Dorian Garrick

List of Publications by Year
in descending order

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	Extension of the bayesian alphabet for genomic selection. BMC Bioinformatics, 2011, 12, 186.	2.6	942
2	Deregressing estimated breeding values and weighting information for genomic regression analyses. Genetics Selection Evolution, 2009, 41, 55.	3.0	500
3	Accuracy of Genomic Selection Methods in a Standard Data Set of Loblolly Pine (<i>Pinus taeda</i>L.). Genetics, 2012, 190, 1503-1510.	2.9	363
4	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.	21.4	286
5	Genomic BLUP Decoded: A Look into the Black Box of Genomic Prediction. Genetics, 2013, 194, 597-607.	2.9	279
6	Genomic prediction of simulated multibreed and purebred performance using observed fifty thousand single nucleotide polymorphism genotypes1. Journal of Animal Science, 2010, 88, 544-551.	0.5	228
7	Technical note: Derivation of equivalent computing algorithms for genomic predictions and reliabilities of animal merit. Journal of Dairy Science, 2009, 92, 2971-2975.	3.4	216
8	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. BMC Genomics, 2014, 15, 442.	2.8	191
9	Genome-Wide Association Study Identifies Loci for Body Composition and Structural Soundness Traits in Pigs. PLoS ONE, 2011, 6, e14726.	2.5	189
10	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. Genetics Selection Evolution, 2011, 43, 40.	3.0	174
11	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. BMC Genomics, 2017, 18, 386.	2.8	159
12	A whole€genome association study for pig reproductive traits. Animal Genetics, 2012, 43, 18-26.	1.7	152
13	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.	3.0	147
14	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.	0.5	145
15	Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. Genetics Selection Evolution, 2011, 43, 5.	3.0	130
16	Genome-wide association study for intramuscular fat deposition and composition in Nellore cattle. BMC Genetics, 2014, 15, 39.	2.7	121
17	Novel genomic approaches unravel genetic architecture of complex traits in apple. BMC Genomics, 2013, 14, 393.	2.8	115
18	Bayesian Methods Applied to GWAS. Methods in Molecular Biology, 2013, 1019, 237-274.	0.9	115

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19	Functionally reciprocal mutations of the prolactin signalling pathway define hairy and slick cattle. Nature Communications, 2014, 5, 5861.	12.8	108
20	Whole Genome Association Studies of Residual Feed Intake and Related Traits in the Pig. PLoS ONE, 2013, 8, e61756.	2.5	104
21	Influence of Free-Stall Base on Tarsal Joint Lesions and Hygiene in Dairy Cows. Journal of Dairy Science, 2007, 90, 3559-3566.	3.4	101
22	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.	2.8	97
23	Genome€wide association analysis and genetic architecture of egg weight and egg uniformity in layer chickens. Animal Genetics, 2012, 43, 87-96.	1.7	95
24	Efficient strategies for leave-one-out cross validation for genomic best linear unbiased prediction. Journal of Animal Science and Biotechnology, 2017, 8, 38.	5.3	94
25	Identification of genomic regions associated with feed efficiency in Nelore cattle. BMC Genetics, 2014, 15, 100.	2.7	87
26	Profitabilities of Some Mating Systems for Dairy Herds in New Zealand. Journal of Dairy Science, 2000, 83, 144-153.	3.4	86
27	Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. Genetics Selection Evolution, 2011, 43, 23.	3.0	86
28	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.	0.5	86
29	Implementing a QTL Detection Study (GWAS) Using Genomic Prediction Methodology. Methods in Molecular Biology, 2013, 1019, 275-298.	0.9	80
30	The nature, scope and impact of genomic prediction in beef cattle in the United States. Genetics Selection Evolution, 2011, 43, 17.	3.0	79
31	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. Genetics Selection Evolution, 2013, 45, 11.	3.0	79
32	Variance Heterogeneity in Direct and Maternal Weight Traits by Sex and Percent Purebred for Simmental-Sired Calves. Journal of Animal Science, 1989, 67, 2515.	0.5	75
33	Whole-genome association analyses for lifetime reproductive traits in the pig. Journal of Animal Science, 2011, 89, 988-995.	0.5	74
34	Genome€wide association study for egg production and quality in layer chickens. Journal of Animal Breeding and Genetics, 2014, 131, 173-182.	2.0	72
35	Correction for Amino Acid Loss during Acid Hydrolysis of a Purified Protein. Analytical Biochemistry, 1996, 236, 199-207.	2.4	69
36	Genome-wide association and prediction of direct genomic breeding values for composition of fatty acids in Angus beef cattlea. BMC Genomics, 2013, 14, 730.	2.8	67

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37	Response and inbreeding from a genomic selection experiment in layer chickens. Genetics Selection Evolution, 2015, 47, 59.	3.0	67
38	Accuracy of direct genomic breeding values for nationally evaluated traits in US Limousin and Simmental beef cattle. Genetics Selection Evolution, 2012, 44, 38.	3.0	63
39	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. Frontiers in Genetics, 2017, 8, 171.	2.3	63
40	Implementation of genomic selection in the poultry industry. Animal Frontiers, 2016, 6, 23-31.	1.7	62
41	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.	1.7	61
42	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. Genetics, 2018, 209, 89-103.	2.9	61
43	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.	1.4	60
44	Heritability and Bayesian genome-wide association study of first service conception and pregnancy in Brangus heifers1. Journal of Animal Science, 2013, 91, 605-612.	0.5	58
45	Computational strategies for alternative single-step Bayesian regression models with large numbers of genotyped and non-genotyped animals. Genetics Selection Evolution, 2016, 48, 96.	3.0	57
46	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. Genetics Selection Evolution, 2013, 45, 30.	3.0	56
47	Aspects of Selection for Performance in Several Environments with Heterogeneous Variances. Journal of Animal Science, 1987, 65, 409-421.	0.5	55
48	The effect of food dry matter intake on endogenous ileal amino acid excretion determined under peptide alimentation in the 50 kg liveweight pig. Journal of the Science of Food and Agriculture, 1993, 62, 235-243.	3.5	54
49	An Upper Bound for Accuracy of Prediction Using GBLUP. PLoS ONE, 2016, 11, e0161054.	2.5	53
50	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. Genetics Selection Evolution, 2014, 46, 34.	3.0	52
51	Fixed-length haplotypes can improve genomic prediction accuracy in an admixed dairy cattle population. Genetics Selection Evolution, 2017, 49, 54.	3.0	52
52	Development and implementation of genomic predictions in beef cattle. Animal Frontiers, 2016, 6, 32-38.	1.7	51
53	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. BMC Genomics, 2018, 19, 499.	2.8	51
54	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.	0.5	51

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55	DNA-based paternity analysis and genetic evaluation in a large, commercial cattle ranch setting1. Journal of Animal Science, 2007, 85, 3159-3169.	0.5	49
56	Population structure and genomic inbreeding in nine Swiss dairy cattle populations. Genetics Selection Evolution, 2017, 49, 83.	3.0	49
57	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.	3.4	48
58	Single nucleotide variants and InDels identified from whole-genome re-sequencing of Guzerat, Gyr, Girolando and Holstein cattle breeds. PLoS ONE, 2017, 12, e0173954.	2.5	47
59	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.	2.5	45
60	Genomic breeding value prediction and QTL mapping of QTLMAS2010 data using Bayesian Methods. BMC Proceedings, 2011, 5, S13.	1.6	45
61	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.	0.5	45
62	Accuracies of direct genomic breeding values in Hereford beef cattle using national or international training populations1. Journal of Animal Science, 2013, 91, 1538-1551.	0.5	44
63	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. BMC Genomics, 2014, 15, 948.	2.8	44
64	Environmental Sensitivity in New Zealand Dairy Cattle. Journal of Dairy Science, 2007, 90, 1538-1547.	3.4	42
65	Inheritance of pulmonary arterial pressure in Angus cattle and its correlation with growth1. Journal of Animal Science, 2008, 86, 815-819.	0.5	41
66	Development and application of a processing model for the Irish dairy industry. Journal of Dairy Science, 2010, 93, 5091-5100.	3.4	41
67	Genome-wide association study of insect bite hypersensitivity in two horse populations in the Netherlands. Genetics Selection Evolution, 2012, 44, 31.	3.0	40
68	Genome-wide prediction of age at puberty and reproductive longevity in sows. Animal Genetics, 2013, 44, 387-397.	1.7	40
69	Changes in inbreeding of U.S. Herefords during the twentieth century1. Journal of Animal Science, 2005, 83, 992-1001.	0.5	38
70	Trends in milk production, calving rate and survival of cows in 14 Irish dairy herds as a result of the introgression of Holstein-Friesian genes. Animal Science, 2006, 82, 423-433.	1.3	38
71	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. Genetics Selection Evolution, 2015, 47, 23.	3.0	38
72	‹i›â€˜Ovar-Mhcâ€‹‹/i›â€" Ovine major histocompatibility complex: Role in genetic resistance to diseases. New Zealand Veterinary Journal, 2006, 54, 153-160.	0.9	37

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73	Financial implications of recent declines in reproduction and survival of Holstein-Friesian cows in spring-calving Irish dairy herds. Agricultural Systems, 2006, 89, 165-183.	6.1	37
74	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. BMC Genomics, 2017, 18, 910.	2.8	36
75	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. Journal of Dairy Science, 2018, 101, 1292-1296.	3.4	35
76	Producing and using genetic evaluations in the United States beef industry of today1. Journal of Animal Science, 2009, 87, E11-E18.	0.5	34
77	Non-additive association analysis using proxy phenotypes identifies novel cattle syndromes. Nature Genetics, 2021, 53, 949-954.	21.4	34
78	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.	0.5	33
79	Comparison of alternative approaches to single-trait genomic prediction using genotyped and non-genotyped Hanwoo beef cattle. Genetics Selection Evolution, 2017, 49, 2.	3.0	33
80	Utilisation of marker assisted selection in a commercial dairy cow population. Livestock Science, 1997, 47, 139-147.	1.2	32
81	Genetic and Economic Responses for Within-Family Marker-Assisted Selection in Dairy Cattle Breeding Schemes. Journal of Dairy Science, 1998, 81, 2942-2950.	3.4	32
82	Multiple-marker mapping of wood density loci in an outbred pedigree of radiata pine. Theoretical and Applied Genetics, 2000, 100, 926-933.	3.6	32
83	'Ovar-Mhc' - ovine major histocompatibility complex: structure and gene polymorphisms. Genetics and Molecular Research, 2006, 5, 581-608.	0.2	32
84	A fast and efficient Gibbs sampler for BayesB in whole-genome analyses. Genetics Selection Evolution, 2015, 47, 80.	3.0	31
85	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.	0.5	31
86	Utilisation of genetic variation by marker assisted selection in commercial dairy cattle populations. Livestock Science, 1999, 59, 51-60.	1.2	30
87	Genetic diversity and population structure of American Red Angus cattle1. Journal of Animal Science, 2010, 88, 59-68.	0.5	30
88	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.	0.5	30
89	Effect of Live Weight and Differing Economic Values on Responses to Selection for Milk Fat, Protein, Volume, and Live Weight. Journal of Dairy Science, 1997, 80, 2557-2562.	3.4	29
90	Effects of age at slaughter and sire genotype on fatness, muscularity, and the quality of meat from ram lambs born to Romney ewes. New Zealand Journal of Agricultural Research, 2002, 45, 77-86.	1.6	29

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91	Effects of calving age, breed fraction and month of calving on calving interval and survival across parities in Irish spring-calving dairy cows. Livestock Science, 2006, 100, 216-230.	1.6	29
92	Genome-wide association study of growth and body composition traits in Brangus beef cattle. Livestock Science, 2016, 183, 4-11.	1.6	29
93	The Accuracy and Bias of Single-Step Genomic Prediction for Populations Under Selection. G3: Genes, Genomes, Genetics, 2017, 7, 2685-2694.	1.8	29
94	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. Scientific Reports, 2018, 8, 16222.	3.3	29
95	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. American Journal of Human Genetics, 2020, 106, 893-904.	6.2	29
96	A missense mutation in AGTPBP1 was identified in sheep with a lower motor neuron disease. Heredity, 2012, 109, 156-162.	2.6	28
97	Identification of breeding objectives using a bioeconomic model for a beef cattle production system in Uruguay. Livestock Science, 2014, 160, 21-28.	1.6	28
98	Host genetic influence on papillomavirusâ€induced tumors in the horse. International Journal of Cancer, 2016, 139, 784-792.	5.1	28
99	A genome-wide association study reveals novel genomic regions and positional candidate genes for fat deposition in broiler chickens. BMC Genomics, 2018, 19, 374.	2.8	28
100	Possible Effects of 25 Years of Selection and Crossbreeding on the Genetic Merit and Productivity of New Zealand Dairy Cattle. Journal of Dairy Science, 2000, 83, 154-163.	3.4	27
101	Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. Poultry Science, 2013, 92, 1712-1723.	3.4	27
102	A Fast EM Algorithm for BayesA-Like Prediction of Genomic Breeding Values. PLoS ONE, 2012, 7, e49157.	2.5	27
103	Milestones in beef cattle genetic evaluation1. Journal of Animal Science, 2009, 87, E3-E10.	0.5	26
104	Short Communication: Quantitative Trait Loci Analysis on 17 Nonproduction Traits in the New Zealand Dairy Population. Journal of Dairy Science, 1999, 82, 2514-2516.	3.4	25
105	Breeding objectives for three silvicultural regimes of radiata pine. Canadian Journal of Forest Research, 2001, 31, 654-662.	1.7	25
106	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.	1.7	25
107	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. Poultry Science, 2013, 92, 2270-2275.	3.4	25
108	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.	5.3	25

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109	Short Communication: Effect of Environment on the Expression of Breed and Heterosis Effects for Production Traits. Journal of Dairy Science, 2007, 90, 1548-1553.	3.4	24
110	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.	2.0	24
111	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.	0.5	23
112	Sterol regulatory element binding transcription factor 1 (SREBF1) polymorphism and milk fatty acid composition. Journal of Dairy Science, 2013, 96, 2605-2616.	3.4	23
113	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.	5.3	23
114	Genome-wide association analysis reveals QTL and candidate mutations involved in white spotting in cattle. Genetics Selection Evolution, 2019, 51, 62.	3.0	23
115	Whole genome analysis of infectious bovine keratoconjunctivitis in Angus cattle using Bayesian threshold models. BMC Proceedings, 2011, 5, S22.	1.6	22
116	Genome-Wide Association Study for Marek's Disease Mortality in Layer Chickens. Avian Diseases, 2013, 57, 395-400.	1.0	22
117	Genome-wide association study of temperament and tenderness using different Bayesian approaches in a Nelloreâ€"Angus crossbred population. Livestock Science, 2014, 161, 17-27.	1.6	22
118	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. BMC Genomics, 2017, 18, 999.	2.8	22
119	Strategies for noise reduction and standardization of milk mid-infrared spectra from dairy cattle. Journal of Dairy Science, 2019, 102, 6357-6372.	3.4	22
120	Inheritance of adult velvet antler weights and live weights in farmed red deer. Livestock Science, 1997, 49, 287-295.	1.2	21
121	Variance modelling of longitudinal height data from a <i>Pinus radiata</i> progeny test. Canadian Journal of Forest Research, 2000, 30, 645-654.	1.7	21
122	Maternal effects on docility in Limousin cattle1. Journal of Animal Science, 2007, 85, 650-657.	0.5	20
123	Analysis of egg production in layer chickens using a random regression model with genomic relationships. Poultry Science, 2013, 92, 1486-1491.	3.4	20
124	The evolution of methodologies for genomic prediction. Livestock Science, 2014, 166, 10-18.	1.6	20
125	XSim: Simulation of Descendants from Ancestors with Sequence Data. G3: Genes, Genomes, Genetics, 2015, 5, 1415-1417.	1.8	20
126	The evolving role of Fourier-transform mid-infrared spectroscopy in genetic improvement of dairy cattle. Journal of Animal Science and Biotechnology, 2020, 11, 39.	5.3	20

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127	Parasitism and production in fleece‐weight‐selected and control sheep. New Zealand Journal of Agricultural Research, 1995, 38, 381-387.	1.6	19
128	Predicting breeding values and accuracies from group in comparison to individual observations. Journal of Animal Science, 2006, 84, 88-92.	0.5	19
129	Reduction in accuracy of genomic prediction for ordered categorical data compared to continuous observations. Genetics Selection Evolution, 2014, 46, 37.	3.0	19
130	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. Genetics Selection Evolution, 2016, 48, 22.	3.0	19
131	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.	1.8	19
132	Genome-wide association study of infectious bovine keratoconjunctivitis in Angus cattle. BMC Genetics, 2013, 14, 23.	2.7	18
133	An efficient exact method to obtain GBLUP and single-step GBLUP when the genomic relationship matrix is singular. Genetics Selection Evolution, 2016, 48, 80.	3.0	18
134	Effects of Selection and Crossbreeding Strategies on Industry Profit in the New Zealand Dairy Industry. Journal of Dairy Science, 2000, 83, 164-172.	3.4	17
135	Genomic breeding value prediction and QTL mapping of QTLMAS2011 data using Bayesian and GBLUP methods. BMC Proceedings, 2012, 6, S7.	1.6	17
136	The Effect of Calf Gender on Milk Production in Seasonal Calving Cows and Its Impact on Genetic Evaluations. PLoS ONE, 2016, 11, e0151236.	2.5	17
137	A FAS-ligand variant associated with autoimmune lymphoproliferative syndrome in cats. Mammalian Genome, 2017, 28, 47-55.	2.2	17
138	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. BMC Genomics, 2019, 20, 669.	2.8	17
139	Identification of recombination hotspots and quantitative trait loci for recombination rate in layer chickens. Journal of Animal Science and Biotechnology, 2019, 10, 20.	5.3	17
140	An animal breeding approach to the estimation of genetic and environmental trends from field populations1. Journal of Animal Science, 2010, 88, E3-E10.	0.5	16
141	Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. Genomics, 2014, 104, 572-581.	2.9	16
142	Genetic parameters and genetic correlations among triacylglycerol and phospholipid fractions in Angus cattle1. Journal of Animal Science, 2015, 93, 522-528.	0.5	16
143	Variance modelling of longitudinal height data from a *Pinus radiata* progeny test. Canadian Journal of Forest Research, 2000, 30, 645-654.	1.7	16
144	The influence of allyl trenbolone (Regumate) on the timing, duration and endocrinology of parturition in sows. Animal Reproduction Science, 1985, 9, 163-171.	1.5	15

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145	Breeding objectives for Holstein cattle in South Africa. South African Journal of Animal Sciences, 2014, 44, 199.	0.5	15
146	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.	1.4	15
147	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.	2.0	15
148	A model of mammalian energetics and growth: model development. Agricultural Systems, 2001, 68, 55-68.	6.1	14
149	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.	1.3	14
150	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.	1.4	14
151	Sequence-based genome-wide association study of individual milk mid-infrared wavenumbers in mixed-breed dairy cattle. Genetics Selection Evolution, 2021, 53, 62.	3.0	14
152	Genetic approaches for increasing fitness in endangered species. Trends in Ecology and Evolution, 2022, 37, 332-345.	8.7	14
153	Estimates of genetic parameters for production and reproduction traits in three breeds of pigs. New Zealand Journal of Agricultural Research, 1996, 39, 387-395.	1.6	13
154	Genetic response to within-family selection using molecular markers in some radiata pine breeding schemes. Canadian Journal of Forest Research, 2001, 31, 779-785.	1.7	13
155	Genetic polymorphisms in bovine *transferrin receptor 2* (*TFR2*) and *solute carrier family 40* (*iron‐regulated transporter*)*, member 1* (*SLC40A1*) genes and their association with beef iron content. Animal Genetics, 2012, 43, 115-122.	1.7	13
156	Genotype imputation in a tropical crossbred dairy cattle population. Journal of Dairy Science, 2017, 100, 9623-9634.	3.4	13
157	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 *MSTN*. Animal Genetics, 2019, 50, 621-633.	1.7	13
158	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.	5.3	13
159	Selection responses in New Zealand Romney sheep. New Zealand Journal of Agricultural Research, 1985, 28, 257-264.	1.6	12
160	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.	0.5	12
161	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.	2.4	12
162	Effects of oestradiol benzoate treatment on the reproductive performance and endocrine status of sows after lactations of 10 or 35 days. Reproduction, 1984, 72, 329-337.	2.6	11

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163	Parasitological characteristics of fleece‐weight‐selected and control sheep. New Zealand Journal of Agricultural Research, 1995, 38, 389-397.	1.6	11
164	Weaning weight inheritance in environments classified by maternal body weight change1. Journal of Animal Science, 2007, 85, 610-617.	0.5	11
165	A genome‐wide association study for canine cryptorchidism in Siberian Huskies. Journal of Animal Breeding and Genetics, 2014, 131, 202-209.	2.0	11
166	Some relationships between weights of growing heifers and their subsequent lactation performances. New Zealand Journal of Agricultural Research, 1997, 40, 87-92.	1.6	10
167	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.	0.5	10
168	The economic value of somatic cell count in South African Holstein and Jersey cattle. South African Journal of Animal Sciences, 2014, 44, 173.	0.5	10
169	Deriving Gene Networks from SNP Associated with Triacylglycerol and Phospholipid Fatty Acid Fractions from Ribeyes of Angus Cattle. Frontiers in Genetics, 2016, 7, 116.	2.3	10
170	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. BMC Genetics, 2019, 20, 83.	2.7	10
171	Economic values of traits for pig improvement. I. A simulation model. Australian Journal of Agricultural Research, 1995, 46, 285.	1.5	10
172	Threshold model analysis of lamb survivability in Romney sheep. New Zealand Journal of Agricultural Research, 2006, 49, 411-418.	1.6	9
173	Use of linear mixed models for genetic evaluation of gestation length and birth weight allowing for heavy-tailed residual effects. Genetics Selection Evolution, 2010, 42, 26.	3.0	9
174	Genome-wide detection of autosomal copy number variants in several sheep breeds using Illumina OvineSNP50 BeadChips. Small Ruminant Research, 2017, 155, 24-32.	1.2	9
175	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.	1.7	9
176	Can Nitrogen Excretion of Dairy Cows Be Reduced by Genetic Selection for Low Milk Urea Nitrogen Concentration?. Animals, 2021, 11, 737.	2.3	9
177	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.	2.3	9
178	A nested mixture model for genomic prediction using whole-genome SNP genotypes. PLoS ONE, 2018, 13, e0194683.	2.5	9
179	Selection response in New Zealand Romney sheep. New Zealand Journal of Agricultural Research, 1984, 27, 329-336.	1.6	8
180	Multiple Trait Prediction for a Type of Model with Heterogeneous Genetic and Residual Covariance Structures. Journal of Animal Science, 1989, 67, 2529.	0.5	8

#	Article	IF	Citations
181	Emerging technologies for identifying superior dairy cows in New Zealand. New Zealand Veterinary Journal, 2005, 53, 390-399.	0.9	8
182	Phenotypic relationships between hair whorl characteristics and spermatozoal attributes in Holstein bulls. Animal Reproduction Science, 2005, 85, 95-103.	1.5	8
183	Application of new technologies in sheep breeding. New Zealand Journal of Agricultural Research, 2007, 50, 89-102.	1.6	8
184	Reducing bias in maintenance energy expected progeny difference by accounting for selection on weaning and yearling weights1. Journal of Animal Science, 2009, 87, 1628-1637.	0.5	8
185	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.	0.5	8
186	β-Mannosidosis in German Shepherd Dogs. Veterinary Pathology, 2019, 56, 743-748.	1.7	8
187	Fast parallelized sampling of Bayesian regression models for whole-genome prediction. Genetics Selection Evolution, 2020, 52, 16.	3.0	8
188	Comparison of Genotype Imputation for SNP Array and Low-Coverage Whole-Genome Sequencing Data. Frontiers in Genetics, 2021, 12, 704118.	2.3	8
189	The effect of simulated censored data on estimates of heritability of longevity in the Thoroughbred racing industry. Genetics and Molecular Research, 2006, 5, 7-15.	0.2	8
190	Association of microsatellite polymorphisms with immune responses to a killed Mycobacterium avium subsp. paratuberculosis vaccine in Merino sheep. New Zealand Veterinary Journal, 2010, 58, 237-245.	0.9	7
191	Growth, feed intake and maternal performance of Angus heifers from high and low feed efficiency selection lines. Animal Production Science, 2014, 54, 1428.	1.3	7
192	Epistatic interactions associated with fatty acid concentrations of beef from angus sired beef cattle. BMC Genomics, 2016, 17, 891.	2.8	7
193	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.	1.6	7
194	The role of genomics in pig improvement. Animal Production Science, 2017, 57, 2360.	1.3	7
195	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.	5.3	7
196	Genetic Parameters for Maternal Performance Traits in Commercially Farmed New Zealand Beef Cattle. Animals, 2021, 11, 2509.	2.3	7
197	Non-additive QTL mapping of lactation traits in 124,000 cattle reveals novel recessive loci. Genetics Selection Evolution, 2022, 54, 5.	3.0	7
198	Economic values of traits for pig improvement. II. Estimates for New Zealand conditions. Australian Journal of Agricultural Research, 1995, 46, 305.	1.5	6

#	Article	IF	Citations
199	A model of mammalian energetics and growth: model testing (sheep). Agricultural Systems, 2001, 68, 69-91.	6.1	6
200	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.	2.0	6
201	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.	1.3	6
202	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.	3.0	6
203	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.	1.6	6
204	Accuracy of genomic prediction of shell quality in a White Leghorn line. Poultry Science, 2020, 99, 2833-2840.	3.4	6
205	The genomes of precision edited cloned calves show no evidence for off-target events or increased de novo mutagenesis. BMC Genomics, 2021, 22, 457.	2.8	6
206	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.	2.3	6
207	Discovering Copy Number Variation in Dual-Purpose XinJiang Brown Cattle. Frontiers in Genetics, 2021, 12, 747431.	2.3	6
208	XSim version 2: simulation of modern breeding programs. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	6
209	Evaluation of the Duroc in comparison with the Landrace and Large White as a terminal sire of crossbred pigs slaughtered at 85 kg liveweight. New Zealand Journal of Agricultural Research, 1988, 31, 421-430.	1.6	5
210	Economic values for dairy production traits under different milk payment systems in South Africa. South African Journal of Animal Sciences, 2010, 39, .	0.5	5
211	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.	1.3	5
212	Exact Distribution of Linkage Disequilibrium in the Presence of Mutation, Selection, or Minor Allele Frequency Filtering. Frontiers in Genetics, 2020, 11, 362.	2.3	5
213	Breeding objectives for three silvicultural regimes of radiata pine. Canadian Journal of Forest Research, 2001, 31, 654-662.	1.7	5
214	Genetic Parameters for Growth, Ultrasound and Carcass Traits in New Zealand Beef Cattle and Their Correlations with Maternal Performance. Animals, 2022, 12, 25.	2.3	5
215	Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. Animals, 2022, 12, 1632.	2.3	5
216	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.	0.5	4

#	Article	IF	Citations
217	Familial episodic ataxia in lambs is potentially associated with a mutation in the fibroblast growth factor 14 (FGF14) gene. PLoS ONE, 2017, 12, e0190030.	2.5	4
218	Economic selection index to improve fiber quality in Mongolian Cashmere goats. Livestock Science, 2020, 232, 103898.	1.6	4
219	Economic values for index improvement of dual-purpose Simmental cattle. Livestock Science, 2020, 240, 104224.	1.6	4
220	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.	1.6	4
221	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.	1.6	4
222	A Missense Mutation in the MYBPH Gene Is Associated With Abdominal Fat Traits in Meat-Type Chickens. Frontiers in Genetics, 2021, 12, 698163.	2.3	4
223	Genetic response to within-family selection using molecular markers in some radiata pine breeding schemes. Canadian Journal of Forest Research, 2001, 31, 779-785.	1.7	4
224	Effects of estimation accuracy on potential payment premiums for superior beef carcasses. New Zealand Journal of Agricultural Research, 1999, 42, 305-314.	1.6	3
225	Invited review: Genomic analysis of data from physiological studies. Journal of Dairy Science, 2012, 95, 499-507.	3.4	3
226	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.	0.5	3
227	Reduced Animal Models Fitting Only Equations for Phenotyped Animals. Frontiers in Genetics, 2021, 12, 637626.	2.3	3
228	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.	1.5	3
229	Alternative Ways of Computing the Numerator Relationship Matrix. Frontiers in Genetics, 2021, 12, 655638.	2.3	3
230	Growth, feed intake and maternal performance of Angus heifers selected for high or low growth and milk production. Animal Production Science, 2010, 50, 349.	1.3	3
231	Pregnancy status predicted using milk mid-infrared spectra from dairy cattle. Journal of Dairy Science, 2022, 105, 3615-3632.	3.4	3
232	Variance parameter estimation for age at puberty phenotypes under 2 levels of phenotype censorship. JDS Communications, 2022, 3, 339-342.	1.5	3
233	Potential for economic benefits to the producer from altering the composition of milk. BSAP Occasional Publication, 2000, 25, 93-108.	0.0	2
234	Cattle. , 2009, , 1-17.		2

#	Article	IF	Citations
235	SNPlotz: a generic genome plot tool to aid the SNP association studies. BMC Bioinformatics, 2010, 11, .	2.6	2
236	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.	0.5	2
237	Cross-validation of genetic and genomic predictions of temperament in Nelloreâ€"Angus crossbreds. Livestock Science, 2015, 182, 28-33.	1.6	2
238	027 Performance of genomic prediction using haplotypes in New Zealand dairy cattle. Journal of Animal Science, 2016, 94, 13-13.	0.5	2
239	331 The genetic improvement of feed efficiency in beef cattle. Journal of Animal Science, 2017, 95, 161-161.	0.5	2
240	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.	1.5	2
241	Identification of an immune modulation locus utilising a bovine mammary gland infection challenge model. Journal of Dairy Research, 2018, 85, 185-192.	1.4	2
242	A certain invariance property of <scp>BLUE</scp> in a wholeâ€genome regression context. Journal of Animal Breeding and Genetics, 2019, 136, 113-117.	2.0	2
243	Accuracies of direct genomic breeding values for birth and weaning weights of registered Charolais cattle in Mexico. Animal Production Science, 2020, 60, 772.	1.3	2
244	Sire selection and genetic improvement of dairy cattle assuming pure market competition. Journal of Dairy Science, 2020, 103, 4532-4544.	3.4	2
245	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.	0.4	2
246	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.	1.7	2
247	Effect of Stall Base Type on Herd Health, Costs, and Producer Satisfaction. , 2007, , .		1
248	Estimates of phenotypic and genetic parameters for weaning and yearling weights in Bali beef cattle. Asian-Australasian Journal of Animal Sciences, 1992, 5, 623-628.	2.4	1
249	Early Career Achievement Awards: Recognizing achievement of young scholars working to foster the discovery, sharing, and application of knowledge concerning the responsible use of animals to enhance human life and well-being1. Journal of Animal Science, 2009, 87, E109-E110.	0.5	0
250	2009 Early Careers Achievement Awards: Recognizing achievement of young scholars working to foster the discovery, sharing, and application of knowledge concerning the responsible use of animals to enhance human life and well-being1. Journal of Animal Science, 2010, 88, E170-E171.	0.5	0
251	Genetics: Population. , 2011, , 514-516.		0
252	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.	1.6	0

#	Article	IF	Citations
253	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.	0.5	0
254	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.	0.5	0
255	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.	0.5	0
256	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.	0.5	0
257	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.	0.9	0
258	Genetics: Quantitative. , 2011, , 517-518.		0
259	An inherited night blindness in Wiltshire sheep. Veterinary Pathology, 2022, , 030098582110674.	1.7	0
260	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 ETQq0 0 0 rgBT /Overlock 10 T	0.5	0