

Michael E Goddard

List of Publications by Year in descending order

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201
papers

53,690
citations

5569

82
h-index

2178

202
g-index

225
all docs

225
docs citations

225
times ranked

45856
citing authors

#	ARTICLE	IF	CITATIONS
1	Assortative mating biases marker-based heritability estimators. <i>Nature Communications</i> , 2022, 13, 660.	5.8	35
2	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.	9.4	156
3	William G. Hill (August 7, 1940 – December 17, 2021). <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 817-820.	1.1	0
4	BayesR3 enables fast MCMC blocked processing for largescale multi-trait genomic prediction and QTN mapping analysis. <i>Communications Biology</i> , 2022, 5, .	2.0	6
5	From Mendel to quantitative genetics in the genome era: the scientific legacy of W. G. Hill. <i>Nature Genetics</i> , 2022, 54, 934-939.	9.4	3
6	Bayesian genome-wide analysis of cattle traits using variants with functional and evolutionary significance. <i>Animal Production Science</i> , 2021, 61, 1818-1827.	0.6	6
7	Genome-wide fine-mapping identifies pleiotropic and functional variants that predict many traits across global cattle populations. <i>Nature Communications</i> , 2021, 12, 860.	5.8	60
8	Widespread signatures of natural selection across human complex traits and functional genomic categories. <i>Nature Communications</i> , 2021, 12, 1164.	5.8	50
9	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. <i>Nature Communications</i> , 2021, 12, 1050.	5.8	19
10	Quantifying genetic heterogeneity between continental populations for human height and body mass index. <i>Scientific Reports</i> , 2021, 11, 5240.	1.6	19
11	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.	2.6	70
12	Putative Causal Variants Are Enriched in Annotated Functional Regions From Six Bovine Tissues. <i>Frontiers in Genetics</i> , 2021, 12, 664379.	1.1	20
13	Genomic partitioning of inbreeding depression in humans. <i>American Journal of Human Genetics</i> , 2021, 108, 1488-1501.	2.6	6
14	Phantom epistasis between unlinked loci. <i>Nature</i> , 2021, 596, E1-E3.	13.7	16
15	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 2070-2081.	4.1	48
16	Mutant alleles differentially shape fitness and other complex traits in cattle. <i>Communications Biology</i> , 2021, 4, 1353.	2.0	6
17	Improving Genomic Prediction of Crossbred and Purebred Dairy Cattle. <i>Frontiers in Genetics</i> , 2020, 11, 598580.	1.1	21
18	Effect direction meta-analysis of GWAS identifies extreme, prevalent and shared pleiotropy in a large mammal. <i>Communications Biology</i> , 2020, 3, 88.	2.0	25

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19	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019, 5, eaaw3538.	4.7	123
20	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.	3.3	99
21	From R.A. Fisher's 1918 Paper to GWAS a Century Later. <i>Genetics</i> , 2019, 211, 1125-1130.	1.2	56
22	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. <i>Genetics</i> , 2019, 211, 1131-1141.	1.2	99
23	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019, 10, 5086.	5.8	291
24	Narrow-sense heritability estimation of complex traits using identity-by-descent information. <i>Heredity</i> , 2018, 121, 616-630.	1.2	20
25	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.	9.4	205
26	Multibreed genomic prediction using multitrait genomic residual maximum likelihood and multitask Bayesian variable selection. <i>Journal of Dairy Science</i> , 2018, 101, 4279-4294.	1.4	20
27	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.	1.2	26
28	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018, 2, 948-954.	6.2	97
29	The feasibility of using low-density marker panels for genotype imputation and genomic prediction of crossbred dairy cattle of East Africa. <i>Journal of Dairy Science</i> , 2018, 101, 9108-9127.	1.4	33
30	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. <i>BMC Genomics</i> , 2018, 19, 521.	1.2	34
31	A multi-trait Bayesian method for mapping QTL and genomic prediction. <i>Genetics Selection Evolution</i> , 2018, 50, 10.	1.2	32
32	Using information of relatives in genomic prediction to apply effective stratified medicine. <i>Scientific Reports</i> , 2017, 7, 42091.	1.6	38
33	Including nonadditive genetic effects in mating programs to maximize dairy farm profitability. <i>Journal of Dairy Science</i> , 2017, 100, 1203-1222.	1.4	46
34	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017, 49, 1304-1310.	9.4	378
35	Genome-wide comparative analyses of correlated and uncorrelated phenotypes identify major pleiotropic variants in dairy cattle. <i>Scientific Reports</i> , 2017, 7, 9248.	1.6	34
36	Can we make genomic selection 100% accurate?. <i>Journal of Animal Breeding and Genetics</i> , 2017, 134, 287-288.	0.8	8

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37	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.	1.2	94
38	Gene expression analysis of blood, liver, and muscle in cattle divergently selected for high and low residual feed intake1. <i>Journal of Animal Science</i> , 2017, 95, 4764-4775.	0.2	31
39	Application of a Bayesian non-linear model hybrid scheme to sequence data for genomic prediction and QTL mapping. <i>BMC Genomics</i> , 2017, 18, 618.	1.2	17
40	Multiple-trait QTL mapping and genomic prediction for wool traits in sheep. <i>Genetics Selection Evolution</i> , 2017, 49, 62.	1.2	46
41	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.	1.2	61
42	Copy number variants in the sheep genome detected using multiple approaches. <i>BMC Genomics</i> , 2016, 17, 441.	1.2	27
43	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.	1.2	18
44	Inflammatory-Related Genetic Variants in Non-Muscle-Invasive Bladder Cancer Prognosis: A Multimarker Bayesian Assessment. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1144-1150.	1.1	8
45	Risk of psychiatric illness from advanced paternal age is not predominantly from de novo mutations. <i>Nature Genetics</i> , 2016, 48, 718-724.	9.4	98
46	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.	3.3	45
47	Detailed phenotyping identifies genes with pleiotropic effects on body composition. <i>BMC Genomics</i> , 2016, 17, 224.	1.2	52
48	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016, 48, 481-487.	9.4	1,757
49	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.	1.0	75
50	A computationally efficient algorithm for genomic prediction using a Bayesian model. <i>Genetics Selection Evolution</i> , 2015, 47, 34.	1.2	23
51	Extensive variation between tissues in allele specific expression in an outbred mammal. <i>BMC Genomics</i> , 2015, 16, 993.	1.2	86
52	Rare Variants in Transcript and Potential Regulatory Regions Explain a Small Percentage of the Missing Heritability of Complex Traits in Cattle. <i>PLoS ONE</i> , 2015, 10, e0143945.	1.1	16
53	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
54	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. <i>American Journal of Human Genetics</i> , 2015, 96, 377-385.	2.6	191

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55	Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. <i>PLoS Genetics</i> , 2015, 11, e1004969.	1.5	339
56	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.	1.2	61
57	Mixed Model with Correction for Case-Control Ascertainment Increases Association Power. <i>American Journal of Human Genetics</i> , 2015, 96, 720-730.	2.6	60
58	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.	1.2	113
59	Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 26.	1.2	56
60	Impact of QTL properties on the accuracy of multi-breed genomic prediction. <i>Genetics Selection Evolution</i> , 2015, 47, 42.	1.2	49
61	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
62	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. <i>American Journal of Human Genetics</i> , 2015, 97, 677-690.	2.6	26
63	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.	1.4	99
64	How old are quantitative trait loci and how widely do they segregate?. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 121-134.	0.8	31
65	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.	9.4	709
66	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	9.4	227
67	The Genetic Architecture of Climatic Adaptation of Tropical Cattle. <i>PLoS ONE</i> , 2014, 9, e113284.	1.1	128
68	Estimation of genomic breeding values for residual feed intake in a multibreed cattle population1. <i>Journal of Animal Science</i> , 2014, 92, 3270-3283.	0.2	38
69	The Effects of Demography and Long-Term Selection on the Accuracy of Genomic Prediction with Sequence Data. <i>Genetics</i> , 2014, 198, 1671-1684.	1.2	74
70	Identification of genomic regions associated with inbreeding depression in Holstein and Jersey dairy cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 71.	1.2	182
71	Statistical Power to Detect Genetic (Co)Variance of Complex Traits Using SNP Data in Unrelated Samples. <i>PLoS Genetics</i> , 2014, 10, e1004269.	1.5	303
72	Erratum to "Improving accuracy of genomic predictions within and between dairy cattle breeds with imputed high-density single nucleotide polymorphism panels" (J. Dairy Sci. 95:4114-4129). <i>Journal of Dairy Science</i> , 2014, 97, 6622.	1.4	6

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73	A Multi-Trait, Meta-analysis for Detecting Pleiotropic Polymorphisms for Stature, Fatness and Reproduction in Beef Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004198.	1.5	247
74	The use of epigenetic phenomena for the improvement of sheep and cattle. <i>Frontiers in Genetics</i> , 2014, 5, 247.	1.1	51
75	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.	1.2	38
76	A single-step genomic model with direct estimation of marker effects. <i>Journal of Dairy Science</i> , 2014, 97, 5833-5850.	1.4	81
77	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
78	Next generation modeling in GWAS: comparing different genetic architectures. <i>Human Genetics</i> , 2014, 133, 1235-1253.	1.8	17
79	Selection for complex traits leaves little or no classic signatures of selection. <i>BMC Genomics</i> , 2014, 15, 246.	1.2	124
80	A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle. <i>Journal of Animal Science</i> , 2014, 92, 2832-2845.	0.2	77
81	Advantages and pitfalls in the application of mixed-model association methods. <i>Nature Genetics</i> , 2014, 46, 100-106.	9.4	876
82	Inferring the recent ancestry of <i>myostatin</i> alleles affecting muscle mass in cattle. <i>Animal Genetics</i> , 2013, 44, 86-90.	0.6	16
83	Evidence for pleiotropism and recent selection in the <i>PLAG1</i> region in Australian beef cattle. <i>Animal Genetics</i> , 2013, 44, 636-647.	0.6	96
84	Adaptation of gastrointestinal nematode parasites to host genotype: single locus simulation models. <i>Genetics Selection Evolution</i> , 2013, 45, 14.	1.2	21
85	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 894-894.	7.7	6
86	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	9.4	2,067
87	Estimation and Partition of Heritability in Human Populations Using Whole-Genome Analysis Methods. <i>Annual Review of Genetics</i> , 2013, 47, 75-95.	3.2	145
88	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.	1.4	186
89	Estimation of SNP Heritability from Dense Genotype Data. <i>American Journal of Human Genetics</i> , 2013, 93, 1151-1155.	2.6	103
90	Kernel methods and haplotypes used in selection of sparse DNA markers for protein yield in dairy cattle. <i>Mathematical Biosciences</i> , 2013, 243, 57-66.	0.9	1

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91	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.	2.6	72
92	The future of livestock breeding: genomic selection for efficiency, reduced emissions intensity, and adaptation. <i>Trends in Genetics</i> , 2013, 29, 206-214.	2.9	527
93	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 507-515.	7.7	617
94	Prospects for genomic selection in forage plant species. <i>Plant Breeding</i> , 2013, 132, 133-143.	1.0	125
95	Genome-Wide Complex Trait Analysis (GCTA): Methods, Data Analyses, and Interpretations. <i>Methods in Molecular Biology</i> , 2013, 1019, 215-236.	0.4	200
96	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. <i>Journal of Animal Science</i> , 2013, 91, 3088-3104.	0.2	138
97	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.	3.3	67
98	Next generation sequencing of African and Indicine cattle to identify single nucleotide polymorphisms. <i>Animal Production Science</i> , 2012, 52, 133.	0.6	11
99	Comparing linkage and association analyses in sheep points to a better way of doing GWAS. <i>Genetical Research</i> , 2012, 94, 191-203.	0.3	22
100	Validation of single nucleotide polymorphisms associated with milk production traits in dairy cattle. <i>Journal of Dairy Science</i> , 2012, 95, 864-875.	1.4	40
101	Novel strategies to minimize progeny inbreeding while maximizing genetic gain using genomic information. <i>Journal of Dairy Science</i> , 2012, 95, 377-388.	1.4	107
102	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.	1.4	516
103	Long-term selection strategies for complex traits using high-density genetic markers. <i>Journal of Dairy Science</i> , 2012, 95, 4646-4656.	1.4	27
104	Genetic architecture of body size in mammals. <i>Genome Biology</i> , 2012, 13, 244.	13.9	68
105	Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. <i>Nature Genetics</i> , 2012, 44, 369-375.	9.4	1,338
106	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. <i>Nature Genetics</i> , 2012, 44, 247-250.	9.4	578
107	Genome position specific priors for genomic prediction. <i>BMC Genomics</i> , 2012, 13, 543.	1.2	38
108	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383

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109	Evidence-based psychiatric genetics, AKA the false dichotomy between common and rare variant hypotheses. <i>Molecular Psychiatry</i> , 2012, 17, 474-485.	4.1	124
110	Genetic contributions to stability and change in intelligence from childhood to old age. <i>Nature</i> , 2012, 482, 212-215.	13.7	228
111	Uses of genomics in livestock agriculture. <i>Animal Production Science</i> , 2012, 52, 73.	0.6	27
112	A Better Coefficient of Determination for Genetic Profile Analysis. <i>Genetic Epidemiology</i> , 2012, 36, 214-224.	0.6	274
113	Polymorphic Regions Affecting Human Height Also Control Stature in Cattle. <i>Genetics</i> , 2011, 187, 981-984.	1.2	154
114	Genome-wide association studies establish that human intelligence is highly heritable and polygenic. <i>Molecular Psychiatry</i> , 2011, 16, 996-1005.	4.1	571
115	Short communication: Genomic selection using a multi-breed, across-country reference population. <i>Journal of Dairy Science</i> , 2011, 94, 2625-2630.	1.4	77
116	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.	0.2	25
117	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.	0.3	67
118	Using the genomic relationship matrix to predict the accuracy of genomic selection. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 409-421.	0.8	262
119	Cattle gain stature. <i>Nature Genetics</i> , 2011, 43, 397-398.	9.4	9
120	Genome partitioning of genetic variation for complex traits using common SNPs. <i>Nature Genetics</i> , 2011, 43, 519-525.	9.4	834
121	Genomic inflation factors under polygenic inheritance. <i>European Journal of Human Genetics</i> , 2011, 19, 807-812.	1.4	460
122	GCTA: A Tool for Genome-wide Complex Trait Analysis. <i>American Journal of Human Genetics</i> , 2011, 88, 76-82.	2.6	6,212
123	Estimating Missing Heritability for Disease from Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2011, 88, 294-305.	2.6	949
124	Response to Browning and Browning. <i>American Journal of Human Genetics</i> , 2011, 89, 193-195.	2.6	27
125	Genome-wide association studies for feedlot and growth traits in cattle ¹ . <i>Journal of Animal Science</i> , 2011, 89, 1684-1697.	0.2	156
126	Quantification of Inbreeding Due to Distant Ancestors and Its Detection Using Dense Single Nucleotide Polymorphism Data. <i>Genetics</i> , 2011, 189, 237-249.	1.2	367

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127	Human population dispersal "Out of Africa" estimated from linkage disequilibrium and allele frequencies of SNPs. <i>Genome Research</i> , 2011, 21, 821-829.	2.4	137
128	A genome-wide association study of meat and carcass traits in Australian cattle1. <i>Journal of Animal Science</i> , 2011, 89, 2297-2309.	0.2	112
129	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.	0.2	41
130	Calculation of lifetime net income per year (LTNI/year) of Australian Holstein cows to validate the Australian profit ranking of their sires. 1. Genetic analyses and prediction of LTNI/year for cows still in the herd. <i>Animal Production Science</i> , 2010, 50, 757.	0.6	2
131	The use of communal rearing of families and DNA pooling in aquaculture genomic selection schemes. <i>Genetics Selection Evolution</i> , 2010, 42, 41.	1.2	32
132	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.	1.2	58
133	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
134	Common SNPs explain a large proportion of the heritability for human height. <i>Nature Genetics</i> , 2010, 42, 565-569.	9.4	3,888
135	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.	9.4	836
136	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
137	Reconciling the analysis of IBD and IBS in complex trait studies. <i>Nature Reviews Genetics</i> , 2010, 11, 800-805.	7.7	295
138	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.	0.8	36
139	Genomic selection in livestock populations. <i>Genetical Research</i> , 2010, 92, 413-421.	0.3	90
140	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.	0.3	184
141	Calculation of lifetime net income per year (LTNI/year) of Australian Holstein cows to validate the Australian profit ranking of their sires. 2. Validation of the Australian profit ranking of sires and test for genotype by environment interaction based on LTNI/year. <i>Animal Production Science</i> , 2010, 50, 767.	0.6	4
142	Sensitivity of genomic selection to using different prior distributions. <i>BMC Proceedings</i> , 2010, 4, S5.	1.8	33
143	The Genetic Interpretation of Area under the ROC Curve in Genomic Profiling. <i>PLoS Genetics</i> , 2010, 6, e1000864.	1.5	291
144	Genetic markers for lactation persistency in primiparous Australian dairy cows. <i>Journal of Dairy Science</i> , 2010, 93, 2202-2214.	1.4	23

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145	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.	1.4	135
146	Multivariate analysis of a genome-wide association study in dairy cattle. <i>Journal of Dairy Science</i> , 2010, 93, 3818-3833.	1.4	72
147	Deterministic models of breeding scheme designs that incorporate genomic selection. <i>Journal of Dairy Science</i> , 2010, 93, 5455-5466.	1.4	64
148	Multi-locus models of genetic risk of disease. <i>Genome Medicine</i> , 2010, 2, 10.	3.6	69
149	Systems genetics: The added value of gene expression. <i>HFSP Journal</i> , 2010, 4, 6-10.	2.5	3
150	Preliminary genetic analyses of voluntarily supplied disease data in Australian dairy herds. <i>Animal Production Science</i> , 2010, 50, 186.	0.6	9
151	Accuracy of genomic selection using stochastic search variable selection in Australian Holstein Friesian dairy cattle. <i>Genetical Research</i> , 2009, 91, 307-311.	0.3	104
152	Reliability of Genomic Predictions Across Multiple Populations. <i>Genetics</i> , 2009, 183, 1545-1553.	1.2	280
153	A novel predictor of multilocus haplotype homozygosity: comparison with existing predictors. <i>Genetical Research</i> , 2009, 91, 413-426.	0.3	31
154	<i>Haemonchus contortus</i> and <i>Trichostrongylus colubriformis</i> did not adapt to long-term exposure to sheep that were genetically resistant or susceptible to nematode infections. <i>International Journal for Parasitology</i> , 2009, 39, 607-614.	1.3	37
155	A note on permutation tests for genetic association analysis of quantitative traits when variances are heterogeneous. <i>Genetic Epidemiology</i> , 2009, 33, 710-716.	0.6	0
156	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.	0.6	104
157	Mapping genes for complex traits in domestic animals and their use in breeding programmes. <i>Nature Reviews Genetics</i> , 2009, 10, 381-391.	7.7	1,053
158	Genetic evaluation of Australian dairy cattle for somatic cell scores using multi-trait random regression test-day model. <i>Journal of Animal Breeding and Genetics</i> , 2009, 126, 209-215.	0.8	3
159	Increased accuracy of artificial selection by using the realized relationship matrix. <i>Genetical Research</i> , 2009, 91, 47-60.	0.3	544
160	Invited review: Genomic selection in dairy cattle: Progress and challenges. <i>Journal of Dairy Science</i> , 2009, 92, 433-443.	1.4	1,359
161	Increased accuracy of artificial selection by using the realized relationship matrix: Erratum. <i>Genetical Research</i> , 2009, 91, 143-143.	0.3	4
162	Estimating Effects and Making Predictions from Genome-Wide Marker Data. <i>Statistical Science</i> , 2009, 24, .	1.6	127

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163	Prediction of individual genetic risk of complex disease. <i>Current Opinion in Genetics and Development</i> , 2008, 18, 257-263.	1.5	147
164	Holstein-Friesian Dairy Cows Under a Predominantly Grazing System: Interaction Between Genotype and Environment. <i>Journal of Dairy Science</i> , 2008, 91, 826-839.	1.4	55
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