

Ben Hayes

List of Publications by Year in descending order

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Version: 2024-02-01

301
papers

33,013
citations

5574

82
h-index

4885

168
g-index

314
all docs

314
docs citations

314
times ranked

18598
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. <i>Genetics</i> , 2001, 157, 1819-1829.	2.9	5,963
2	Invited review: Genomic selection in dairy cattle: Progress and challenges. <i>Journal of Dairy Science</i> , 2009, 92, 433-443.	3.4	1,359
3	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
4	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
5	Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. <i>PLoS Biology</i> , 2012, 10, e1001258.	5.6	719
6	Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. <i>Nature Genetics</i> , 2014, 46, 858-865.	21.4	697
7	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 507-515.	16.3	617
8	Genomic selection. <i>Journal of Animal Breeding and Genetics</i> , 2007, 124, 323-330.	2.0	595
9	Breeding crops to feed 10 billion. <i>Nature Biotechnology</i> , 2019, 37, 744-754.	17.5	577
10	Increased accuracy of artificial selection by using the realized relationship matrix. <i>Genetical Research</i> , 2009, 91, 47-60.	0.9	544
11	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
12	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
13	Linkage Disequilibrium and Persistence of Phase in Holstein-Friesian, Jersey and Angus Cattle. <i>Genetics</i> , 2008, 179, 1503-1512.	2.9	439
14	Novel Multilocus Measure of Linkage Disequilibrium to Estimate Past Effective Population Size. <i>Genome Research</i> , 2003, 13, 635-643.	5.5	398
15	Recent human effective population size estimated from linkage disequilibrium. <i>Genome Research</i> , 2007, 17, 520-526.	5.5	381
16	Genetic Architecture of Complex Traits and Accuracy of Genomic Prediction: Coat Colour, Milk-Fat Percentage, and Type in Holstein Cattle as Contrasting Model Traits. <i>PLoS Genetics</i> , 2010, 6, e1001139.	3.5	381
17	Accuracy of genomic breeding values in multi-breed dairy cattle populations. <i>Genetics Selection Evolution</i> , 2009, 41, 51.	3.0	371
18	Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. <i>PLoS Genetics</i> , 2015, 11, e1004969.	3.5	339

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19	Genomic selection: A paradigm shift in animal breeding. <i>Animal Frontiers</i> , 2016, 6, 6-14.	1.7	332
20	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. <i>Genome Biology</i> , 2015, 16, 57.	8.8	331
21	The distribution of the effects of genes affecting quantitative traits in livestock. <i>Genetics Selection Evolution</i> , 2001, 33, 209-29.	3.0	301
22	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. <i>Nature Genetics</i> , 2018, 50, 362-367.	21.4	286
23	Reliability of Genomic Predictions Across Multiple Populations. <i>Genetics</i> , 2009, 183, 1545-1553.	2.9	280
24	Exploiting biological priors and sequence variants enhances QTL discovery and genomic prediction of complex traits. <i>BMC Genomics</i> , 2016, 17, 144.	2.8	266
25	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
26	Harnessing genomic information for livestock improvement. <i>Nature Reviews Genetics</i> , 2019, 20, 135-156.	16.3	262
27	Accelerating Improvement of Livestock with Genomic Selection. <i>Annual Review of Animal Biosciences</i> , 2013, 1, 221-237.	7.4	258
28	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
29	Genome-wide association and genomic selection in animal breeding This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 876-883.	2.0	245
30	1000 Bull Genomes Project to Map Simple and Complex Genetic Traits in Cattle: Applications and Outcomes. <i>Annual Review of Animal Biosciences</i> , 2019, 7, 89-102.	7.4	241
31	A dense SNP-based linkage map for Atlantic salmon (<i>Salmo salar</i>) reveals extended chromosome homeologies and striking differences in sex-specific recombination patterns. <i>BMC Genomics</i> , 2011, 12, 615.	2.8	226
32	Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome. <i>Nature Genetics</i> , 2019, 51, 896-904.	21.4	225
33	Accelerating crop genetic gains with genomic selection. <i>Theoretical and Applied Genetics</i> , 2019, 132, 669-686.	3.6	218
34	Selection Signatures in Worldwide Sheep Populations. <i>PLoS ONE</i> , 2014, 9, e103813.	2.5	197
35	Breeding improves wheat productivity under contrasting agrochemical input levels. <i>Nature Plants</i> , 2019, 5, 706-714.	9.3	194
36	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

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37	Predicting Unobserved Phenotypes for Complex Traits from Whole-Genome SNP Data. <i>PLoS Genetics</i> , 2008, 4, e1000231.	3.5	175
38	Toward genomic prediction from whole-genome sequence data: impact of sequencing design on genotype imputation and accuracy of predictions. <i>Heredity</i> , 2014, 112, 39-47.	2.6	170
39	Design of a Bovine Low-Density SNP Array Optimized for Imputation. <i>PLoS ONE</i> , 2012, 7, e34130.	2.5	159
40	Genome-wide association studies for feedlot and growth traits in cattle ¹ . <i>Journal of Animal Science</i> , 2011, 89, 1684-1697.	0.5	156
41	Polymorphic Regions Affecting Human Height Also Control Stature in Cattle. <i>Genetics</i> , 2011, 187, 981-984.	2.9	154
42	A linkage map of the Atlantic salmon (<i>Salmo salar</i>) based on EST-derived SNP markers. <i>BMC Genomics</i> , 2008, 9, 223.	2.8	150
43	Genomic selection for tolerance to heat stress in Australian dairy cattle. <i>Journal of Dairy Science</i> , 2016, 99, 2849-2862.	3.4	143
44	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
45	LASSO with cross-validation for genomic selection. <i>Genetical Research</i> , 2009, 91, 427-436.	0.9	137
46	Components of the accuracy of genomic prediction in a multi-breed sheep population ¹ . <i>Journal of Animal Science</i> , 2012, 90, 3375-3384.	0.5	137
47	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
48	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. <i>BMC Genomics</i> , 2011, 12, 318.	2.8	135
49	A catalogue of novel bovine long noncoding RNA across 18 tissues. <i>PLoS ONE</i> , 2015, 10, e0141225.	2.5	130
50	Accuracy of imputation to whole-genome sequence data in Holstein Friesian cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 41.	3.0	128
51	Genomic selection in crops, trees and forages: a review. <i>Crop and Pasture Science</i> , 2014, 65, 1177.	1.5	128
52	Overview of Statistical Methods for Genome-Wide Association Studies (GWAS). <i>Methods in Molecular Biology</i> , 2013, 1019, 149-169.	0.9	127
53	Accuracy of genomic predictions of residual feed intake and 250-day body weight in growing heifers using 625,000 single nucleotide polymorphism markers. <i>Journal of Dairy Science</i> , 2012, 95, 2108-2119.	3.4	125
54	Prospects for genomic selection in forage plant species. <i>Plant Breeding</i> , 2013, 132, 133-143.	1.9	125

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55	Selection for complex traits leaves little or no classic signatures of selection. BMC Genomics, 2014, 15, 246.	2.8	124
56	A Validated Genome Wide Association Study to Breed Cattle Adapted to an Environment Altered by Climate Change. PLoS ONE, 2009, 4, e6676.	2.5	122
57	Animal board invited review: genetic possibilities to reduce enteric methane emissions from ruminants. Animal, 2015, 9, 1431-1440.	3.3	119
58	Genetics of complex traits: prediction of phenotype, identification of causal polymorphisms and genetic architecture. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160569.	2.6	118
59	Improving Genetic Gain with Genomic Selection in Autotetraploid Potato. Plant Genome, 2016, 9, plantgenome2016.02.0021.	2.8	115
60	Genomic prediction for rust resistance in diverse wheat landraces. Theoretical and Applied Genetics, 2014, 127, 1795-1803.	3.6	114
61	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. Animal Genetics, 2014, 45, 754-757.	1.7	113
62	Improved precision of QTL mapping using a nonlinear Bayesian method in a multi-breed population leads to greater accuracy of across-breed genomic predictions. Genetics Selection Evolution, 2015, 47, 29.	3.0	113
63	Identification and characterisation of novel SNP markers in Atlantic cod: Evidence for directional selection. BMC Genetics, 2008, 9, 18.	2.7	112
64	Genomic Selection Improves Heat Tolerance in Dairy Cattle. Scientific Reports, 2016, 6, 34114.	3.3	112
65	An extensive resource of single nucleotide polymorphism markers associated with Atlantic salmon (<i>Salmo salar</i>) expressed sequences. Aquaculture, 2007, 265, 82-90.	3.5	110
66	Novel strategies to minimize progeny inbreeding while maximizing genetic gain using genomic information. Journal of Dairy Science, 2012, 95, 377-388.	3.4	107
67	Technical note: Prediction of breeding values using marker-derived relationship matrices. Journal of Animal Science, 2008, 86, 2089-2092.	0.5	106
68	A chickpea genetic variation map based on the sequencing of 3,366 genomes. Nature, 2021, 599, 622-627.	27.8	106
69	Multibreed genome wide association can improve precision of mapping causative variants underlying milk production in dairy cattle. BMC Genomics, 2014, 15, 62.	2.8	105
70	Accuracy of genomic selection using stochastic search variable selection in Australian Holstein Friesian dairy cattle. Genetical Research, 2009, 91, 307-311.	0.9	104
71	A genome map of divergent artificial selection between <i>Bos taurus</i> dairy cattle and <i>Bos taurus</i> beef cattle. Animal Genetics, 2009, 40, 176-184.	1.7	104
72	Metagenomic Predictions: From Microbiome to Complex Health and Environmental Phenotypes in Humans and Cattle. PLoS ONE, 2013, 8, e73056.	2.5	103

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73	Statistical Epistasis Is a Generic Feature of Gene Regulatory Networks. <i>Genetics</i> , 2007, 175, 411-420.	2.9	99
74	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
75	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
76	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. <i>Genetics</i> , 2019, 211, 1131-1141.	2.9	99
77	Accuracy of genotype imputation in sheep breeds. <i>Animal Genetics</i> , 2012, 43, 72-80.	1.7	98
78	Genomic selection for feed efficiency in dairy cattle. <i>Animal</i> , 2014, 8, 1-10.	3.3	98
79	Accelerating wheat breeding for end-use quality with multi-trait genomic predictions incorporating near infrared and nuclear magnetic resonance-derived phenotypes. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2505-2519.	3.6	98
80	Accuracy of pedigree and genomic predictions of carcass and novel meat quality traits in multi-breed sheep data assessed by cross-validation. <i>Genetics Selection Evolution</i> , 2012, 44, 33.	3.0	96
81	Accuracy of estimated genomic breeding values for wool and meat traits in a multi-breed sheep population. <i>Animal Production Science</i> , 2010, 50, 1004.	1.3	94
82	Genotype \times 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
83	Inferring Demography from Runs of Homozygosity in Whole-Genome Sequence, with Correction for Sequence Errors. <i>Molecular Biology and Evolution</i> , 2013, 30, 2209-2223.	8.9	91
84	Genomic selection in livestock populations. <i>Genetical Research</i> , 2010, 92, 413-421.	0.9	90
85	Accuracy of marker-assisted selection with single markers and marker haplotypes in cattle. <i>Genetical Research</i> , 2007, 89, 215-220.	0.9	87
86	Extensive variation between tissues in allele specific expression in an outbred mammal. <i>BMC Genomics</i> , 2015, 16, 993.	2.8	86
87	Exploring and Harnessing Haplotype Diversity to Improve Yield Stability in Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 1534.	3.6	86
88	Variation in residual feed intake in Holstein-Friesian dairy heifers in southern Australia. <i>Journal of Dairy Science</i> , 2011, 94, 4715-4725.	3.4	85
89	Selection on Optimal Haploid Value Increases Genetic Gain and Preserves More Genetic Diversity Relative to Genomic Selection. <i>Genetics</i> , 2015, 200, 1341-1348.	2.9	83
90	Genetic Gain and Inbreeding from Genomic Selection in a Simulated Commercial Breeding Program for Perennial Ryegrass. <i>Plant Genome</i> , 2016, 9, plantgenome2015.06.0046.	2.8	83

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91	Accuracy of direct genomic values in Holstein bulls and cows using subsets of SNP markers. <i>Genetics Selection Evolution</i> , 2010, 42, 37.	3.0	82
92	Imputation of Missing Genotypes From Sparse to High Density Using Long-Range Phasing. <i>Genetics</i> , 2011, 189, 317-327.	2.9	79
93	Quantitative trait loci for clinical mastitis on chromosomes 2, 6, 14 and 20 in Norwegian Red cattle. <i>Animal Genetics</i> , 2011, 42, 457-465.	1.7	78
94	Genetic support for a quantitative trait nucleotide in the ABCG2 gene affecting milk composition of dairy cattle. <i>BMC Genetics</i> , 2007, 8, 32.	2.7	77
95	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
96	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
97	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
98	Improving breeding efficiency in potato using molecular and quantitative genetics. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2279-2292.	3.6	74
99	Accounting for dominance to improve genomic evaluations of dairy cows for fertility and milk production traits. <i>Genetics Selection Evolution</i> , 2016, 48, 8.	3.0	74
100	An examination of positive selection and changing effective population size in Angus and Holstein cattle populations (<i>Bos taurus</i>) using a high density SNP genotyping platform and the contribution of ancient polymorphism to genomic diversity in Domestic cattle. <i>BMC Genomics</i> , 2009, 10, 181.	2.8	72
101	Multivariate analysis of a genome-wide association study in dairy cattle. <i>Journal of Dairy Science</i> , 2010, 93, 3818-3833.	3.4	72
102	Casein haplotypes and their association with milk production traits in Norwegian Red cattle. <i>Genetics Selection Evolution</i> , 2009, 41, 24.	3.0	68
103	High throughput whole rumen metagenome profiling using untargeted massively parallel sequencing. <i>BMC Genetics</i> , 2012, 13, 53.	2.7	68
104	Strategies and utility of imputed SNP genotypes for genomic analysis in dairy cattle. <i>BMC Genomics</i> , 2012, 13, 538.	2.8	68
105	The origin of selection signatures on bovine chromosome 6. <i>Animal Genetics</i> , 2008, 39, 105-111.	1.7	67
106	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
107	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
108	Responses of dairy cows to short-term heat stress in controlled-climate chambers. <i>Animal Production Science</i> , 2017, 57, 1233.	1.3	67

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109	Genotype calling and mapping of multisite variants using an Atlantic salmon iSelect SNP array. <i>Bioinformatics</i> , 2011, 27, 303-310.	4.1	66
110	Improving the analysis of low heritability complex traits for enhanced genetic gain in potato. <i>Theoretical and Applied Genetics</i> , 2014, 127, 809-820.	3.6	66
111	<sc>GO</sc>â€œ<sc>FAANG</sc> meeting: a Gathering On Functional Annotation of <sc>Animal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	1.7	65
112	Mapping of a quantitative trait locus for resistance against infectious salmon anaemia in Atlantic salmon (<i>Salmo Salar</i>): comparing survival analysis with analysis on affected/resistant data. <i>BMC Genetics</i> , 2007, 8, 53.	2.7	64
113	Deterministic models of breeding scheme designs that incorporate genomic selection. <i>Journal of Dairy Science</i> , 2010, 93, 5455-5466.	3.4	64
114	Technical note: Efficient parentage assignment and pedigree reconstruction with dense single nucleotide polymorphism data. <i>Journal of Dairy Science</i> , 2011, 94, 2114-2117.	3.4	64
115	Improved accuracy of genomic prediction for dry matter intake of dairy cattle from combined European and Australian data sets. <i>Journal of Dairy Science</i> , 2012, 95, 6103-6112.	3.4	64
116	Effects on Production Traits of Haplotypes Among Casein Genes in Norwegian Goats and Evidence for a Site of Preferential Recombination. <i>Genetics</i> , 2006, 174, 455-464.	2.9	62
117	Genetic parameters and response to selection in blue mussel (<i>Mytilus galloprovincialis</i>) using a SNP-based pedigree. <i>Aquaculture</i> , 2014, 420-421, 295-301.	3.5	61
118	Rapid Discovery of De Novo Deleterious Mutations in Cattle Enhances the Value of Livestock as Model Species. <i>Scientific Reports</i> , 2017, 7, 11466.	3.3	61
119	Accelerating Genetic Gain in Sugarcane Breeding Using Genomic Selection. <i>Agronomy</i> , 2020, 10, 585.	3.0	60
120	Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 26.	3.0	56
121	Investigating the effect of two methane-mitigating diets on the rumen microbiome using massively parallel sequencing. <i>Journal of Dairy Science</i> , 2013, 96, 6030-6046.	3.4	54
122	Differentially Expressed Genes in Endometrium and Corpus Luteum of Holstein Cows Selected for High and Low Fertility Are Enriched for Sequence Variants Associated with Fertility1. <i>Biology of Reproduction</i> , 2016, 94, 19.	2.7	53
123	Mitigation of inbreeding while preserving genetic gain in genomic breeding programs for outbred plants. <i>Theoretical and Applied Genetics</i> , 2017, 130, 969-980.	3.6	53
124	Holstein-Friesian calves selected for divergence in residual feed intake during growth exhibited significant but reduced residual feed intake divergence in their first lactation. <i>Journal of Dairy Science</i> , 2014, 97, 1427-1435.	3.4	52
125	Detailed phenotyping identifies genes with pleiotropic effects on body composition. <i>BMC Genomics</i> , 2016, 17, 224.	2.8	52
126	Metagenomics of rumen bacteriophage from thirteen lactating dairy cattle. <i>BMC Microbiology</i> , 2013, 13, 242.	3.3	51

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127	Multivariate Genomic Selection and Potential of Rapid Indirect Selection with Speed Breeding in Spring Wheat. <i>Crop Science</i> , 2019, 59, 1945-1959.	1.8	51
128	Power of QTL mapping experiments in commercial Atlantic salmon populations, exploiting linkage and linkage disequilibrium and effect of limited recombination in males. <i>Heredity</i> , 2006, 97, 19-26.	2.6	50
129	Short communication: Implementation of a breeding value for heat tolerance in Australian dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 7362-7367.	3.4	50
130	Impact of QTL properties on the accuracy of multi-breed genomic prediction. <i>Genetics Selection Evolution</i> , 2015, 47, 42.	3.0	49
131	Regulatory and coding genome regions are enriched for trait associated variants in dairy and beef cattle. <i>BMC Genomics</i> , 2014, 15, 436.	2.8	47
132	Evaluation of three strategies using DNA markers for traceability in aquaculture species. <i>Aquaculture</i> , 2005, 250, 70-81.	3.5	46
133	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
134	Detection of quantitative trait loci in <i>Bos indicus</i> and <i>Bos taurus</i> cattle using genome-wide association studies. <i>Genetics Selection Evolution</i> , 2013, 45, 43.	3.0	44
135	Models for Genome \times Environment Interaction: Examples in Livestock. <i>Crop Science</i> , 2016, 56, 2251-2259.	1.8	43
136	Genomic heritabilities and genomic estimated breeding values for methane traits in Angus cattle ¹ . <i>Journal of Animal Science</i> , 2016, 94, 902-908.	0.5	43
137	Genome-wide association mapping in Norwegian Red cattle identifies quantitative trait loci for fertility and milk production on BTA12. <i>Animal Genetics</i> , 2011, 42, 466-474.	1.7	42
138	Leveraging genetically simple traits to identify small-effect variants for complex phenotypes. <i>BMC Genomics</i> , 2016, 17, 858.	2.8	42
139	Reducing the carbon footprint of Australian milk production by mitigation of enteric methane emissions. <i>Animal Production Science</i> , 2016, 56, 1017.	1.3	42
140	Genome-wide association study and annotating candidate gene networks affecting age at first calving in Nellore cattle. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 484-492.	2.0	42
141	Putative bovine topological association domains and CTCF binding motifs can reduce the search space for causative regulatory variants of complex traits. <i>BMC Genomics</i> , 2018, 19, 395.	2.8	42
142	Detection of chromosome segments of zebu and taurine origin and their effect on beef production and growth ¹ . <i>Journal of Animal Science</i> , 2011, 89, 2050-2060.	0.5	41
143	Genomewide association study of methane emissions in Angus beef cattle with validation in dairy cattle ¹ . <i>Journal of Animal Science</i> , 2016, 94, 4151-4166.	0.5	41
144	Putative enhancer sites in the bovine genome are enriched with variants affecting complex traits. <i>Genetics Selection Evolution</i> , 2017, 49, 56.	3.0	41

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145	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
146	Sequencing the mosaic genome of Brahman cattle identifies historic and recent introgression including polled. <i>Scientific Reports</i> , 2018, 8, 17761.	3.3	39
147	Towards a new phenotype for tick resistance in beef and dairy cattle: a review. <i>Animal Production Science</i> , 2019, 59, 1401.	1.3	39
148	SNP detection exploiting multiple sources of redundancy in large EST collections improves validation rates. <i>Bioinformatics</i> , 2007, 23, 1692-1693.	4.1	38
149	Weight and time of onset of female-superior sexual dimorphism in pond reared <i>Penaeus monodon</i> . <i>Aquaculture</i> , 2010, 300, 237-239.	3.5	38
150	Genome position specific priors for genomic prediction. <i>BMC Genomics</i> , 2012, 13, 543.	2.8	38
151	Comparison of heritabilities of dairy traits in Australian Holstein-Friesian cattle from genomic and pedigree data and implications for genomic evaluations. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 20-31.	2.0	38
152	Genetic variants in mammary development, prolactin signalling and involution pathways explain considerable variation in bovine milk production and milk composition. <i>Genetics Selection Evolution</i> , 2014, 46, 29.	3.0	38
153	Design of a low-density SNP chip for the main Australian sheep breeds and its effect on imputation and genomic prediction accuracy. <i>Animal Genetics</i> , 2015, 46, 544-556.	1.7	38
154	Genetic parameters for growth and survival in <i>Penaeus monodon</i> cultured in India. <i>Aquaculture</i> , 2011, 318, 74-78.	3.5	37
155	Power of a genome scan to detect and locate quantitative trait loci in cattle using dense single nucleotide polymorphisms. <i>Journal of Animal Breeding and Genetics</i> , 2010, 127, 133-142.	2.0	36
156	Unraveling genetic sensitivity of beef cattle to environmental variation under tropical conditions. <i>Genetics Selection Evolution</i> , 2019, 51, 29.	3.0	35
157	“SpeedGS” to Accelerate Genetic Gain in Spring Wheat. , 2019, , 303-327.		35
158	Boosting Genetic Gain in Allogamous Crops via Speed Breeding and Genomic Selection. <i>Frontiers in Plant Science</i> , 2019, 10, 1364.	3.6	35
159	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. <i>BMC Genomics</i> , 2018, 19, 521.	2.8	34
160	Gene by environment interactions for production traits in Australian dairy cattle. <i>Journal of Dairy Science</i> , 2009, 92, 4008-4017.	3.4	33
161	Sensitivity of genomic selection to using different prior distributions. <i>BMC Proceedings</i> , 2010, 4, S5.	1.6	33
162	Genomic selection for recovery of original genetic background from hybrids of endangered and common breeds. <i>Evolutionary Applications</i> , 2014, 7, 227-237.	3.1	33

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163	Gene expression of the heat stress response in bovine peripheral white blood cells and milk somatic cells in vivo. <i>Scientific Reports</i> , 2020, 10, 19181.	3.3	33
164	Evaluation of marker assisted selection in pig enterprises. <i>Livestock Science</i> , 2003, 81, 197-211.	1.2	32
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