. Animals, 2021, 11, 737.	1.0	9
18	Non-additive association analysis using proxy phenotypes identifies novel cattle syndromes. Nature Genetics, 2021, 53, 949-954.	9.4	34

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19	The genomes of precision edited cloned calves show no evidence for off-target events or increased de novo mutagenesis. BMC Genomics, 2021, 22, 457.	1.2	6
20	Animal medical genetics: a historical perspective on more than 50 years of research into genetic disorders of animals at Massey University. New Zealand Veterinary Journal, 2021, 69, 255-266.	0.4	0
21	Alternative Ways of Computing the Numerator Relationship Matrix. Frontiers in Genetics, 2021, 12, 655638.	1.1	3
22	Sequence-based genome-wide association study of individual milk mid-infrared wavenumbers in mixed-breed dairy cattle. Genetics Selection Evolution, 2021, 53, 62.	1.2	14
23	A Missense Mutation in the MYBPH Gene Is Associated With Abdominal Fat Traits in Meat-Type Chickens. Frontiers in Genetics, 2021, 12, 698163.	1.1	4
24	Genetic Parameters for Maternal Performance Traits in Commercially Farmed New Zealand Beef Cattle. Animals, 2021, 11, 2509.	1.0	7
25	Estimates of genomic inbreeding and identification of candidate regions that differ between Chinese indigenous sheep breeds. Journal of Animal Science and Biotechnology, 2021, 12, 95.	2.1	13
26	HandyCNV: Standardized Summary, Annotation, Comparison, and Visualization of Copy Number Variant, Copy Number Variation Region, and Runs of Homozygosity. Frontiers in Genetics, 2021, 12, 731355.	1.1	9
27	Advantage of including Genomic Information to Predict Breeding Values for Lactation Yields of Milk, Fat, and Protein or Somatic Cell Score in a New Zealand Dairy Goat Herd. Animals, 2021, 11, 24.	1.0	6
28	Comparison of Genotype Imputation for SNP Array and Low-Coverage Whole-Genome Sequencing Data. Frontiers in Genetics, 2021, 12, 704118.	1.1	8
29	Discovering Copy Number Variation in Dual-Purpose XinJiang Brown Cattle. Frontiers in Genetics, 2021, 12, 747431.	1.1	6
30	Genetic parameters for total lactation yields of milk, fat, protein, and somatic cell score in New Zealand dairy goats. Animal Science Journal, 2020, 91, e13310.	0.6	14
31	Economic selection index to improve fiber quality in Mongolian Cashmere goats. Livestock Science, 2020, 232, 103898.	0.6	4
32	Economic values for index improvement of dual-purpose Simmental cattle. Livestock Science, 2020, 240, 104224.	0.6	4
33	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. American Journal of Human Genetics, 2020, 106, 893-904.	2.6	29
34	Genome-wide association studies of lactation yields of milk, fat, protein and somatic cell score in New Zealand dairy goats. Journal of Animal Science and Biotechnology, 2020, 11, 55.	2.1	25
35	Accuracies of direct genomic breeding values for birth and weaning weights of registered Charolais cattle in Mexico. Animal Production Science, 2020, 60, 772.	0.6	2
36	Sire selection and genetic improvement of dairy cattle assuming pure market competition. Journal of Dairy Science, 2020, 103, 4532-4544.	1.4	2

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37	Exact Distribution of Linkage Disequilibrium in the Presence of Mutation, Selection, or Minor Allele Frequency Filtering. Frontiers in Genetics, 2020, 11, 362.	1.1	5
38	Fast parallelized sampling of Bayesian regression models for whole-genome prediction. Genetics Selection Evolution, 2020, 52, 16.	1.2	8
39	Accuracy of genomic prediction of shell quality in a White Leghorn line. Poultry Science, 2020, 99, 2833-2840.	1.5	6
40	The evolving role of Fourier-transform mid-infrared spectroscopy in genetic improvement of dairy cattle. Journal of Animal Science and Biotechnology, 2020, 11, 39.	2.1	20
41	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. BMC Genetics, 2019, 20, 83.	2.7	10
42	Increasing the accuracy of genomic prediction in pure€bred Limousin beef cattle by including cross€bred Limousin data and accounting for an F94L variant in <i><scp>MSTN</scp></i>. Animal Genetics, 2019, 50, 621-633.	0.6	13
43	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. BMC Genomics, 2019, 20, 669.	1.2	17
44	Î²-Mannosidosis in German Shepherd Dogs. Veterinary Pathology, 2019, 56, 743-748.	0.8	8
45	Strategies for noise reduction and standardization of milk mid-infrared spectra from dairy cattle. Journal of Dairy Science, 2019, 102, 6357-6372.	1.4	22
46	Identification of recombination hotspots and quantitative trait loci for recombination rate in layer chickens. Journal of Animal Science and Biotechnology, 2019, 10, 20.	2.1	17
47	Fine mapping of genomic regions associated with female fertility in Nellore beef cattle based on sequence variants from segregating sires. Journal of Animal Science and Biotechnology, 2019, 10, 97.	2.1	7
48	Genome-wide association analysis reveals QTL and candidate mutations involved in white spotting in cattle. Genetics Selection Evolution, 2019, 51, 62.	1.2	23
49	A certain invariance property of <scp>BLUE</scp> in a whole€genome regression context. Journal of Animal Breeding and Genetics, 2019, 136, 113-117.	0.8	2
50	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. Genetics, 2018, 209, 89-103.	1.2	61
51	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	9.4	286
52	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. Journal of Dairy Science, 2018, 101, 1292-1296.	1.4	35
53	Empirical Comparisons of Different Statistical Models To Identify and Validate Kernel Row Number-Associated Variants from Structured Multi-parent Mapping Populations of Maize. G3: Genes, Genomes, Genetics, 2018, 8, 3567-3575.	0.8	19
54	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. Scientific Reports, 2018, 8, 16222.	1.6	29

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55	Variance component estimates for post-thaw sperm variables measured by computer assisted semen analyzer for inbred and non-inbred Hereford bulls. Animal Reproduction Science, 2018, 199, 45-50.	0.5	2
56	Identification of an immune modulation locus utilising a bovine mammary gland infection challenge model. Journal of Dairy Research, 2018, 85, 185-192.	0.7	2
57	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC Genomics, 2018, 19, 499.	1.2	51
58	A genome-wide association study reveals novel genomic regions and positional candidate genes for fat deposition in broiler chickens. BMC Genomics, 2018, 19, 374.	1.2	28
59	A nested mixture model for genomic prediction using whole-genome SNP genotypes. PLoS ONE, 2018, 13, e0194683.	1.1	9
60	Comparison of alternative approaches to single-trait genomic prediction using genotyped and non-genotyped Hanwoo beef cattle. Genetics Selection Evolution, 2017, 49, 2.	1.2	33
61	Efficient strategies for leave-one-out cross validation for genomic best linear unbiased prediction. Journal of Animal Science and Biotechnology, 2017, 8, 38.	2.1	94
62	Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach. Journal of Agricultural, Biological, and Environmental Statistics, 2017, 22, 172-193.	0.7	60
63	A FAS-ligand variant associated with autoimmune lymphoproliferative syndrome in cats. Mammalian Genome, 2017, 28, 47-55.	1.0	17
64	A comparison of identity‐by‐descent and identity‐by‐state matrices that are used for genetic evaluation and estimation of variance components. Journal of Animal Breeding and Genetics, 2017, 134, 213-223.	0.8	15
65	Genome-wide detection of autosomal copy number variants in several sheep breeds using Illumina OvineSNP50 BeadChips. Small Ruminant Research, 2017, 155, 24-32.	0.6	9
66	Genotype imputation in a tropical crossbred dairy cattle population. Journal of Dairy Science, 2017, 100, 9623-9634.	1.4	13
67	The Accuracy and Bias of Single-Step Genomic Prediction for Populations Under Selection. G3: Genes, Genomes, Genetics, 2017, 7, 2685-2694.	0.8	29
68	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. BMC Genomics, 2017, 18, 386.	1.2	159
69	165 Genetic variants with potential loss of function in Gyr, Girolando, and Guzerat cattle breeds by resequencing. Journal of Animal Science, 2017, 95, 81-81.	0.2	0
70	587 The role of diet composition fed during residual feed intake determinations and the impact of the diet on the gene sets associated with efficiency as determined by a gene set enrichment analysis. Journal of Animal Science, 2017, 95, 287-288.	0.2	0
71	Population structure and genomic inbreeding in nine Swiss dairy cattle populations. Genetics Selection Evolution, 2017, 49, 83.	1.2	49
72	The role of genomics in pig improvement. Animal Production Science, 2017, 57, 2360.	0.6	7

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73	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. Frontiers in Genetics, 2017, 8, 171.	1.1	63
74	Genetic parameters for carcass and ultrasound traits in Hereford and admixed Simmental beef cattle: Accuracy of evaluating carcass traits1. Journal of Animal Science, 2017, 95, 4718-4727.	0.2	12
75	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. BMC Genomics, 2017, 18, 999.	1.2	22
76	Single nucleotide variants and InDels identified from whole-genome re-sequencing of Guzerat, Gyr, Girolando and Holstein cattle breeds. PLoS ONE, 2017, 12, e0173954.	1.1	47
77	Familial episodic ataxia in lambs is potentially associated with a mutation in the fibroblast growth factor 14 (FGF14) gene. PLoS ONE, 2017, 12, e0190030.	1.1	4
78	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers1,2. Journal of Animal Science, 2017, 95, 4796-4812.	0.2	31
79	Fixed-length haplotypes can improve genomic prediction accuracy in an admixed dairy cattle population. Genetics Selection Evolution, 2017, 49, 54.	1.2	52
80	331 The genetic improvement of feed efficiency in beef cattle. Journal of Animal Science, 2017, 95, 161-161.	0.2	2
81	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. BMC Genomics, 2017, 18, 910.	1.2	36
82	164 Single nucleotide variants and indels identified from whole-genome resequencing of Gyr, Girolando, and Holstein cattle breeds. Journal of Animal Science, 2017, 95, 80-81.	0.2	0
83	Development and implementation of genomic predictions in beef cattle. Animal Frontiers, 2016, 6, 32-38.	0.8	51
84	027 Performance of genomic prediction using haplotypes in New Zealand dairy cattle. Journal of Animal Science, 2016, 94, 13-13.	0.2	2
85	Deriving Gene Networks from SNP Associated with Triacylglycerol and Phospholipid Fatty Acid Fractions from Ribeyes of Angus Cattle. Frontiers in Genetics, 2016, 7, 116.	1.1	10
86	Implementation of genomic selection in the poultry industry. Animal Frontiers, 2016, 6, 23-31.	0.8	62
87	The Effect of Calf Gender on Milk Production in Seasonal Calving Cows and Its Impact on Genetic Evaluations. PLoS ONE, 2016, 11, e0151236.	1.1	17
88	An Upper Bound for Accuracy of Prediction Using GBLUP. PLoS ONE, 2016, 11, e0161054.	1.1	53
89	032 Quantitative trait loci and candidate genes associated with heifer pregnancy rate and stayability in beef cattle. Journal of Animal Science, 2016, 94, 15-15.	0.2	3
90	Epistatic interactions associated with fatty acid concentrations of beef from angus sired beef cattle. BMC Genomics, 2016, 17, 891.	1.2	7

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91	036 Discovery of quantitative trait loci using a quantitative trait loci–effects model in a multigenerational pedigree. Journal of Animal Science, 2016, 94, 16-17.	0.2	0
92	Host genetic influence on papillomavirus–induced tumors in the horse. International Journal of Cancer, 2016, 139, 784-792.	2.3	28
93	Computational strategies for alternative single-step Bayesian regression models with large numbers of genotyped and non-genotyped animals. Genetics Selection Evolution, 2016, 48, 96.	1.2	57
94	Estimates of genetic and crossbreeding parameters for milk components and potential yield of dairy products from New Zealand dairy cattle. New Zealand Journal of Agricultural Research, 2016, 59, 79-89.	0.9	6
95	Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in layers. Journal of Animal Breeding and Genetics, 2016, 133, 334-346.	0.8	24
96	An efficient exact method to obtain GBLUP and single-step GBLUP when the genomic relationship matrix is singular. Genetics Selection Evolution, 2016, 48, 80.	1.2	18
97	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. Genetics Selection Evolution, 2016, 48, 22.	1.2	19
98	Mixture models detect large effect QTL better than GBLUP and result in more accurate and persistent predictions. Journal of Animal Science and Biotechnology, 2016, 7, 7.	2.1	23
99	Responses in lactose yield, lactose percentage and protein-to-protein-plus-lactose ratio from index selection in New Zealand dairy cattle. New Zealand Journal of Agricultural Research, 2016, 59, 90-105.	0.9	7
100	Genome-wide association study of growth and body composition traits in Brangus beef cattle. Livestock Science, 2016, 183, 4-11.	0.6	29
101	Dairy product production and lactose demand in New Zealand and Ireland under different simulated milk product-processing portfolios. Irish Journal of Agricultural and Food Research, 2016, 55, 126-135.	0.2	2
102	Response and inbreeding from a genomic selection experiment in layer chickens. Genetics Selection Evolution, 2015, 47, 59.	1.2	67
103	Accuracy of prediction of simulated polygenic phenotypes and their underlying quantitative trait loci genotypes using real or imputed whole-genome markers in cattle. Genetics Selection Evolution, 2015, 47, 99.	1.2	6
104	Genetic parameters and genetic correlations among triacylglycerol and phospholipid fractions in Angus cattle1. Journal of Animal Science, 2015, 93, 522-528.	0.2	16
105	Predicted dairy product yields and deficits of lactose for manufacturing under differing selection and manufacturing scenarios in New Zealand. New Zealand Journal of Agricultural Research, 2015, 58, 432-440.	0.9	0
106	XSim: Simulation of Descendants from Ancestors with Sequence Data. G3: Genes, Genomes, Genetics, 2015, 5, 1415-1417.	0.8	20
107	A fast and efficient Gibbs sampler for BayesB in whole-genome analyses. Genetics Selection Evolution, 2015, 47, 80.	1.2	31
108	Cross-validation of genetic and genomic predictions of temperament in Nellore–Angus crossbreds. Livestock Science, 2015, 182, 28-33.	0.6	2

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109	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. Genetics Selection Evolution, 2015, 47, 23.	1.2	38
110	Genetic parameters for sensory traits in longissimus muscle and their associations with tenderness, marbling score, and intramuscular fat in Angus cattle1. Journal of Animal Science, 2015, 93, 21-27.	0.2	45
111	The economic value of somatic cell count in South African Holstein and Jersey cattle. South African Journal of Animal Sciences, 2014, 44, 173.	0.2	10
112	Comparison of breeding value prediction for two traits in a Nellore-Angus crossbred population using different Bayesian modeling methodologies. Genetics and Molecular Biology, 2014, 37, 631-637.	0.6	5
113	Use of robust multivariate linear mixed models for estimation of genetic parameters for carcass traits in beef cattle. Journal of Animal Breeding and Genetics, 2014, 131, 504-512.	0.8	6
114	QTLs associated with dry matter intake, metabolic mid-test weight, growth and feed efficiency have little overlap across 4 beef cattle studies. BMC Genomics, 2014, 15, 1004.	1.2	97
115	Identification of genomic regions associated with feed efficiency in Nelore cattle. BMC Genetics, 2014, 15, 100.	2.7	87
116	Breeding objectives for Holstein cattle in South Africa. South African Journal of Animal Sciences, 2014, 44, 199.	0.2	15
117	Functionally reciprocal mutations of the prolactin signalling pathway define hairy and slick cattle. Nature Communications, 2014, 5, 5861.	5.8	108
118	Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. Genomics, 2014, 104, 572-581.	1.3	16
119	Validation and further characterization of a major quantitative trait locus associated with host response to experimental infection with porcine reproductive and respiratory syndrome virus. Animal Genetics, 2014, 45, 48-58.	0.6	61
120	Estimating the impact of somatic cell count on the value of milk utilising parameters obtained from the published literature. Journal of Dairy Research, 2014, 81, 223-232.	0.7	15
121	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. Genetics Selection Evolution, 2014, 46, 34.	1.2	52
122	Reduction in accuracy of genomic prediction for ordered categorical data compared to continuous observations. Genetics Selection Evolution, 2014, 46, 37.	1.2	19
123	Genome-wide association study for intramuscular fat deposition and composition in Nellore cattle. BMC Genetics, 2014, 15, 39.	2.7	121
124	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. BMC Genomics, 2014, 15, 948.	1.2	44
125	A class of Bayesian methods to combine large numbers of genotyped and non-genotyped animals for whole-genome analyses. Genetics Selection Evolution, 2014, 46, 50.	1.2	147
126	Identification of breeding objectives using a bioeconomic model for a beef cattle production system in Uruguay. Livestock Science, 2014, 160, 21-28.	0.6	28

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127	Genome-wide association study of temperament and tenderness using different Bayesian approaches in a Nellore–Angus crossbred population. Livestock Science, 2014, 161, 17-27.	0.6	22
128	Genome‐wide association study for egg production and quality in layer chickens. Journal of Animal Breeding and Genetics, 2014, 131, 173-182.	0.8	72
129	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. BMC Genomics, 2014, 15, 442.	1.2	191
130	A genome‐wide association study for canine cryptorchidism in Siberian Huskies. Journal of Animal Breeding and Genetics, 2014, 131, 202-209.	0.8	11
131	The evolution of methodologies for genomic prediction. Livestock Science, 2014, 166, 10-18.	0.6	20
132	Spring calving versus split calving: effects on farm, processor and industry profitability for the Irish dairy industry. Journal of Agricultural Science, 2014, 152, 448-463.	0.6	6
133	Growth, feed intake and maternal performance of Angus heifers from high and low feed efficiency selection lines. Animal Production Science, 2014, 54, 1428.	0.6	7
134	Genomic BLUP Decoded: A Look into the Black Box of Genomic Prediction. Genetics, 2013, 194, 597-607.	1.2	279
135	Association of polymorphisms in solute carrier family 27, isoform A6 (SLC27A6) and fatty acid-binding protein-3 and fatty acid-binding protein-4 (FABP3 and FABP4) with fatty acid composition of bovine milk. Journal of Dairy Science, 2013, 96, 6007-6021.	1.4	48
136	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. Genetics Selection Evolution, 2013, 45, 11.	1.2	79
137	Genome-wide association study of infectious bovine keratoconjunctivitis in Angus cattle. BMC Genetics, 2013, 14, 23.	2.7	18
138	Novel genomic approaches unravel genetic architecture of complex traits in apple. BMC Genomics, 2013, 14, 393.	1.2	115
139	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. Genetics Selection Evolution, 2013, 45, 30.	1.2	56
140	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. Poultry Science, 2013, 92, 2270-2275.	1.5	25
141	Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. Poultry Science, 2013, 92, 1712-1723.	1.5	27
142	Genome-Wide Association Study for Marek's Disease Mortality in Layer Chickens. Avian Diseases, 2013, 57, 395-400.	0.4	22
143	An evaluation of circulating bovine viral diarrhea virus type 2 maternal antibody level and response to vaccination in Angus calves1,2,3,4. Journal of Animal Science, 2013, 91, 4440-4450.	0.2	23
144	Genome-wide prediction of age at puberty and reproductive longevity in sows. Animal Genetics, 2013, 44, 387-397.	0.6	40

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145	Sterol regulatory element binding transcription factor 1 (SREBF1) polymorphism and milk fatty acid composition. Journal of Dairy Science, 2013, 96, 2605-2616.	1.4	23
146	Analysis of egg production in layer chickens using a random regression model with genomic relationships. Poultry Science, 2013, 92, 1486-1491.	1.5	20
147	Bayesian Methods Applied to GWAS. Methods in Molecular Biology, 2013, 1019, 237-274.	0.4	115
148	Implementing a QTL Detection Study (GWAS) Using Genomic Prediction Methodology. Methods in Molecular Biology, 2013, 1019, 275-298.	0.4	80
149	Genome-wide association and prediction of direct genomic breeding values for composition of fatty acids in Angus beef cattlea. BMC Genomics, 2013, 14, 730.	1.2	67
150	Genome-wide association study of concentrations of iron and other minerals in longissimus muscle of Angus cattle1. Journal of Animal Science, 2013, 91, 3593-3600.	0.2	10
151	Accuracies of direct genomic breeding values in Hereford beef cattle using national or international training populations1. Journal of Animal Science, 2013, 91, 1538-1551.	0.2	44
152	Genetic parameters for concentrations of minerals in longissimus muscle and their associations with palatability traits in Angus cattle1. Journal of Animal Science, 2013, 91, 1067-1075.	0.2	30
153	Application of multivariate heavy-tailed distributions to residuals in the estimation of genetic parameters of growth traits in beef cattle1. Journal of Animal Science, 2013, 91, 1552-1561.	0.2	2
154	Evaluation of response to bovine viral diarrhea virus type 2 vaccination and timing of weaning on yearling ultrasound body composition, performance, and carcass quality traits in Angus calves1,2,3. Journal of Animal Science, 2013, 91, 5466-5476.	0.2	4
155	Whole Genome Association Studies of Residual Feed Intake and Related Traits in the Pig. PLoS ONE, 2013, 8, e61756.	1.1	104
156	Heritability and Bayesian genome-wide association study of first service conception and pregnancy in Brangus heifers1. Journal of Animal Science, 2013, 91, 605-612.	0.2	58
157	A missense mutation in AGTPBP1 was identified in sheep with a lower motor neuron disease. Heredity, 2012, 109, 156-162.	1.2	28
158	An analysis of the implications of a change to the seasonal milk supply profile in the Irish dairy industry utilizing a seasonal processing sector model. Journal of Agricultural Science, 2012, 150, 389-407.	0.6	14
159	Invited review: Genomic analysis of data from physiological studies. Journal of Dairy Science, 2012, 95, 499-507.	1.4	3
160	Genome-wide association study of insect bite hypersensitivity in two horse populations in the Netherlands. Genetics Selection Evolution, 2012, 44, 31.	1.2	40
161	Accuracy of direct genomic breeding values for nationally evaluated traits in US Limousin and Simmental beef cattle. Genetics Selection Evolution, 2012, 44, 38.	1.2	63
162	Accuracy of Genomic Selection Methods in a Standard Data Set of Loblolly Pine (<i>Pinus taeda</i>L.). Genetics, 2012, 190, 1503-1510.	1.2	363

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163	Genetic parameters for carnitine, creatine, creatinine, carnosine, and anserine concentration in longissimus muscle and their association with palatability traits in Angus cattle1. Journal of Animal Science, 2012, 90, 4248-4255.	0.2	33
164	Evidence for a major QTL associated with host response to Porcine Reproductive and Respiratory Syndrome Virus challenge1. Journal of Animal Science, 2012, 90, 1733-1746.	0.2	145
165	Bayesian genome-wide association analysis of growth and yearling ultrasound measures of carcass traits in Brangus heifers1. Journal of Animal Science, 2012, 90, 3398-3409.	0.2	86
166	The accuracies of DNA-based estimates of genetic merit derived from Angus or multibreed beef cattle training populations1,2,3. Journal of Animal Science, 2012, 90, 4191-4202.	0.2	8
167	A whole-genome association study for pig reproductive traits. Animal Genetics, 2012, 43, 18-26.	0.6	152
168	Genetic polymorphisms in bovine <i>transferrin receptor 2</i> (<i>TFR2</i>) and <i>solute carrier family 40</i> (<i>iron-regulated transporter</i>)<i>, member 1</i> (<i>SLC40A1</i>) genes and their association with beef iron content. Animal Genetics, 2012, 43, 115-122.	0.6	13
169	In a shake of a lamb's tail: using genomics to unravel a cause of chondrodysplasia in <scp>T</scp>exel sheep. Animal Genetics, 2012, 43, 9-18.	0.6	25
170	Genome-wide association analysis and genetic architecture of egg weight and egg uniformity in layer chickens. Animal Genetics, 2012, 43, 87-96.	0.6	95
171	Genomic breeding value prediction and QTL mapping of QTLMAS2011 data using Bayesian and GBLUP methods. BMC Proceedings, 2012, 6, S7.	1.8	17
172	A Fast EM Algorithm for BayesA-Like Prediction of Genomic Breeding Values. PLoS ONE, 2012, 7, e49157.	1.1	27
173	Bayesian genome-wide association analysis of growth and yearling ultrasound measures of carcass traits in Brangus heifers. Journal of Animal Science, 2012, 90, 3398-3409.	0.2	51
174	Whole-genome association analyses for lifetime reproductive traits in the pig. Journal of Animal Science, 2011, 89, 988-995.	0.2	74
175	A Novel Nonsense Mutation in the DMP1 Gene Identified by a Genome-Wide Association Study Is Responsible for Inherited Rickets in Corriedale Sheep. PLoS ONE, 2011, 6, e21739.	1.1	45
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