

Michael E Goddard

List of Publications by Year in descending order

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201
papers

53,690
citations

5574

82
h-index

2178

202
g-index

225
all docs

225
docs citations

225
times ranked

45856
citing authors

#	ARTICLE	IF	CITATIONS
1	GCTA: A Tool for Genome-wide Complex Trait Analysis. <i>American Journal of Human Genetics</i> , 2011, 88, 76-82.	6.2	6,212
2	Common SNPs explain a large proportion of the heritability for human height. <i>Nature Genetics</i> , 2010, 42, 565-569.	21.4	3,888
3	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
4	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
5	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	21.4	2,067
6	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
8	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016, 48, 481-487.	21.4	1,757
9	Invited review: Genomic selection in dairy cattle: Progress and challenges. <i>Journal of Dairy Science</i> , 2009, 92, 433-443.	3.4	1,359
10	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. <i>Nature Genetics</i> , 2012, 44, 369-375.	21.4	1,338
11	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.2	1,098
12	Mapping genes for complex traits in domestic animals and their use in breeding programmes. <i>Nature Reviews Genetics</i> , 2009, 10, 381-391.	16.3	1,053
13	Estimating Missing Heritability for Disease from Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2011, 88, 294-305.	6.2	949
14	Advantages and pitfalls in the application of mixed-model association methods. <i>Nature Genetics</i> , 2014, 46, 100-106.	21.4	876
15	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
16	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , 2011, 43, 519-525.	21.4	834
17	Data and Theory Point to Mainly Additive Genetic Variance for Complex Traits. <i>PLoS Genetics</i> , 2008, 4, e1000008.	3.5	823
18	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015, 47, 1114-1120.	21.4	709

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19	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 507-515.	16.3	617
20	Genomic selection. <i>Journal of Animal Breeding and Genetics</i> , 2007, 124, 323-330.	2.0	595
21	Prediction of individual genetic risk to disease from genome-wide association studies. <i>Genome Research</i> , 2007, 17, 1520-1528.	5.5	580
22	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. <i>Nature Genetics</i> , 2012, 44, 247-250.	21.4	578
23	Genome-wide association studies establish that human intelligence is highly heritable and polygenic. <i>Molecular Psychiatry</i> , 2011, 16, 996-1005.	7.9	571
24	Increased accuracy of artificial selection by using the realized relationship matrix. <i>Genetical Research</i> , 2009, 91, 47-60.	0.9	544
25	The future of livestock breeding: genomic selection for efficiency, reduced emissions intensity, and adaptation. <i>Trends in Genetics</i> , 2013, 29, 206-214.	6.7	527
26	Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels. <i>Journal of Dairy Science</i> , 2012, 95, 4114-4129.	3.4	516
27	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011, 19, 807-812.	2.8	460
28	Linkage Disequilibrium and Persistence of Phase in Holstein-Friesian, Jersey and Angus Cattle. <i>Genetics</i> , 2008, 179, 1503-1512.	2.9	439
29	Novel Multilocus Measure of Linkage Disequilibrium to Estimate Past Effective Population Size. <i>Genome Research</i> , 2003, 13, 635-643.	5.5	398
30	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	27.8	383
31	Recent human effective population size estimated from linkage disequilibrium. <i>Genome Research</i> , 2007, 17, 520-526.	5.5	381
32	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017, 49, 1304-1310.	21.4	378
33	Quantification of Inbreeding Due to Distant Ancestors and Its Detection Using Dense Single Nucleotide Polymorphism Data. <i>Genetics</i> , 2011, 189, 237-249.	2.9	367
34	Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. <i>PLoS Genetics</i> , 2015, 11, e1004969.	3.5	339
35	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. <i>PLoS Genetics</i> , 2014, 10, e1004269.	3.5	303
36	Reconciling the analysis of IBD and IBS in complex trait studies. <i>Nature Reviews Genetics</i> , 2010, 11, 800-805.	16.3	295

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37	The Genetic Interpretation of Area under the ROC Curve in Genomic Profiling. <i>PLoS Genetics</i> , 2010, 6, e1000864.	3.5	291
38	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	12.8	291
39	Reliability of Genomic Predictions Across Multiple Populations. <i>Genetics</i> , 2009, 183, 1545-1553.	2.9	280
40	A Better Coefficient of Determination for Genetic Profile Analysis. <i>Genetic Epidemiology</i> , 2012, 36, 214-224.	1.3	274
41	Using the genomic relationship matrix to predict the accuracy of genomic selection. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 409-421.	2.0	262
42	A Multi-Trait, Meta-analysis for Detecting Pleiotropic Polymorphisms for Stature, Fatness and Reproduction in Beef Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004198.	3.5	247
43	Genetic contributions to stability and change in intelligence from childhood to old age. <i>Nature</i> , 2012, 482, 212-215.	27.8	228
44	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	21.4	227
45	Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. <i>Nature Genetics</i> , 2018, 50, 737-745.	21.4	205
46	Genome-Wide Complex Trait Analysis (GCTA): Methods, Data Analyses, and Interpretations. <i>Methods in Molecular Biology</i> , 2013, 1019, 215-236.	0.9	200
47	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. <i>American Journal of Human Genetics</i> , 2015, 96, 377-385.	6.2	191
48	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. <i>Human Molecular Genetics</i> , 2013, 22, 832-841.	2.9	186
49	A Commentary on "Common SNPs Explain a Large Proportion of the Heritability for Human Height" by Yang et al. (2010). <i>Twin Research and Human Genetics</i> , 2010, 13, 517-524.	0.6	184
50	Identification of genomic regions associated with inbreeding depression in Holstein and Jersey dairy cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 71.	3.0	182
51	Predicting Unobserved Phenotypes for Complex Traits from Whole-Genome SNP Data. <i>PLoS Genetics</i> , 2008, 4, e1000231.	3.5	175
52	Genome-wide association studies for feedlot and growth traits in cattle1. <i>Journal of Animal Science</i> , 2011, 89, 1684-1697.	0.5	156
53	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	21.4	156
54	Polymorphic Regions Affecting Human Height Also Control Stature in Cattle. <i>Genetics</i> , 2011, 187, 981-984.	2.9	154

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55	The Use of Covariance Functions and Random Regressions for Genetic Evaluation of Milk Production Based on Test Day Records. <i>Journal of Dairy Science</i> , 1998, 81, 3300-3308.	3.4	148
56	Prediction of individual genetic risk of complex disease. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 257-263.	3.3	147
57	Estimation and Partition of Heritability in Human Populations Using Whole-Genome Analysis Methods. <i>Annual Review of Genetics</i> , 2013, 47, 75-95.	7.6	145
58	Accuracy of prediction of genomic breeding values for residual feed intake and carcass and meat quality traits in <i>Bos taurus</i> , <i>Bos indicus</i> , and composite beef cattle ¹ . <i>Journal of Animal Science</i> , 2013, 91, 3088-3104.	0.5	138
59	Human population dispersal “Out of Africa” estimated from linkage disequilibrium and allele frequencies of SNPs. <i>Genome Research</i> , 2011, 21, 821-829.	5.5	137
60	A validated genome-wide association study in 2 dairy cattle breeds for milk production and fertility traits using variable length haplotypes. <i>Journal of Dairy Science</i> , 2010, 93, 3331-3345.	3.4	135
61	Effect of rate of inbreeding on inbreeding depression in <i>Drosophila melanogaster</i> . <i>Theoretical and Applied Genetics</i> , 1989, 77, 123-127.	3.6	128
62	The Genetic Architecture of Climatic Adaptation of Tropical Cattle. <i>PLoS ONE</i> , 2014, 9, e113284.	2.5	128
63	Estimating Effects and Making Predictions from Genome-Wide Marker Data. <i>Statistical Science</i> , 2009, 24, .	2.8	127
64	Prospects for genomic selection in forage plant species. <i>Plant Breeding</i> , 2013, 132, 133-143.	1.9	125
65	Evidence-based psychiatric genetics, AKA the false dichotomy between common and rare variant hypotheses. <i>Molecular Psychiatry</i> , 2012, 17, 474-485.	7.9	124
66	Selection for complex traits leaves little or no classic signatures of selection. <i>BMC Genomics</i> , 2014, 15, 246.	2.8	124
67	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	10.3	123
68	Improved precision of QTL mapping using a nonlinear Bayesian method in a multi-breed population leads to greater accuracy of across-breed genomic predictions. <i>Genetics Selection Evolution</i> , 2015, 47, 29.	3.0	113
69	A genome-wide association study of meat and carcass traits in Australian cattle ¹ . <i>Journal of Animal Science</i> , 2011, 89, 2297-2309.	0.5	112
70	Novel strategies to minimize progeny inbreeding while maximizing genetic gain using genomic information. <i>Journal of Dairy Science</i> , 2012, 95, 377-388.	3.4	107
71	Technical note: Prediction of breeding values using marker-derived relationship matrices. <i>Journal of Animal Science</i> , 2008, 86, 2089-2092.	0.5	106
72	Accuracy of genomic selection using stochastic search variable selection in Australian Holstein Friesian dairy cattle. <i>Genetical Research</i> , 2009, 91, 307-311.	0.9	104

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73	A genome map of divergent artificial selection between <i>Bos taurus</i> dairy cattle and <i>Bos taurus</i> beef cattle. <i>Animal Genetics</i> , 2009, 40, 176-184.	1.7	104
74	Estimation of SNP Heritability from Dense Genotype Data. <i>American Journal of Human Genetics</i> , 2013, 93, 1151-1155.	6.2	103
75	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds. 4. Correlations among animal, carcass, and meat quality traits. <i>Australian Journal of Agricultural Research</i> , 2003, 54, 149.	1.5	100
76	Hot topic: Definition and implementation of a breeding value for feed efficiency in dairy cows. <i>Journal of Dairy Science</i> , 2015, 98, 7340-7350.	3.4	99
77	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19398-19408.	7.1	99
78	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. <i>Genetics</i> , 2019, 211, 1131-1141.	2.9	99
79	Genetic and environmental relationship among calving interval, survival, persistency of milk yield and somatic cell count in dairy cattle. <i>Livestock Science</i> , 2003, 80, 189-200.	1.2	98
80	Risk of psychiatric illness from advanced paternal age is not predominantly from de novo mutations. <i>Nature Genetics</i> , 2016, 48, 718-724.	21.4	98
81	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018, 2, 948-954.	12.0	97
82	Genetic Parameters for Milk Yield, Survival, Workability, and Type Traits for Australian Dairy Cattle. <i>Journal of Dairy Science</i> , 1995, 78, 205-220.	3.4	96
83	Evidence for pleiotropism and recent selection in the <i>PLAGL1</i> region in Australian beef cattle. <i>Animal Genetics</i> , 2013, 44, 636-647.	1.7	96
84	Evaluation of the accuracy of imputed sequence variant genotypes and their utility for causal variant detection in cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 24.	3.0	94
85	Genotype × Environment Interaction for Milk Production of Daughters of Australian Dairy Sires from Test-Day Records. <i>Journal of Dairy Science</i> , 2003, 86, 3736-3744.	3.4	93
86	Genomic selection in livestock populations. <i>Genetical Research</i> , 2010, 92, 413-421.	0.9	90
87	Accuracy of marker-assisted selection with single markers and marker haplotypes in cattle. <i>Genetical Research</i> , 2007, 89, 215-220.	0.9	87
88	Extensive variation between tissues in allele specific expression in an outbred mammal. <i>BMC Genomics</i> , 2015, 16, 993.	2.8	86
89	A single-step genomic model with direct estimation of marker effects. <i>Journal of Dairy Science</i> , 2014, 97, 5833-5850.	3.4	81
90	Short communication: Genomic selection using a multi-breed, across-country reference population. <i>Journal of Dairy Science</i> , 2011, 94, 2625-2630.	3.4	77

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91	A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle ¹ . <i>Journal of Animal Science</i> , 2014, 92, 2832-2845.	0.5	77
92	Targeted imputation of sequence variants and gene expression profiling identifies twelve candidate genes associated with lactation volume, composition and calving interval in dairy cattle. <i>Mammalian Genome</i> , 2016, 27, 81-97.	2.2	75
93	The Effects of Demography and Long-Term Selection on the Accuracy of Genomic Prediction with Sequence Data. <i>Genetics</i> , 2014, 198, 1671-1684.	2.9	74
94	Breeding objectives for pasture based dairy production systems. <i>Livestock Science</i> , 1994, 40, 123-137.	1.2	72
95	Multivariate analysis of a genome-wide association study in dairy cattle. <i>Journal of Dairy Science</i> , 2010, 93, 3818-3833.	3.4	72
96	Additive Genetic Variation in Schizophrenia Risk Is Shared by Populations of African and European Descent. <i>American Journal of Human Genetics</i> , 2013, 93, 463-470.	6.2	72
97	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. <i>American Journal of Human Genetics</i> , 2021, 108, 786-798.	6.2	70
98	Multi-locus models of genetic risk of disease. <i>Genome Medicine</i> , 2010, 2, 10.	8.2	69
99	Selection indices for non-linear profit functions. <i>Theoretical and Applied Genetics</i> , 1983, 64, 339-344.	3.6	68
100	Genetic architecture of body size in mammals. <i>Genome Biology</i> , 2012, 13, 244.	9.6	68
101	The distribution of SNP marker effects for faecal worm egg count in sheep, and the feasibility of using these markers to predict genetic merit for resistance to worm infections. <i>Genetical Research</i> , 2011, 93, 203-219.	0.9	67
102	Whole-genome resequencing of two elite sires for the detection of haplotypes under selection in dairy cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7693-7698.	7.1	67
103	Deterministic models of breeding scheme designs that incorporate genomic selection. <i>Journal of Dairy Science</i> , 2010, 93, 5455-5466.	3.4	64
104	A General Unified Framework to Assess the Sampling Variance of Heritability Estimates Using Pedigree or Marker-Based Relationships. <i>Genetics</i> , 2015, 199, 223-232.	2.9	61
105	Meta-analysis of sequence-based association studies across three cattle breeds reveals 25 QTL for fat and protein percentages in milk at nucleotide resolution. <i>BMC Genomics</i> , 2017, 18, 853.	2.8	61
106	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. <i>American Journal of Human Genetics</i> , 2015, 96, 720-730.	6.2	60
107	Genome-wide fine-mapping identifies pleiotropic and functional variants that predict many traits across global cattle populations. <i>Nature Communications</i> , 2021, 12, 860.	12.8	60
108	Genotype by Environment Interaction for Fertility, Survival, and Milk Production Traits in Australian Dairy Cattle. <i>Journal of Dairy Science</i> , 2008, 91, 4840-4853.	3.4	59

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109	Using the realized relationship matrix to disentangle confounding factors for the estimation of genetic variance components of complex traits. <i>Genetics Selection Evolution</i> , 2010, 42, 22.	3.0	58
110	Genetic and phenotypic characterisation of animal, carcass, and meat quality traits from temperate and tropically adapted beef breeds. 2. Abattoir carcass traits. <i>Australian Journal of Agricultural Research</i> , 2003, 54, 119.	1.5	57
111	Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 26.	3.0	56
112	From R.A. Fisher's 1918 Paper to GWAS a Century Later. <i>Genetics</i> , 2019, 211, 1125-1130.	2.9	56
113	Holstein-Friesian Dairy Cows Under a Predominantly Grazing System: Interaction Between Genotype and Environment. <i>Journal of Dairy Science</i> , 2008, 91, 826-839.	3.4	55
114	Estimates of Genetic Parameters for Daily Somatic Cell Count of Australian Dairy Cattle. <i>Journal of Dairy Science</i> , 2001, 84, 1255-1264.	3.4	52
115	Detailed phenotyping identifies genes with pleiotropic effects on body composition. <i>BMC Genomics</i> , 2016, 17, 224.	2.8	52
116	The use of epigenetic phenomena for the improvement of sheep and cattle. <i>Frontiers in Genetics</i> , 2014, 5, 247.	2.3	51
117	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	12.8	50
118	Impact of QTL properties on the accuracy of multi-breed genomic prediction. <i>Genetics Selection Evolution</i> , 2015, 47, 42.	3.0	49
119	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 2070-2081.	7.9	48
120	Including nonadditive genetic effects in mating programs to maximize dairy farm profitability. <i>Journal of Dairy Science</i> , 2017, 100, 1203-1222.	3.4	46
121	Multiple-trait QTL mapping and genomic prediction for wool traits in sheep. <i>Genetics Selection Evolution</i> , 2017, 49, 62.	3.0	46
122	GCTA-GREML accounts for linkage disequilibrium when estimating genetic variance from genome-wide SNPs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4579-80.	7.1	45
123	Prediction of the Confidence Interval of Quantitative Trait Loci Location. <i>Behavior Genetics</i> , 2004, 34, 477-482.	2.1	44
124	Assessment of heat stress in dairy cattle in papua new guinea. <i>Tropical Animal Health and Production</i> , 1986, 18, 232-242.	1.4	41
125	Detection of chromosome segments of zebu and taurine origin and their effect on beef production and growth1. <i>Journal of Animal Science</i> , 2011, 89, 2050-2060.	0.5	41
126	Validation of single nucleotide polymorphisms associated with milk production traits in dairy cattle. <i>Journal of Dairy Science</i> , 2012, 95, 864-875.	3.4	40

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127	Genome position specific priors for genomic prediction. BMC Genomics, 2012, 13, 543.	2.8	38
128	Estimation of genomic breeding values for residual feed intake in a multibreed cattle population1. Journal of Animal Science, 2014, 92, 3270-3283.	0.5	38
129	Genetic variants in mammary development, prolactin signalling and involution pathways explain considerable variation in bovine milk production and milk composition. Genetics Selection Evolution, 2014, 46, 29.	3.0	38
130	Using information of relatives in genomic prediction to apply effective stratified medicine. Scientific Reports, 2017, 7, 42091.	3.3	38
131	Haemonchus contortus and Trichostrongylus colubriformis did not adapt to long-term exposure to sheep that were genetically resistant or susceptible to nematode infections. International Journal for Parasitology, 2009, 39, 607-614.	3.1	37
132	Genetic parameters of fertility traits and their correlation with production, type, workability, liveweight, survival index, and cell count. Australian Journal of Agricultural Research, 2004, 55, 77.	1.5	36
133	Power of a genome scan to detect and locate quantitative trait loci in cattle using dense single nucleotide polymorphisms. Journal of Animal Breeding and Genetics, 2010, 127, 133-142.	2.0	36
134	Assortative mating biases marker-based heritability estimators. Nature Communications, 2022, 13, 660.	12.8	35
135	Genome-wide comparative analyses of correlated and uncorrelated phenotypes identify major pleiotropic variants in dairy cattle. Scientific Reports, 2017, 7, 9248.	3.3	34
136	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. BMC Genomics, 2018, 19, 521.	2.8	34
137	Sensitivity of genomic selection to using different prior distributions. BMC Proceedings, 2010, 4, S5.	1.6	33
138	The feasibility of using low-density marker panels for genotype imputation and genomic prediction of crossbred dairy cattle of East Africa. Journal of Dairy Science, 2018, 101, 9108-9127.	3.4	33
139	The use of linkage disequilibrium to map quantitative trait loci. Australian Journal of Experimental Agriculture, 2005, 45, 837.	1.0	32
140	The use of communal rearing of families and DNA pooling in aquaculture genomic selection schemes. Genetics Selection Evolution, 2010, 42, 41.	3.0	32
141	A multi-trait Bayesian method for mapping QTL and genomic prediction. Genetics Selection Evolution, 2018, 50, 10.	3.0	32
142	A novel predictor of multilocus haplotype homozygosity: comparison with existing predictors. Genetical Research, 2009, 91, 413-426.	0.9	31
143	How old are quantitative trait loci and how widely do they segregate?. Journal of Animal Breeding and Genetics, 2015, 132, 121-134.	2.0	31
144	Gene expression analysis of blood, liver, and muscle in cattle divergently selected for high and low residual feed intake1. Journal of Animal Science, 2017, 95, 4764-4775.	0.5	31

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145	Genetic and environmental correlations between test-day somatic cell count and milk yield traits. <i>Livestock Science</i> , 2001, 73, 1-13.	1.2	30
146	The Number of Loci That Affect Milk Production Traits in Dairy Cattle. <i>Genetics</i> , 2007, 177, 1117-1123.	2.9	29
147	Response to Browning and Browning. <i>American Journal of Human Genetics</i> , 2011, 89, 193-195.	6.2	27
148	Long-term selection strategies for complex traits using high-density genetic markers. <i>Journal of Dairy Science</i> , 2012, 95, 4646-4656.	3.4	27
149	Uses of genomics in livestock agriculture. <i>Animal Production Science</i> , 2012, 52, 73.	1.3	27
150	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016, 17, 441.	2.8	27
151	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. <i>American Journal of Human Genetics</i> , 2015, 97, 677-690.	6.2	26
152	Comparing allele specific expression and local expression quantitative trait loci and the influence of gene expression on complex trait variation in cattle. <i>BMC Genomics</i> , 2018, 19, 793.	2.8	26
153	The value of using DNA markers for beef bull selection in the seedstock sector ^{1,2} . <i>Journal of Animal Science</i> , 2011, 89, 307-320.	0.5	25
154	Effect direction meta-analysis of GWAS identifies extreme, prevalent and shared pleiotropy in a large mammal. <i>Communications Biology</i> , 2020, 3, 88.	4.4	25
155	The validity of genetic models underlying quantitative traits. <i>Livestock Science</i> , 2001, 72, 117-127.	1.2	23
156	Genetic markers for lactation persistency in primiparous Australian dairy cows. <i>Journal of Dairy Science</i> , 2010, 93, 2202-2214.	3.4	23
157	A computationally efficient algorithm for genomic prediction using a Bayesian model. <i>Genetics Selection Evolution</i> , 2015, 47, 34.	3.0	23
158	Comparing linkage and association analyses in sheep points to a better way of doing GWAS. <i>Genetical Research</i> , 2012, 94, 191-203.	0.9	22
159	Adaptation of gastrointestinal nematode parasites to host genotype: single locus simulation models. <i>Genetics Selection Evolution</i> , 2013, 45, 14.	3.0	21
160	Improving Genomic Prediction of Crossbred and Purebred Dairy Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 598580.	2.3	21
161	Narrow-sense heritability estimation of complex traits using identity-by-descent information. <i>Heredity</i> , 2018, 121, 616-630.	2.6	20
162	Multibreed genomic prediction using multitrait genomic residual maximum likelihood and multitask Bayesian variable selection. <i>Journal of Dairy Science</i> , 2018, 101, 4279-4294.	3.4	20

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163	Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues. <i>Frontiers in Genetics</i> , 2021, 12, 664379.	2.3	20
164	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021, 12, 1050.	12.8	19
165	Quantifying genetic heterogeneity between continental populations for human height and body mass index. <i>Scientific Reports</i> , 2021, 11, 5240.	3.3	19
166	A hybrid expectation maximisation and MCMC sampling algorithm to implement Bayesian mixture model based genomic prediction and QTL mapping. <i>BMC Genomics</i> , 2016, 17, 744.	2.8	18
167	Next generation modeling in GWAS: comparing different genetic architectures. <i>Human Genetics</i> , 2014, 133, 1235-1253.	3.8	17
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