

Dorian Garrick

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247
papers

7,345
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42
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269
ext. papers

9,154
ext. citations

3.2
avg, IF

6.08
L-index

#	Paper	IF	Citations
247	Extension of the bayesian alphabet for genomic selection. <i>BMC Bioinformatics</i> , 2011 , 12, 186	3.6	672
246	Deregressing estimated breeding values and weighting information for genomic regression analyses. <i>Genetics Selection Evolution</i> , 2009 , 41, 55	4.9	402
245	Accuracy of genomic selection methods in a standard data set of loblolly pine (<i>Pinus taeda</i> L.). <i>Genetics</i> , 2012 , 190, 1503-10	4	266
244	Genomic BLUP decoded: a look into the black box of genomic prediction. <i>Genetics</i> , 2013 , 194, 597-607	4	194
243	Genomic prediction of simulated multibreed and purebred performance using observed fifty thousand single nucleotide polymorphism genotypes. <i>Journal of Animal Science</i> , 2010 , 88, 544-51	0.7	179
242	Technical note: Derivation of equivalent computing algorithms for genomic predictions and reliabilities of animal merit. <i>Journal of Dairy Science</i> , 2009 , 92, 2971-5	4	161
241	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. <i>Genetics Selection Evolution</i> , 2011 , 43, 40	4.9	153
240	Genome-wide association study identifies Loci for body composition and structural soundness traits in pigs. <i>PLoS ONE</i> , 2011 , 6, e14726	3.7	149
239	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	36.3	139
238	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. <i>BMC Genomics</i> , 2014 , 15, 442	4.5	124
237	Evidence for a major QTL associated with host response to porcine reproductive and respiratory syndrome virus challenge. <i>Journal of Animal Science</i> , 2012 , 90, 1733-46	0.7	118
236	A whole-genome association study for pig reproductive traits. <i>Animal Genetics</i> , 2012 , 43, 18-26	2.5	112
235	Breeding value prediction for production traits in layer chickens using pedigree or genomic relationships in a reduced animal model. <i>Genetics Selection Evolution</i> , 2011 , 43, 5	4.9	104
234	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	4.9	92
233	Novel genomic approaches unravel genetic architecture of complex traits in apple. <i>BMC Genomics</i> , 2013 , 14, 393	4.5	89
232	Bayesian methods applied to GWAS. <i>Methods in Molecular Biology</i> , 2013 , 1019, 237-74	1.4	89
231	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. <i>BMC Genomics</i> , 2017 , 18, 386	4.5	86

230	Whole Genome Association Studies of Residual Feed Intake and Related Traits in the Pig. <i>PLoS ONE</i> , 2013 , 8, e61756	3.7	81
229	Influence of free-stall base on tarsal joint lesions and hygiene in dairy cows. <i>Journal of Dairy Science</i> , 2007 , 90, 3559-66	4	81
228	Genome-wide association analysis and genetic architecture of egg weight and egg uniformity in layer chickens. <i>Animal Genetics</i> , 2012 , 43 Suppl 1, 87-96	2.5	76
227	Genome-wide association study for intramuscular fat deposition and composition in Nelore cattle. <i>BMC Genetics</i> , 2014 , 15, 39	2.6	73
226	Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. <i>Genetics Selection Evolution</i> , 2011 , 43, 23	4.9	73
225	Functionally reciprocal mutations of the prolactin signalling pathway define hairy and slick cattle. <i>Nature Communications</i> , 2014 , 5, 5861	17.4	72
224	Implementing a QTL detection study (GWAS) using genomic prediction methodology. <i>Methods in Molecular Biology</i> , 2013 , 1019, 275-98	1.4	72
223	Bayesian genome-wide association analysis of growth and yearling ultrasound measures of carcass traits in Brangus heifers. <i>Journal of Animal Science</i> , 2012 , 90, 3398-3409	0.7	69
222	Profitabilities of some mating systems for dairy herds in New Zealand. <i>Journal of Dairy Science</i> , 2000 , 83, 144-53	4	68
221	The nature, scope and impact of genomic prediction in beef cattle in the United States. <i>Genetics Selection Evolution</i> , 2011 , 43, 17	4.9	66
220	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. <i>Genetics Selection Evolution</i> , 2013 , 45, 11	4.9	65
219	Whole-genome association analyses for lifetime reproductive traits in the pig. <i>Journal of Animal Science</i> , 2011 , 89, 988-95	0.7	63
218	Correction for amino acid loss during acid hydrolysis of a purified protein. <i>Analytical Biochemistry</i> , 1996 , 236, 199-207	3.1	63
217	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	4.5	59
216	Accuracy of direct genomic breeding values for nationally evaluated traits in US Limousin and Simmental beef cattle. <i>Genetics Selection Evolution</i> , 2012 , 44, 38	4.9	56
215	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	2.5	53
214	Identification of genomic regions associated with feed efficiency in Nelore cattle. <i>BMC Genetics</i> , 2014 , 15, 100	2.6	52
213	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	4.5	51

212	Heritability and Bayesian genome-wide association study of first service conception and pregnancy in Brangus heifers. <i>Journal of Animal Science</i> , 2013 , 91, 605-12	0.7	51
211	Genome-wide association study for egg production and quality in layer chickens. <i>Journal of Animal Breeding and Genetics</i> , 2014 , 131, 173-82	2.9	50
210	The effect of food dry matter intake on endogenous ileal amino acid excretion determined under peptide alimentation in the 50 kg liveweight pig. <i>Journal of the Science of Food and Agriculture</i> , 1993 , 62, 235-243	4.3	46
209	Aspects of Selection for Performance in Several Environments with Heterogeneous Variances. <i>Journal of Animal Science</i> , 1987 , 65, 409-421	0.7	46
208	Response and inbreeding from a genomic selection experiment in layer chickens. <i>Genetics Selection Evolution</i> , 2015 , 47, 59	4.9	44
207	Genomic breeding value prediction and QTL mapping of QTLMAS2010 data using Bayesian Methods. <i>BMC Proceedings</i> , 2011 , 5 Suppl 3, S13	2.3	43
206	Bayesian genome-wide association analysis of growth and yearling ultrasound measures of carcass traits in Brangus heifers. <i>Journal of Animal Science</i> , 2012 , 90, 3398-409	0.7	43
205	Variance heterogeneity in direct and maternal weight traits by sex and percent purebred for Simmental-sired calves. <i>Journal of Animal Science</i> , 1989 , 67, 2515-28	0.7	42
204	A novel nonsense mutation in the DMP1 gene identified by a genome-wide association study is responsible for inherited rickets in Corriedale sheep. <i>PLoS ONE</i> , 2011 , 6, e21739	3.7	40
203	DNA-based paternity analysis and genetic evaluation in a large, commercial cattle ranch setting. <i>Journal of Animal Science</i> , 2007 , 85, 3159-69	0.7	40
202	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. <i>Genetics Selection Evolution</i> , 2013 , 45, 30	4.9	39
201	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, 6007-21	4	38
200	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. <i>Animal Science</i> , 2006 , 82, 423-433		38
199	An Upper Bound for Accuracy of Prediction Using GBLUP. <i>PLoS ONE</i> , 2016 , 11, e0161054	3.7	38
198	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. <i>BMC Genomics</i> , 2014 , 15, 948	4.5	37
197	Accuracies of direct genomic breeding values in Hereford beef cattle using national or international training populations. <i>Journal of Animal Science</i> , 2013 , 91, 1538-51	0.7	37
196	Inheritance of pulmonary arterial pressure in Angus cattle and its correlation with growth. <i>Journal of Animal Science</i> , 2008 , 86, 815-9	0.7	37
195	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	4.9	37

194	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	1.9	36
193	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	6	35
192	Changes in inbreeding of U.S. Herefords during the twentieth century. <i>Journal of Animal Science</i> , 2005 , 83, 992-1001	0.7	35
191	Genome-wide association study of insect bite hypersensitivity in two horse populations in the Netherlands. <i>Genetics Selection Evolution</i> , 2012 , 44, 31	4.9	34
190	Development and application of a processing model for the Irish dairy industry. <i>Journal of Dairy Science</i> , 2010 , 93, 5091-100	4	34
189	Financial implications of recent declines in reproduction and survival of Holstein-Friesian cows in spring-calving Irish dairy herds. <i>Agricultural Systems</i> , 2006 , 89, 165-183	6.1	34
188	Implementation of genomic selection in the poultry industry. <i>Animal Frontiers</i> , 2016 , 6, 23-31	5.5	34
187	Development and implementation of genomic predictions in beef cattle. <i>Animal Frontiers</i> , 2016 , 6, 32-38	5.5	32
186	Population structure and genomic inbreeding in nine Swiss dairy cattle populations. <i>Genetics Selection Evolution</i> , 2017 , 49, 83	4.9	32
185	Environmental sensitivity in New Zealand dairy cattle. <i>Journal of Dairy Science</i> , 2007 , 90, 1538-47	4	32
184	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, 21-7	0.7	31
183	Fixed-length haplotypes can improve genomic prediction accuracy in an admixed dairy cattle population. <i>Genetics Selection Evolution</i> , 2017 , 49, 54	4.9	30
182	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. <i>Genetics Selection Evolution</i> , 2014 , 46, 34	4.9	30
181	Ovar-Mhc--ovine major histocompatibility complex: role in genetic resistance to diseases. <i>New Zealand Veterinary Journal</i> , 2006 , 54, 153-60	1.7	30
180	'Ovar-Mhc' - ovine major histocompatibility complex: structure and gene polymorphisms. <i>Genetics and Molecular Research</i> , 2006 , 5, 581-608	1.2	30
179	Genome-wide prediction of age at puberty and reproductive longevity in sows. <i>Animal Genetics</i> , 2013 , 44, 387-97	2.5	29
178	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. <i>Frontiers in Genetics</i> , 2017 , 8, 171	4.5	29
177	Genetic parameters for carnitine, creatine, creatinine, carnosine, and anserine concentration in longissimus muscle and their association with palatability traits in Angus cattle. <i>Journal of Animal Science</i> , 2012 , 90, 4248-55	0.7	29

176	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. <i>Genetics Selection Evolution</i> , 2015 , 47, 23	4.9	28
175	Producing and using genetic evaluations in the United States beef industry of today. <i>Journal of Animal Science</i> , 2009 , 87, E11-8	0.7	28
174	Multiple-marker mapping of wood density loci in an outbred pedigree of radiata pine. <i>Theoretical and Applied Genetics</i> , 2000 , 100, 926-933	6	28
173	Utilisation of marker assisted selection in a commercial dairy cow population. <i>Livestock Science</i> , 1997 , 47, 139-147		27
172	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	4.5	26
171	Effects of age at slaughter and sire genotype on fatness, muscularity, and the quality of meat from ram lambs born to Romney ewes. <i>New Zealand Journal of Agricultural Research</i> , 2002 , 45, 77-86	1.9	26
170	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, 1067-75	0.7	25
169	Effect of live weight and differing economic values on responses to selection for milk fat, protein, volume, and live weight. <i>Journal of Dairy Science</i> , 1997 , 80, 2557-62	4	25
168	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	4.9	24
167	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	3.7	24
166	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. <i>Genetics</i> , 2018 , 209, 89-103	4	24
165	Effects of calving age, breed fraction and month of calving on calving interval and survival across parities in Irish spring-calving dairy cows. <i>Livestock Science</i> , 2006 , 100, 216-230	1.7	24
164	Utilisation of genetic variation by marker assisted selection in commercial dairy cattle populations. <i>Livestock Science</i> , 1999 , 59, 51-60		24
163	A missense mutation in AGTPBP1 was identified in sheep with a lower motor neuron disease. <i>Heredity</i> , 2012 , 109, 156-62	3.6	23
162	Possible effects of 25 years of selection and crossbreeding on the genetic merit and productivity of New Zealand dairy cattle. <i>Journal of Dairy Science</i> , 2000 , 83, 154-63	4	23
161	Genetic diversity and population structure of American Red Angus cattle. <i>Journal of Animal Science</i> , 2010 , 88, 59-68	0.7	22
160	Short communication: Effect of environment on the expression of breed and heterosis effects for production traits. <i>Journal of Dairy Science</i> , 2007 , 90, 1548-53	4	22
159	Short communication: quantitative trait loci analysis on 17 nonproduction traits in the New Zealand dairy population. <i>Journal of Dairy Science</i> , 1999 , 82, 2514-6	4	22

158	A fast EM algorithm for BayesA-like prediction of genomic breeding values. <i>PLoS ONE</i> , 2012 , 7, e49157	3.7	22
157	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. <i>Poultry Science</i> , 2013 , 92, 2270-5	3.9	21
156	Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. <i>Poultry Science</i> , 2013 , 92, 1712-23	3.9	21
155	Identification of breeding objectives using a bioeconomic model for a beef cattle production system in Uruguay. <i>Livestock Science</i> , 2014 , 160, 21-28	1.7	21
154	Breeding objectives for three silvicultural regimes of radiata pine. <i>Canadian Journal of Forest Research</i> , 2001 , 31, 654-662	1.9	21
153	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers. <i>Journal of Animal Science</i> , 2017 , 95, 4796-4812	0.7	20
152	In a shake of a lamb's tail: using genomics to unravel a cause of chondrodysplasia in Texel sheep. <i>Animal Genetics</i> , 2012 , 43 Suppl 1, 9-18	2.5	20
151	An evaluation of circulating bovine viral diarrhoea virus type 2 maternal antibody level and response to vaccination in Angus calves. <i>Journal of Animal Science</i> , 2013 , 91, 4440-50	0.7	20
150	A fast and efficient Gibbs sampler for BayesB in whole-genome analyses. <i>Genetics Selection Evolution</i> , 2015 , 47, 80	4.9	19
149	Genome-wide association study of temperament and tenderness using different Bayesian approaches in a Nellore-Angus crossbred population. <i>Livestock Science</i> , 2014 , 161, 17-27	1.7	19
148	Genetic and economic responses for within-family marker-assisted selection in dairy cattle breeding schemes. <i>Journal of Dairy Science</i> , 1998 , 81, 2942-50	4	19
147	Variance modelling of longitudinal height data from a Pinus radiata progeny test. <i>Canadian Journal of Forest Research</i> , 2000 , 30, 645-654	1.9	19
146	Host genetic influence on papillomavirus-induced tumors in the horse. <i>International Journal of Cancer</i> , 2016 , 139, 784-92	7.5	19
145	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, 334-46	2.9	18
144	Genome-wide association study of growth and body composition traits in Brangus beef cattle. <i>Livestock Science</i> , 2016 , 183, 4-11	1.7	18
143	Whole genome analysis of infectious bovine keratoconjunctivitis in Angus cattle using Bayesian threshold models. <i>BMC Proceedings</i> , 2011 , 5 Suppl 4, S22	2.3	18
142	Milestones in beef cattle genetic evaluation. <i>Journal of Animal Science</i> , 2009 , 87, E3-10	0.7	18
141	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , 2018 , 19, 499	4.5	17

140	The evolution of methodologies for genomic prediction. <i>Livestock Science</i> , 2014 , 166, 10-18	1.7	17
139	Maternal effects on docility in Limousin cattle. <i>Journal of Animal Science</i> , 2007 , 85, 650-7	0.7	17
138	Predicting breeding values and accuracies from group in comparison to individual observations. <i>Journal of Animal Science</i> , 2006 , 84, 88-92	0.7	17
137	Parasitism and production in fleece-weight-selected and control sheep. <i>New Zealand Journal of Agricultural Research</i> , 1995 , 38, 381-387	1.9	17
136	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	6	16
135	Analysis of egg production in layer chickens using a random regression model with genomic relationships. <i>Poultry Science</i> , 2013 , 92, 1486-91	3.9	16
134	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	4.9	16
133	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	4.5	15
132	Genome-wide association study of infectious bovine keratoconjunctivitis in Angus cattle. <i>BMC Genetics</i> , 2013 , 14, 23	2.6	15
131	Genome-wide association study for Marek's disease mortality in layer chickens. <i>Avian Diseases</i> , 2013 , 57, 395-400	1.6	15
130	The Accuracy and Bias of Single-Step Genomic Prediction for Populations Under Selection. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2685-2694	3.2	15
129	Sterol regulatory element binding transcription factor 1 (SREBF1) polymorphism and milk fatty acid composition. <i>Journal of Dairy Science</i> , 2013 , 96, 2605-2616	4	15
128	Inheritance of adult velvet antler weights and live weights in farmed red deer. <i>Livestock Science</i> , 1997 , 49, 287-295		15
127	Effects of selection and crossbreeding strategies on industry profit in the New Zealand dairy industry. <i>Journal of Dairy Science</i> , 2000 , 83, 164-72	4	15
126	A FAS-ligand variant associated with autoimmune lymphoproliferative syndrome in cats. <i>Mammalian Genome</i> , 2017 , 28, 47-55	3.2	14
125	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. <i>American Journal of Human Genetics</i> , 2020 , 106, 893-904	11	14
124	Genomic breeding value prediction and QTL mapping of QTLMAS2011 data using Bayesian and GBLUP methods. <i>BMC Proceedings</i> , 2012 , 6 Suppl 2, S7	2.3	14
123	Genetic parameters and genetic correlations among triacylglycerol and phospholipid fractions in Angus cattle. <i>Journal of Animal Science</i> , 2015 , 93, 522-8	0.7	14

122	Genome-wide association analysis reveals QTL and candidate mutations involved in white spotting in cattle. <i>Genetics Selection Evolution</i> , 2019 , 51, 62	4.9	14
121	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	4.9	13
120	XSim: Simulation of Descendants from Ancestors with Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 1415-7	3.2	13
119	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, 223-32	1.6	13
118	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	3.7	13
117	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. <i>Journal of Dairy Science</i> , 2018 , 101, 1292-1296	4	13
116	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	2.9	12
115	Strategies for noise reduction and standardization of milk mid-infrared spectra from dairy cattle. <i>Journal of Dairy Science</i> , 2019 , 102, 6357-6372	4	12
114	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	4.9	12
113	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. <i>Animal Genetics</i> , 2012 , 43, 115-22	2.5	12
112	Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. <i>Genomics</i> , 2014 , 104, 572-81	4.3	12
111	The influence of allyl trenbolone (Regumate) on the timing, duration and endocrinology of parturition in sows. <i>Animal Reproduction Science</i> , 1985 , 9, 163-171	2.1	12
110	Variance modelling of longitudinal height data from a Pinus radiata progeny test. <i>Canadian Journal of Forest Research</i> , 2000 , 30, 645-654	1.9	12
109	Genetic parameters for carcass and ultrasound traits in Hereford and admixed Simmental beef cattle: Accuracy of evaluating carcass traits. <i>Journal of Animal Science</i> , 2017 , 95, 4718-4727	0.7	11
108	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. <i>Journal of Agricultural Science</i> , 2012 , 150, 389-407 ¹		11
107	Weaning weight inheritance in environments classified by maternal body weight change. <i>Journal of Animal Science</i> , 2007 , 85, 610-7	0.7	11
106	A model of mammalian energetics and growth: model development. <i>Agricultural Systems</i> , 2001 , 68, 55-68.1		11
105	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	6	10

104	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. <i>BMC Genomics</i> , 2017 , 18, 999	4.5	10
103	A genome-wide association study for canine cryptorchidism in Siberian Huskies. <i>Journal of Animal Breeding and Genetics</i> , 2014 , 131, 202-9	2.9	10
102	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, 3593-600	0.7	10
101	Genetic response to within-family selection using molecular markers in some radiata pine breeding schemes. <i>Canadian Journal of Forest Research</i> , 2001 , 31, 779-785	1.9	10
100	Economic values of traits for pig improvement. I. A simulation model. <i>Australian Journal of Agricultural Research</i> , 1995 , 46, 285		10
99	Reduction in accuracy of genomic prediction for ordered categorical data compared to continuous observations. <i>Genetics Selection Evolution</i> , 2014 , 46, 37	4.9	9
98	Some relationships between weights of growing heifers and their subsequent lactation performances. <i>New Zealand Journal of Agricultural Research</i> , 1997 , 40, 87-92	1.9	9
97	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	3.2	9
96	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	1	8
95	Breeding objectives for Holstein cattle in South Africa. <i>South African Journal of Animal Sciences</i> , 2014 , 44, 199	1	8
94	An animal breeding approach to the estimation of genetic and environmental trends from field populations. <i>Journal of Animal Science</i> , 2010 , 88, E3-E10	0.7	8
93	Reducing bias in maintenance energy expected progeny difference by accounting for selection on weaning and yearling weights. <i>Journal of Animal Science</i> , 2009 , 87, 1628-37	0.7	8
92	Application of new technologies in sheep breeding. <i>New Zealand Journal of Agricultural Research</i> , 2007 , 50, 89-102	1.9	8
91	Parasitological characteristics of fleece-weight-selected and control sheep. <i>New Zealand Journal of Agricultural Research</i> , 1995 , 38, 389-397	1.9	8
90	Non-additive association analysis using proxy phenotypes identifies novel cattle syndromes. <i>Nature Genetics</i> , 2021 , 53, 949-954	36.3	8
89	The effect of simulated censored data on estimates of heritability of longevity in the Thoroughbred racing industry. <i>Genetics and Molecular Research</i> , 2006 , 5, 7-15	1.2	8
88	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	1.7	7
87	Association of microsatellite polymorphisms with immune responses to a killed Mycobacterium avium subsp. paratuberculosis vaccine in Merino sheep. <i>New Zealand Veterinary Journal</i> , 2010 , 58, 237-45	1.7	7

86	Use of linear mixed models for genetic evaluation of gestation length and birth weight allowing for heavy-tailed residual effects. <i>Genetics Selection Evolution</i> , 2010 , 42, 26	4.9	7
85	Emerging technologies for identifying superior dairy cows in New Zealand. <i>New Zealand Veterinary Journal</i> , 2005 , 53, 390-399	1.7	7
84	Phenotypic relationships between hair whorl characteristics and spermatozoal attributes in Holstein bulls. <i>Animal Reproduction Science</i> , 2005 , 85, 95-103	2.1	7
83	Threshold model analysis of lamb survivability in Romney sheep. <i>New Zealand Journal of Agricultural Research</i> , 2006 , 49, 411-418	1.9	7
82	Estimates of genetic parameters for production and reproduction traits in three breeds of pigs. <i>New Zealand Journal of Agricultural Research</i> , 1996 , 39, 387-395	1.9	7
81	Selection responses in New Zealand Romney sheep. <i>New Zealand Journal of Agricultural Research</i> , 1985 , 28, 257-264	1.9	7
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