

Dorian Garrick

List of Publications by Year in descending order

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Version: 2024-02-01

260
papers

10,295
citations

44069

48
h-index

48315

88
g-index

271
all docs

271
docs citations

271
times ranked

7104
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. <i>New Zealand Journal of Agricultural Research</i> , 2022, 65, 172-187.	1.6	4
2	Non-additive QTL mapping of lactation traits in 124,000 cattle reveals novel recessive loci. <i>Genetics Selection Evolution</i> , 2022, 54, 5.	3.0	7
3	An inherited night blindness in Wiltshire sheep. <i>Veterinary Pathology</i> , 2022, , 030098582110674.	1.7	0
4	Genetic approaches for increasing fitness in endangered species. <i>Trends in Ecology and Evolution</i> , 2022, 37, 332-345.	8.7	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.) <i>J Dairy Sci</i> 105:7843-7844 (2022)		
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> . <i>Veterinary Pathology</i> , 2022, 59, 442-450.	1.7	2
7	XSim version 2: simulation of modern breeding programs. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	6
8	Pregnancy status predicted using milk mid-infrared spectra from dairy cattle. <i>Journal of Dairy Science</i> , 2022, 105, 3615-3632.	3.4	3
9	Genetic Parameters for Growth, Ultrasound and Carcass Traits in New Zealand Beef Cattle and Their Correlations with Maternal Performance. <i>Animals</i> , 2022, 12, 25.	2.3	5
10	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. <i>Animals</i> , 2022, 12, 1632.	2.3	5
11	Variance parameter estimation for age at puberty phenotypes under 2 levels of phenotype censorship. <i>JDS Communications</i> , 2022, 3, 339-342.	1.5	3
12	Genetic parameters for efficiency of crude protein utilisation and its relationship with production traits across lactations in grazing dairy cows. <i>New Zealand Journal of Agricultural Research</i> , 2021, 64, 62-82.	1.6	4
13	Reduced Animal Models Fitting Only Equations for Phenotyped Animals. <i>Frontiers in Genetics</i> , 2021, 12, 637626.	2.3	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. <i>JDS Communications</i> , 2021, 2, 51-54.	1.5	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>Felis catus</i>). <i>Animal Genetics</i> , 2021, 52, 321-332.	1.7	9
16	Identification of Genomic Regions Associated with Concentrations of Milk Fat, Protein, Urea and Efficiency of Crude Protein Utilization in Grazing Dairy Cows. <i>Genes</i> , 2021, 12, 456.	2.4	12
17	Can Nitrogen Excretion of Dairy Cows Be Reduced by Genetic Selection for Low Milk Urea Nitrogen Concentration?. <i>Animals</i> , 2021, 11, 737.	2.3	9
18	Non-additive association analysis using proxy phenotypes identifies novel cattle syndromes. <i>Nature Genetics</i> , 2021, 53, 949-954.	21.4	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. <i>BMC Genomics</i> , 2021, 22, 457.	2.8	6
20	Animal medical genetics: a historical perspective on more than 50 years of research into genetic disorders of animals at Massey University. <i>New Zealand Veterinary Journal</i> , 2021, 69, 255-266.	0.9	0
21	Alternative Ways of Computing the Numerator Relationship Matrix. <i>Frontiers in Genetics</i> , 2021, 12, 655638.	2.3	3
22	Sequence-based genome-wide association study of individual milk mid-infrared wavenumbers in mixed-breed dairy cattle. <i>Genetics Selection Evolution</i> , 2021, 53, 62.	3.0	14
23	A Missense Mutation in the MYBPH Gene Is Associated With Abdominal Fat Traits in Meat-Type Chickens. <i>Frontiers in Genetics</i> , 2021, 12, 698163.	2.3	4
24	Genetic Parameters for Maternal Performance Traits in Commercially Farmed New Zealand Beef Cattle. <i>Animals</i> , 2021, 11, 2509.	2.3	7
25	Estimates of genomic inbreeding and identification of candidate regions that differ between Chinese indigenous sheep breeds. <i>Journal of Animal Science and Biotechnology</i> , 2021, 12, 95.	5.3	13
26	HandyCNV: Standardized Summary, Annotation, Comparison, and Visualization of Copy Number Variant, Copy Number Variation Region, and Runs of Homozygosity. <i>Frontiers in Genetics</i> , 2021, 12, 731355.	2.3	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. <i>Animals</i> , 2021, 11, 24.	2.3	6
28	Comparison of Genotype Imputation for SNP Array and Low-Coverage Whole-Genome Sequencing Data. <i>Frontiers in Genetics</i> , 2021, 12, 704118.	2.3	8
29	Discovering Copy Number Variation in Dual-Purpose Xinjiang Brown Cattle. <i>Frontiers in Genetics</i> , 2021, 12, 747431.	2.3	6
30	Genetic parameters for total lactation yields of milk, fat, protein, and somatic cell score in New Zealand dairy goats. <i>Animal Science Journal</i> , 2020, 91, e13310.	1.4	14
31	Economic selection index to improve fiber quality in Mongolian Cashmere goats. <i>Livestock Science</i> , 2020, 232, 103898.	1.6	4
32	Economic values for index improvement of dual-purpose Simmental cattle. <i>Livestock Science</i> , 2020, 240, 104224.	1.6	4
33	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. <i>American Journal of Human Genetics</i> , 2020, 106, 893-904.	6.2	29
34	Genome-wide association studies of lactation yields of milk, fat, protein and somatic cell score in New Zealand dairy goats. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 55.	5.3	25
35	Accuracies of direct genomic breeding values for birth and weaning weights of registered Charolais cattle in Mexico. <i>Animal Production Science</i> , 2020, 60, 772.	1.3	2
36	Sire selection and genetic improvement of dairy cattle assuming pure market competition. <i>Journal of Dairy Science</i> , 2020, 103, 4532-4544.	3.4	2

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37	Exact Distribution of Linkage Disequilibrium in the Presence of Mutation, Selection, or Minor Allele Frequency Filtering. <i>Frontiers in Genetics</i> , 2020, 11, 362.	2.3	5
38	Fast parallelized sampling of Bayesian regression models for whole-genome prediction. <i>Genetics Selection Evolution</i> , 2020, 52, 16.	3.0	8
39	Accuracy of genomic prediction of shell quality in a White Leghorn line. <i>Poultry Science</i> , 2020, 99, 2833-2840.	3.4	6
40	The evolving role of Fourier-transform mid-infrared spectroscopy in genetic improvement of dairy cattle. <i>Journal of Animal Science and Biotechnology</i> , 2020, 11, 39.	5.3	20
41	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. <i>BMC Genetics</i> , 2019, 20, 83.	2.7	10
42	Increasing the accuracy of genomic prediction in purebred Limousin beef cattle by including crossbred Limousin data and accounting for an F94L variant in <i>MSTN</i> . <i>Animal Genetics</i> , 2019, 50, 621-633.	1.7	13
43	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. <i>BMC Genomics</i> , 2019, 20, 669.	2.8	17
44	Î2-Mannosidosis in German Shepherd Dogs. <i>Veterinary Pathology</i> , 2019, 56, 743-748.	1.7	8
45	Strategies for noise reduction and standardization of milk mid-infrared spectra from dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 6357-6372.	3.4	22
46	Identification of recombination hotspots and quantitative trait loci for recombination rate in layer chickens. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 20.	5.3	17
47	Fine mapping of genomic regions associated with female fertility in Nellore beef cattle based on sequence variants from segregating sires. <i>Journal of Animal Science and Biotechnology</i> , 2019, 10, 97.	5.3	7
48	Genome-wide association analysis reveals QTL and candidate mutations involved in white spotting in cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 62.	3.0	23
49	A certain invariance property of <i>BLUE</i> in a whole-genome regression context. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 113-117.	2.0	2
50	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. <i>Genetics</i> , 2018, 209, 89-103.	2.9	61
51	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. <i>Nature Genetics</i> , 2018, 50, 362-367.	21.4	286
52	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. <i>Journal of Dairy Science</i> , 2018, 101, 1292-1296.	3.4	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. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3567-3575.	1.8	19
54	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. <i>Scientific Reports</i> , 2018, 8, 16222.	3.3	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. <i>Animal Reproduction Science</i> , 2018, 199, 45-50.	1.5	2
56	Identification of an immune modulation locus utilising a bovine mammary gland infection challenge model. <i>Journal of Dairy Research</i> , 2018, 85, 185-192.	1.4	2
57	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018, 19, 499.	2.8	51
58	A genome-wide association study reveals novel genomic regions and positional candidate genes for fat deposition in broiler chickens. <i>BMC Genomics</i> , 2018, 19, 374.	2.8	28
59	A nested mixture model for genomic prediction using whole-genome SNP genotypes. <i>PLoS ONE</i> , 2018, 13, e0194683.	2.5	9
60	Comparison of alternative approaches to single-trait genomic prediction using genotyped and non-genotyped Hanwoo beef cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 2.	3.0	33
61	Efficient strategies for leave-one-out cross validation for genomic best linear unbiased prediction. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 38.	5.3	94
62	Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2017, 22, 172-193.	1.4	60
63	A FAS-ligand variant associated with autoimmune lymphoproliferative syndrome in cats. <i>Mammalian Genome</i> , 2017, 28, 47-55.	2.2	17
64	A comparison of identity-by-descent and identity-by-state matrices that are used for genetic evaluation and estimation of variance components. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 213-223.	2.0	15
65	Genome-wide detection of autosomal copy number variants in several sheep breeds using Illumina OvineSNP50 BeadChips. <i>Small Ruminant Research</i> , 2017, 155, 24-32.	1.2	9
66	Genotype imputation in a tropical crossbred dairy cattle population. <i>Journal of Dairy Science</i> , 2017, 100, 9623-9634.	3.4	13
67	The Accuracy and Bias of Single-Step Genomic Prediction for Populations Under Selection. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2685-2694.	1.8	29
68	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. <i>BMC Genomics</i> , 2017, 18, 386.	2.8	159
69	165 Genetic variants with potential loss of function in Gyr, Girolando, and Guzerat cattle breeds by resequencing. <i>Journal of Animal Science</i> , 2017, 95, 81-81.	0.5	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. <i>Journal of Animal Science</i> , 2017, 95, 287-288.	0.5	0
71	Population structure and genomic inbreeding in nine Swiss dairy cattle populations. <i>Genetics Selection Evolution</i> , 2017, 49, 83.	3.0	49
72	The role of genomics in pig improvement. <i>Animal Production Science</i> , 2017, 57, 2360.	1.3	7

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73	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. <i>Frontiers in Genetics</i> , 2017, 8, 171.	2.3	63
74	Genetic parameters for carcass and ultrasound traits in Hereford and admixed Simmental beef cattle: Accuracy of evaluating carcass traits ¹ . <i>Journal of Animal Science</i> , 2017, 95, 4718-4727.	0.5	12
75	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. <i>BMC Genomics</i> , 2017, 18, 999.	2.8	22
76	Single nucleotide variants and InDels identified from whole-genome re-sequencing of Guzerat, Gyr, Girolando and Holstein cattle breeds. <i>PLoS ONE</i> , 2017, 12, e0173954.	2.5	47
77	Familial episodic ataxia in lambs is potentially associated with a mutation in the fibroblast growth factor 14 (FGF14) gene. <i>PLoS ONE</i> , 2017, 12, e0190030.	2.5	4
78	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers ^{1,2} . <i>Journal of Animal Science</i> , 2017, 95, 4796-4812.	0.5	31
79	Fixed-length haplotypes can improve genomic prediction accuracy in an admixed dairy cattle population. <i>Genetics Selection Evolution</i> , 2017, 49, 54.	3.0	52
80	331 The genetic improvement of feed efficiency in beef cattle. <i>Journal of Animal Science</i> , 2017, 95, 161-161.	0.5	2
81	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. <i>BMC Genomics</i> , 2017, 18, 910.	2.8	36
82	164 Single nucleotide variants and indels identified from whole-genome resequencing of Gyr, Girolando, and Holstein cattle breeds. <i>Journal of Animal Science</i> , 2017, 95, 80-81.	0.5	0
83	Development and implementation of genomic predictions in beef cattle. <i>Animal Frontiers</i> , 2016, 6, 32-38.	1.7	51
84	027 Performance of genomic prediction using haplotypes in New Zealand dairy cattle. <i>Journal of Animal Science</i> , 2016, 94, 13-13.	0.5	2
85	Deriving Gene Networks from SNP Associated with Triacylglycerol and Phospholipid Fatty Acid Fractions from Ribeyes of Angus Cattle. <i>Frontiers in Genetics</i> , 2016, 7, 116.	2.3	10
86	Implementation of genomic selection in the poultry industry. <i>Animal Frontiers</i> , 2016, 6, 23-31.	1.7	62
87	The Effect of Calf Gender on Milk Production in Seasonal Calving Cows and Its Impact on Genetic Evaluations. <i>PLoS ONE</i> , 2016, 11, e0151236.	2.5	17
88	An Upper Bound for Accuracy of Prediction Using GBLUP. <i>PLoS ONE</i> , 2016, 11, e0161054.	2.5	53
89	032 Quantitative trait loci and candidate genes associated with heifer pregnancy rate and stayability in beef cattle. <i>Journal of Animal Science</i> , 2016, 94, 15-15.	0.5	3
90	Epistatic interactions associated with fatty acid concentrations of beef from angus sired beef cattle. <i>BMC Genomics</i> , 2016, 17, 891.	2.8	7

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91	036 Discovery of quantitative trait loci using a quantitative trait loci effects model in a multigenerational pedigree. <i>Journal of Animal Science</i> , 2016, 94, 16-17.	0.5	0
92	Host genetic influence on papillomavirus-induced tumors in the horse. <i>International Journal of Cancer</i> , 2016, 139, 784-792.	5.1	28
93	Computational strategies for alternative single-step Bayesian regression models with large numbers of genotyped and non-genotyped animals. <i>Genetics Selection Evolution</i> , 2016, 48, 96.	3.0	57
94	Estimates of genetic and crossbreeding parameters for milk components and potential yield of dairy products from New Zealand dairy cattle. <i>New Zealand Journal of Agricultural Research</i> , 2016, 59, 79-89.	1.6	6
95	Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in layers. <i>Journal of Animal Breeding and Genetics</i> , 2016, 133, 334-346.	2.0	24
96	An efficient exact method to obtain GBLUP and single-step GBLUP when the genomic relationship matrix is singular. <i>Genetics Selection Evolution</i> , 2016, 48, 80.	3.0	18
97	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. <i>Genetics Selection Evolution</i> , 2016, 48, 22.	3.0	19
98	Mixture models detect large effect QTL better than GBLUP and result in more accurate and persistent predictions. <i>Journal of Animal Science and Biotechnology</i> , 2016, 7, 7.	5.3	23
99	Responses in lactose yield, lactose percentage and protein-to-protein-plus-lactose ratio from index selection in New Zealand dairy cattle. <i>New Zealand Journal of Agricultural Research</i> , 2016, 59, 90-105.	1.6	7
100	Genome-wide association study of growth and body composition traits in Brangus beef cattle. <i>Livestock Science</i> , 2016, 183, 4-11.	1.6	29
101	Dairy product production and lactose demand in New Zealand and Ireland under different simulated milk product-processing portfolios. <i>Irish Journal of Agricultural and Food Research</i> , 2016, 55, 126-135.	0.4	2
102	Response and inbreeding from a genomic selection experiment in layer chickens. <i>Genetics Selection Evolution</i> , 2015, 47, 59.	3.0	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. <i>Genetics Selection Evolution</i> , 2015, 47, 99.	3.0	6
104	Genetic parameters and genetic correlations among triacylglycerol and phospholipid fractions in Angus cattle. <i>Journal of Animal Science</i> , 2015, 93, 522-528.	0.5	16
105	Predicted dairy product yields and deficits of lactose for manufacturing under differing selection and manufacturing scenarios in New Zealand. <i>New Zealand Journal of Agricultural Research</i> , 2015, 58, 432-440.	1.6	0
106	XSim: Simulation of Descendants from Ancestors with Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1415-1417.	1.8	20
107	A fast and efficient Gibbs sampler for BayesB in whole-genome analyses. <i>Genetics Selection Evolution</i> , 2015, 47, 80.	3.0	31
108	Cross-validation of genetic and genomic predictions of temperament in Nellore Angus crossbreds. <i>Livestock Science</i> , 2015, 182, 28-33.	1.6	2

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109	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 23.	3.0	38
110	Genetic parameters for sensory traits in longissimus muscle and their associations with tenderness, marbling score, and intramuscular fat in Angus cattle. <i>Journal of Animal Science</i> , 2015, 93, 21-27.	0.5	45
111	The economic value of somatic cell count in South African Holstein and Jersey cattle. <i>South African Journal of Animal Sciences</i> , 2014, 44, 173.	0.5	10
112	Comparison of breeding value prediction for two traits in a Nelore-Angus crossbred population using different Bayesian modeling methodologies. <i>Genetics and Molecular Biology</i> , 2014, 37, 631-637.	1.3	5
113	Use of robust multivariate linear mixed models for estimation of genetic parameters for carcass traits in beef cattle. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 504-512.	2.0	6
114	QTLs associated with dry matter intake, metabolic mid-test weight, growth and feed efficiency have little overlap across 4 beef cattle studies. <i>BMC Genomics</i> , 2014, 15, 1004.	2.8	97
115	Identification of genomic regions associated with feed efficiency in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 100.	2.7	87
116	Breeding objectives for Holstein cattle in South Africa. <i>South African Journal of Animal Sciences</i> , 2014, 44, 199.	0.5	15
117	Functionally reciprocal mutations of the prolactin signalling pathway define hairy and slick cattle. <i>Nature Communications</i> , 2014, 5, 5861.	12.8	108
118	Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. <i>Genomics</i> , 2014, 104, 572-581.	2.9	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. <i>Animal Genetics</i> , 2014, 45, 48-58.	1.7	61
120	Estimating the impact of somatic cell count on the value of milk utilising parameters obtained from the published literature. <i>Journal of Dairy Research</i> , 2014, 81, 223-232.	1.4	15
121	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. <i>Genetics Selection Evolution</i> , 2014, 46, 34.	3.0	52
122	Reduction in accuracy of genomic prediction for ordered categorical data compared to continuous observations. <i>Genetics Selection Evolution</i> , 2014, 46, 37.	3.0	19
123	Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle. <i>BMC Genetics</i> , 2014, 15, 39.	2.7	121
124	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. <i>BMC Genomics</i> , 2014, 15, 948.	2.8	44
125	A class of Bayesian methods to combine large numbers of genotyped and non-genotyped animals for whole-genome analyses. <i>Genetics Selection Evolution</i> , 2014, 46, 50.	3.0	147
126	Identification of breeding objectives using a bioeconomic model for a beef cattle production system in Uruguay. <i>Livestock Science</i> , 2014, 160, 21-28.	1.6	28

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127	Genome-wide association study of temperament and tenderness using different Bayesian approaches in a Nelloreâ€“Angus crossbred population. <i>Livestock Science</i> , 2014, 161, 17-27.	1.6	22
128	Genome-wide association study for egg production and quality in layer chickens. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 173-182.	2.0	72
129	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. <i>BMC Genomics</i> , 2014, 15, 442.	2.8	191
130	A genome-wide association study for canine cryptorchidism in Siberian Huskies. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 202-209.	2.0	11
131	The evolution of methodologies for genomic prediction. <i>Livestock Science</i> , 2014, 166, 10-18.	1.6	20
132	Spring calving versus split calving: effects on farm, processor and industry profitability for the Irish dairy industry. <i>Journal of Agricultural Science</i> , 2014, 152, 448-463.	1.3	6
133	Growth, feed intake and maternal performance of Angus heifers from high and low feed efficiency selection lines. <i>Animal Production Science</i> , 2014, 54, 1428.	1.3	7
134	Genomic BLUP Decoded: A Look into the Black Box of Genomic Prediction. <i>Genetics</i> , 2013, 194, 597-607.	2.9	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. <i>Journal of Dairy Science</i> , 2013, 96, 6007-6021.	3.4	48
136	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. <i>Genetics Selection Evolution</i> , 2013, 45, 11.	3.0	79
137	Genome-wide association study of infectious bovine keratoconjunctivitis in Angus cattle. <i>BMC Genetics</i> , 2013, 14, 23.	2.7	18
138	Novel genomic approaches unravel genetic architecture of complex traits in apple. <i>BMC Genomics</i> , 2013, 14, 393.	2.8	115
139	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. <i>Genetics Selection Evolution</i> , 2013, 45, 30.	3.0	56
140	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. <i>Poultry Science</i> , 2013, 92, 2270-2275.	3.4	25
141	Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. <i>Poultry Science</i> , 2013, 92, 1712-1723.	3.4	27
142	Genome-Wide Association Study for Marek's Disease Mortality in Layer Chickens. <i>Avian Diseases</i> , 2013, 57, 395-400.	1.0	22
143	An evaluation of circulating bovine viral diarrhea virus type 2 maternal antibody level and response to vaccination in Angus calves ^{1,2,3,4} . <i>Journal of Animal Science</i> , 2013, 91, 4440-4450.	0.5	23
144	Genome-wide prediction of age at puberty and reproductive longevity in sows. <i>Animal Genetics</i> , 2013, 44, 387-397.	1.7	40

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145	Sterol regulatory element binding transcription factor 1 (SREBF1) polymorphism and milk fatty acid composition. <i>Journal of Dairy Science</i> , 2013, 96, 2605-2616.	3.4	23
146	Analysis of egg production in layer chickens using a random regression model with genomic relationships. <i>Poultry Science</i> , 2013, 92, 1486-1491.	3.4	20
147	Bayesian Methods Applied to GWAS. <i>Methods in Molecular Biology</i> , 2013, 1019, 237-274.	0.9	115
148	Implementing a QTL Detection Study (GWAS) Using Genomic Prediction Methodology. <i>Methods in Molecular Biology</i> , 2013, 1019, 275-298.	0.9	80
149	Genome-wide association and prediction of direct genomic breeding values for composition of fatty acids in Angus beef cattle. <i>BMC Genomics</i> , 2013, 14, 730.	2.8	67
150	Genome-wide association study of concentrations of iron and other minerals in longissimus muscle of Angus cattle. <i>Journal of Animal Science</i> , 2013, 91, 3593-3600.	0.5	10
151	Accuracies of direct genomic breeding values in Hereford beef cattle using national or international training populations. <i>Journal of Animal Science</i> , 2013, 91, 1538-1551.	0.5	44
152	Genetic parameters for concentrations of minerals in longissimus muscle and their associations with palatability traits in Angus cattle. <i>Journal of Animal Science</i> , 2013, 91, 1067-1075.	0.5	30
153	Application of multivariate heavy-tailed distributions to residuals in the estimation of genetic parameters of growth traits in beef cattle. <i>Journal of Animal Science</i> , 2013, 91, 1552-1561.	0.5	2
154	Evaluation of response to bovine viral diarrhoea virus type 2 vaccination and timing of weaning on yearling ultrasound body composition, performance, and carcass quality traits in Angus calves. <i>Journal of Animal Science</i> , 2013, 91, 5466-5476.	0.5	4
155	Whole Genome Association Studies of Residual Feed Intake and Related Traits in the Pig. <i>PLoS ONE</i> , 2013, 8, e61756.	2.5	104
156	Heritability and Bayesian genome-wide association study of first service conception and pregnancy in Brangus heifers. <i>Journal of Animal Science</i> , 2013, 91, 605-612.	0.5	58
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