

# Dorian Garrick

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

247  
papers

7,345  
citations

42  
h-index

76  
g-index

269  
ext. papers

9,154  
ext. citations

3.2  
avg, IF

6.08  
L-index

#	Paper	IF	Citations
247	Non-additive QTL mapping of lactation traits in 124,000 cattle reveals novel recessive loci.. <i>Genetics Selection Evolution</i> , <b>2022</b> , 54, 5	4.9	0
246	An inherited night blindness in Wiltshire sheep.. <i>Veterinary Pathology</i> , <b>2022</b> , 3009858211067461	2.8	
245	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. 2:51B4). <i>JDS Communications</i> , <b>2022</b> , 3, 164	1.4	
244	Pathology of the peripheral neuropathy Charcot-Marie-Tooth disease type 4H in Holstein Friesian cattle with a splice site mutation in .. <i>Veterinary Pathology</i> , <b>2022</b> , 3009858221083041	2.8	0
243	Pregnancy status predicted using milk mid-infrared spectra from dairy cattle.. <i>Journal of Dairy Science</i> , <b>2022</b> , 105, 3615-3632	4	2
242	Discovering Copy Number Variation in Dual-Purpose XinJiang Brown Cattle.. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 747431	4.5	0
241	Comparison of Genotype Imputation for SNP Array and Low-Coverage Whole-Genome Sequencing Data.. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 704118	4.5	1
240	Reduced Animal Models Fitting Only Equations for Phenotyped Animals. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 637626	4.5	0
239	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> , <b>2021</b> , 2, 51-54	1.4	2
238	Mining the 99 Lives Cat Genome Sequencing Consortium database implicates genes and variants for the Ticked locus in domestic cats ( <i>Felis tatus</i> ). <i>Animal Genetics</i> , <b>2021</b> , 52, 321-332	2.5	3
237	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> , <b>2021</b> , 12,	4.2	4
236	Can Nitrogen Excretion of Dairy Cows Be Reduced by Genetic Selection for Low Milk Urea Nitrogen Concentration?. <i>Animals</i> , <b>2021</b> , 11,	3.1	3
235	Non-additive association analysis using proxy phenotypes identifies novel cattle syndromes. <i>Nature Genetics</i> , <b>2021</b> , 53, 949-954	36.3	8
234	The genomes of precision edited cloned calves show no evidence for off-target events or increased de novo mutagenesis. <i>BMC Genomics</i> , <b>2021</b> , 22, 457	4.5	1
233	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> , <b>2021</b> , 69, 255-266	1.7	
232	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> , <b>2021</b> , 64, 62-82	1.9	2
231	Alternative Ways of Computing the Numerator Relationship Matrix. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 655638	4.5	1

230	Sequence-based genome-wide association study of individual milk mid-infrared wavenumbers in mixed-breed dairy cattle. <i>Genetics Selection Evolution</i> , <b>2021</b> , 53, 62	4.9	4
229	A Missense Mutation in the Gene Is Associated With Abdominal Fat Traits in Meat-Type Chickens. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 698163	4.5	2
228	Estimates of genomic inbreeding and identification of candidate regions that differ between Chinese indigenous sheep breeds. <i>Journal of Animal Science and Biotechnology</i> , <b>2021</b> , 12, 95	6	2
227	HandyCNV: Standardized Summary, Annotation, Comparison, and Visualization of Copy Number Variant, Copy Number Variation Region, and Runs of Homozygosity. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 731355	4.5	2
226	Mutations in the Kinesin-2 Motor KIF3B Cause an Autosomal-Dominant Ciliopathy. <i>American Journal of Human Genetics</i> , <b>2020</b> , 106, 893-904	11	14
225	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> , <b>2020</b> , 11, 55	6	10
224	Accuracies of direct genomic breeding values for birth and weaning weights of registered Charolais cattle in Mexico. <i>Animal Production Science</i> , <b>2020</b> , 60, 772	1.4	0
223	Sire selection and genetic improvement of dairy cattle assuming pure market competition. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 4532-4544	4	0
222	Exact Distribution of Linkage Disequilibrium in the Presence of Mutation, Selection, or Minor Allele Frequency Filtering. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 362	4.5	0
221	Fast parallelized sampling of Bayesian regression models for whole-genome prediction. <i>Genetics Selection Evolution</i> , <b>2020</b> , 52, 16	4.9	2
220	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> , <b>2020</b> , 11,	3.1	2
219	Genetic parameters for total lactation yields of milk, fat, protein, and somatic cell score in New Zealand dairy goats. <i>Animal Science Journal</i> , <b>2020</b> , 91, e13310	1.8	7
218	Economic selection index to improve fiber quality in Mongolian Cashmere goats. <i>Livestock Science</i> , <b>2020</b> , 232, 103898	1.7	1
217	Economic values for index improvement of dual-purpose Simmental cattle. <i>Livestock Science</i> , <b>2020</b> , 240, 104224	1.7	1
216	Accuracy of genomic prediction of shell quality in a White Leghorn line. <i>Poultry Science</i> , <b>2020</b> , 99, 2833-2840	3.9	5
215	The evolving role of Fourier-transform mid-infrared spectroscopy in genetic improvement of dairy cattle. <i>Journal of Animal Science and Biotechnology</i> , <b>2020</b> , 11, 39	6	6
214	Genome-wide association scan for QTL and their positional candidate genes associated with internal organ traits in chickens. <i>BMC Genomics</i> , <b>2019</b> , 20, 669	4.5	6
213	EMannosidosis in German Shepherd Dogs. <i>Veterinary Pathology</i> , <b>2019</b> , 56, 743-748	2.8	3

212	Strategies for noise reduction and standardization of milk mid-infrared spectra from dairy cattle. <i>Journal of Dairy Science</i> , <b>2019</b> , 102, 6357-6372	4	12
211	Identification of recombination hotspots and quantitative trait loci for recombination rate in layer chickens. <i>Journal of Animal Science and Biotechnology</i> , <b>2019</b> , 10, 20	6	6
210	Unraveling genomic associations with feed efficiency and body weight traits in chickens through an integrative approach. <i>BMC Genetics</i> , <b>2019</b> , 20, 83	2.6	6
209	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. <i>Animal Genetics</i> , <b>2019</b> , 50, 621-633 <sup>2.5</sup>	3.5	6
208	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> , <b>2019</b> , 10, 97	6	3
207	Genome-wide association analysis reveals QTL and candidate mutations involved in white spotting in cattle. <i>Genetics Selection Evolution</i> , <b>2019</b> , 51, 62	4.9	14
206	A certain invariance property of BLUE in a whole-genome regression context. <i>Journal of Animal Breeding and Genetics</i> , <b>2019</b> , 136, 113-117	2.9	2
205	Genomic Prediction from Multiple-Trait Bayesian Regression Methods Using Mixture Priors. <i>Genetics</i> , <b>2018</b> , 209, 89-103	4	24
204	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. <i>Nature Genetics</i> , <b>2018</b> , 50, 362-367	36.3	139
203	Identification of putative regulatory regions and transcription factors associated with intramuscular fat content traits. <i>BMC Genomics</i> , <b>2018</b> , 19, 499	4.5	17
202	A genome-wide association study reveals novel genomic regions and positional candidate genes for fat deposition in broiler chickens. <i>BMC Genomics</i> , <b>2018</b> , 19, 374	4.5	15
201	A nested mixture model for genomic prediction using whole-genome SNP genotypes. <i>PLoS ONE</i> , <b>2018</b> , 13, e0194683	3.7	5
200	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. <i>Journal of Dairy Science</i> , <b>2018</b> , 101, 1292-1296	4	13
199	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> , <b>2018</b> , 8, 3567-3575	3.2	9
198	Integration of genome wide association studies and whole genome sequencing provides novel insights into fat deposition in chicken. <i>Scientific Reports</i> , <b>2018</b> , 8, 16222	4.9	16
197	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> , <b>2018</b> , 199, 45-50 <sup>2.1</sup>	2.1	2
196	Identification of an immune modulation locus utilising a bovine mammary gland infection challenge model. <i>Journal of Dairy Research</i> , <b>2018</b> , 85, 185-192	1.6	2
195	Comparison of alternative approaches to single-trait genomic prediction using genotyped and non-genotyped Hanwoo beef cattle. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 2	4.9	24

194	Efficient strategies for leave-one-out cross validation for genomic best linear unbiased prediction. <i>Journal of Animal Science and Biotechnology</i> , <b>2017</b> , 8, 38	6	35
193	Application of Whole-Genome Prediction Methods for Genome-Wide Association Studies: A Bayesian Approach. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , <b>2017</b> , 22, 172-193	1.9	36
192	A FAS-ligand variant associated with autoimmune lymphoproliferative syndrome in cats. <i>Mammalian Genome</i> , <b>2017</b> , 28, 47-55	3.2	14
191	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> , <b>2017</b> , 134, 213-223	2.9	12
190	Genome-wide detection of autosomal copy number variants in several sheep breeds using Illumina OvineSNP50 BeadChips. <i>Small Ruminant Research</i> , <b>2017</b> , 155, 24-32	1.7	7
189	Genotype imputation in a tropical crossbred dairy cattle population. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 9623-9634	4	6
188	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. <i>BMC Genomics</i> , <b>2017</b> , 18, 999	4.5	10
187	Single nucleotide variants and InDels identified from whole-genome re-sequencing of Guzerat, Gyr, Girolando and Holstein cattle breeds. <i>PLoS ONE</i> , <b>2017</b> , 12, e0173954	3.7	24
186	Familial episodic ataxia in lambs is potentially associated with a mutation in the fibroblast growth factor 14 (FGF14) gene. <i>PLoS ONE</i> , <b>2017</b> , 12, e0190030	3.7	4
185	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> , <b>2017</b> , 95, 4796-4812	0.7	20
184	Fixed-length haplotypes can improve genomic prediction accuracy in an admixed dairy cattle population. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 54	4.9	30
183	331 The genetic improvement of feed efficiency in beef cattle. <i>Journal of Animal Science</i> , <b>2017</b> , 95, 161-164	1.4	2
182	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. <i>BMC Genomics</i> , <b>2017</b> , 18, 910	4.5	26
181	The Accuracy and Bias of Single-Step Genomic Prediction for Populations Under Selection. <i>G3: Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 2685-2694	3.2	15
180	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. <i>BMC Genomics</i> , <b>2017</b> , 18, 386	4.5	86
179	165 Genetic variants with potential loss of function in Gyr, Girolando, and Guzerat cattle breeds by resequencing. <i>Journal of Animal Science</i> , <b>2017</b> , 95, 81-81	0.7	
178	Population structure and genomic inbreeding in nine Swiss dairy cattle populations. <i>Genetics Selection Evolution</i> , <b>2017</b> , 49, 83	4.9	32
177	The role of genomics in pig improvement. <i>Animal Production Science</i> , <b>2017</b> , 57, 2360	1.4	2

176	Network Analysis Reveals Putative Genes Affecting Meat Quality in Angus Cattle. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 171	4.5	29
175	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> , <b>2017</b> , 95, 4718-4727	0.7	11
174	Development and implementation of genomic predictions in beef cattle. <i>Animal Frontiers</i> , <b>2016</b> , 6, 32-38	5.5	32
173	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> , <b>2016</b> , 133, 334-46	2.9	18
172	An efficient exact method to obtain GBLUP and single-step GBLUP when the genomic relationship matrix is singular. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 80	4.9	13
171	Effects of number of training generations on genomic prediction for various traits in a layer chicken population. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 22	4.9	12
170	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> , <b>2016</b> , 7, 7	6	16
169	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> , <b>2016</b> , 59, 90-105	1.9	5
168	Genome-wide association study of growth and body composition traits in Brangus beef cattle. <i>Livestock Science</i> , <b>2016</b> , 183, 4-11	1.7	18
167	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> , <b>2016</b> , 55, 126-135	1.1	2
166	Deriving Gene Networks from SNP Associated with Triacylglycerol and Phospholipid Fatty Acid Fractions from Ribeyes of Angus Cattle. <i>Frontiers in Genetics</i> , <b>2016</b> , 7, 116	4.5	4
165	Implementation of genomic selection in the poultry industry. <i>Animal Frontiers</i> , <b>2016</b> , 6, 23-31	5.5	34
164	The Effect of Calf Gender on Milk Production in Seasonal Calving Cows and Its Impact on Genetic Evaluations. <i>PLoS ONE</i> , <b>2016</b> , 11, e0151236	3.7	13
163	An Upper Bound for Accuracy of Prediction Using GBLUP. <i>PLoS ONE</i> , <b>2016</b> , 11, e0161054	3.7	38
162	032 Quantitative trait loci and candidate genes associated with heifer pregnancy rate and stayability in beef cattle. <i>Journal of Animal Science</i> , <b>2016</b> , 94, 15-15	0.7	3
161	Epistatic interactions associated with fatty acid concentrations of beef from angus sired beef cattle. <i>BMC Genomics</i> , <b>2016</b> , 17, 891	4.5	3
160	036 Discovery of quantitative trait loci using a quantitative trait loci effects model in a multigenerational pedigree. <i>Journal of Animal Science</i> , <b>2016</b> , 94, 16-17	0.7	
159	Host genetic influence on papillomavirus-induced tumors in the horse. <i>International Journal of Cancer</i> , <b>2016</b> , 139, 784-92	7.5	19

158	Computational strategies for alternative single-step Bayesian regression models with large numbers of genotyped and non-genotyped animals. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 96	4.9	37
157	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> , <b>2016</b> , 59, 79-89	1.9	4
156	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 23	4.9	28
155	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> , <b>2015</b> , 93, 21-7	0.7	31
154	Response and inbreeding from a genomic selection experiment in layer chickens. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 59	4.9	44
153	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> , <b>2015</b> , 47, 99	4.9	6
152	Genetic parameters and genetic correlations among triacylglycerol and phospholipid fractions in Angus cattle. <i>Journal of Animal Science</i> , <b>2015</b> , 93, 522-8	0.7	14
151	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> , <b>2015</b> , 58, 432-440	1.9	
150	XSim: Simulation of Descendants from Ancestors with Sequence Data. <i>G3: Genes, Genomes, Genetics</i> , <b>2015</b> , 5, 1415-7	3.2	13
149	A fast and efficient Gibbs sampler for BayesB in whole-genome analyses. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 80	4.9	19
148	Cross-validation of genetic and genomic predictions of temperament in Nellore-Angus crossbreds. <i>Livestock Science</i> , <b>2015</b> , 182, 28-33	1.7	2
147	Genome-wide association study for egg production and quality in layer chickens. <i>Journal of Animal Breeding and Genetics</i> , <b>2014</b> , 131, 173-82	2.9	50
146	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. <i>BMC Genomics</i> , <b>2014</b> , 15, 442	4.5	124
145	A genome-wide association study for canine cryptorchidism in Siberian Huskies. <i>Journal of Animal Breeding and Genetics</i> , <b>2014</b> , 131, 202-9	2.9	10
144	The evolution of methodologies for genomic prediction. <i>Livestock Science</i> , <b>2014</b> , 166, 10-18	1.7	17
143	Spring calving versus split calving: effects on farm, processor and industry profitability for the Irish dairy industry. <i>Journal of Agricultural Science</i> , <b>2014</b> , 152, 448-463	1	5
142	Growth, feed intake and maternal performance of Angus heifers from high and low feed efficiency selection lines. <i>Animal Production Science</i> , <b>2014</b> , 54, 1428	1.4	6
141	The economic value of somatic cell count in South African Holstein and Jersey cattle. <i>South African Journal of Animal Sciences</i> , <b>2014</b> , 44, 173	1	8

140	Comparison of breeding value prediction for two traits in a Nellore-Angus crossbred population using different Bayesian modeling methodologies. <i>Genetics and Molecular Biology</i> , <b>2014</b> , 37, 631-7	2	4
139	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> , <b>2014</b> , 131, 504-12	2.9	2
138	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> , <b>2014</b> , 15, 1004	4.5	59
137	Identification of genomic regions associated with feed efficiency in Nelore cattle. <i>BMC Genetics</i> , <b>2014</b> , 15, 100	2.6	52
136	Breeding objectives for Holstein cattle in South Africa. <i>South African Journal of Animal Sciences</i> , <b>2014</b> , 44, 199	1	8
135	Functionally reciprocal mutations of the prolactin signalling pathway define hairy and slick cattle. <i>Nature Communications</i> , <b>2014</b> , 5, 5861	17.4	72
134	Polymorphisms in lipogenic genes and milk fatty acid composition in Holstein dairy cattle. <i>Genomics</i> , <b>2014</b> , 104, 572-81	4.3	12
133	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> , <b>2014</b> , 45, 48-58	2.5	53
132	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> , <b>2014</b> , 81, 223-32	1.6	13
131	Recombination locations and rates in beef cattle assessed from parent-offspring pairs. <i>Genetics Selection Evolution</i> , <b>2014</b> , 46, 34	4.9	30
130	Reduction in accuracy of genomic prediction for ordered categorical data compared to continuous observations. <i>Genetics Selection Evolution</i> , <b>2014</b> , 46, 37	4.9	9
129	Genome-wide association study for intramuscular fat deposition and composition in Nellore cattle. <i>BMC Genetics</i> , <b>2014</b> , 15, 39	2.6	73
128	Evaluation of variant identification methods for whole genome sequencing data in dairy cattle. <i>BMC Genomics</i> , <b>2014</b> , 15, 948	4.5	37
127	A class of Bayesian methods to combine large numbers of genotyped and non-genotyped animals for whole-genome analyses. <i>Genetics Selection Evolution</i> , <b>2014</b> , 46, 50	4.9	92
126	Identification of breeding objectives using a bioeconomic model for a beef cattle production system in Uruguay. <i>Livestock Science</i> , <b>2014</b> , 160, 21-28	1.7	21
125	Genome-wide association study of temperament and tenderness using different Bayesian approaches in a Nellore-Angus crossbred population. <i>Livestock Science</i> , <b>2014</b> , 161, 17-27	1.7	19
124	Genomic BLUP decoded: a look into the black box of genomic prediction. <i>Genetics</i> , <b>2013</b> , 194, 597-607	4	194
123	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> , <b>2013</b> , 96, 6007-21	4	38



122	Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. <i>Genetics Selection Evolution</i> , <b>2013</b> , 45, 11	4.9	65
121	Genome-wide association study of infectious bovine keratoconjunctivitis in Angus cattle. <i>BMC Genetics</i> , <b>2013</b> , 14, 23	2.6	15
120	Novel genomic approaches unravel genetic architecture of complex traits in apple. <i>BMC Genomics</i> , <b>2013</b> , 14, 393	4.5	89
119	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. <i>Genetics Selection Evolution</i> , <b>2013</b> , 45, 30	4.9	39
118	Pedigree and genomic analyses of feed consumption and residual feed intake in laying hens. <i>Poultry Science</i> , <b>2013</b> , 92, 2270-5	3.9	21
117	Accuracy of genomic prediction using an evenly spaced, low-density single nucleotide polymorphism panel in broiler chickens. <i>Poultry Science</i> , <b>2013</b> , 92, 1712-23	3.9	21
116	Genome-wide association study for Marek's disease mortality in layer chickens. <i>Avian Diseases</i> , <b>2013</b> , 57, 395-400	1.6	15
115	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> , <b>2013</b> , 91, 4440-50	0.7	20
114	Genome-wide prediction of age at puberty and reproductive longevity in sows. <i>Animal Genetics</i> , <b>2013</b> , 44, 387-97	2.5	29
113	Sterol regulatory element binding transcription factor 1 (SREBF1) polymorphism and milk fatty acid composition. <i>Journal of Dairy Science</i> , <b>2013</b> , 96, 2605-2616	4	15
112	Analysis of egg production in layer chickens using a random regression model with genomic relationships. <i>Poultry Science</i> , <b>2013</b> , 92, 1486-91	3.9	16
111	Bayesian methods applied to GWAS. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1019, 237-74	1.4	89
110	Implementing a QTL detection study (GWAS) using genomic prediction methodology. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1019, 275-98	1.4	72
109	Genome-wide association and prediction of direct genomic breeding values for composition of fatty acids in Angus beef cattle. <i>BMC Genomics</i> , <b>2013</b> , 14, 730	4.5	51
108	Genome-wide association study of concentrations of iron and other minerals in longissimus muscle of Angus cattle. <i>Journal of Animal Science</i> , <b>2013</b> , 91, 3593-600	0.7	10
107	Accuracies of direct genomic breeding values in Hereford beef cattle using national or international training populations. <i>Journal of Animal Science</i> , <b>2013</b> , 91, 1538-51	0.7	37
106	Genetic parameters for concentrations of minerals in longissimus muscle and their associations with palatability traits in Angus cattle. <i>Journal of Animal Science</i> , <b>2013</b> , 91, 1067-75	0.7	25
105	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> , <b>2013</b> , 91, 1552-61	0.7	2

104	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 calves. <i>Journal of Animal Science</i> , <b>2013</b> , 91, 5466-76	0.7	4
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