

Ben Hayes

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5079742/publications.pdf>

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	Genomic diversity and breed composition of Vietnamese smallholder dairy cows. <i>Journal of Animal Breeding and Genetics</i> , 2022, 139, 145-160.	2.0	3
2	Technical note: overcoming host contamination in bovine vaginal metagenomic samples with nanopore adaptive sequencing. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	10
3	Sleep in an At Risk Adolescent Group: A Qualitative Exploration of the Perspectives, Experiences and Needs of Youth Who Have Been Excluded From Mainstream Education. <i>Inquiry (United States)</i> , 2022, 59, 004695802110624.	0.9	0
4	Extensive Variation in Gene Expression is Revealed in 13 Fertility-Related Genes Using RNA-Seq, ISO-Seq, and CAGE-Seq From Brahman Cattle. <i>Frontiers in Genetics</i> , 2022, 13, 784663.	2.3	4
5	Genetic variation in <i>PLAG1</i> is associated with early fertility in Australian Brahman cattle. <i>Journal of Animal Science</i> , 2022, 100, .	0.5	5
6	Genomics applied to livestock and aquaculture breeding. <i>Evolutionary Applications</i> , 2022, 15, 517-522.	3.1	11
7	Transcriptional changes in the peripheral blood leukocytes from Brangus cattle before and after tick challenge with <i>Rhipicephalus australis</i> . <i>BMC Genomics</i> , 2022, 23, .	2.8	3
8	Characteristics of Cowsheds in Vietnamese Smallholder Dairy Farms and Their Associations with Microclimate—A Preliminary Study. <i>Animals</i> , 2021, 11, 351.	2.3	12
9	Breed-adjusted genomic relationship matrices as a method to account for population stratification in multibreed populations of tropically adapted beef heifers. <i>Animal Production Science</i> , 2021, , .	1.3	1
10	Genetic parameter estimates for male and female fertility traits using genomic data to improve fertility in Australian beef cattle. <i>Animal Production Science</i> , 2021, , .	1.3	7
11	Investigating the Effect of Imputed Structural Variants from Whole-Genome Sequence on Genome-Wide Association and Genomic Prediction in Dairy Cattle. <i>Animals</i> , 2021, 11, 541.	2.3	12
12	Accuracy of genomic prediction of complex traits in sugarcane. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1455-1462.	3.6	26
13	Strategies and considerations for implementing genomic selection to improve traits with additive and non-additive genetic architectures in sugarcane breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1493-1511.	3.6	16
14	Imputation accuracy to whole-genome sequence in Nellore cattle. <i>Genetics Selection Evolution</i> , 2021, 53, 27.	3.0	17
15	Issues of Feeding Strategy for Lactating Cows in Vietnamese Smallholder Dairy Farms. <i>Animals</i> , 2021, 11, 729.	2.3	3
16	Comparison of Genetic Merit for Weight and Meat Traits between the Polled and Horned Cattle in Multiple Beef Breeds. <i>Animals</i> , 2021, 11, 870.	2.3	6
17	Assessment of Performance and Some Welfare Indicators of Cows in Vietnamese Smallholder Dairy Farms. <i>Animals</i> , 2021, 11, 674.	2.3	6
18	Improved genomic prediction of clonal performance in sugarcane by exploiting non-additive genetic effects. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2235-2252.	3.6	27

#	ARTICLE	IF	CITATIONS
19	Variants at the ASIP locus contribute to coat color darkening in Nellore cattle. <i>Genetics Selection Evolution</i> , 2021, 53, 40.	3.0	25
20	Genomic selection and genetic gain for nut yield in an Australian macadamia breeding population. <i>BMC Genomics</i> , 2021, 22, 370.	2.8	13
21	Interrogating the bovine reproductive tract metagenomes using culture-independent approaches: a systematic review. <i>Animal Microbiome</i> , 2021, 3, 41.	3.8	22
22	Multiple Country and Breed Genomic Prediction of Tick Resistance in Beef Cattle. <i>Frontiers in Immunology</i> , 2021, 12, 620847.	4.8	14
23	Evolution of tissue and developmental specificity of transcription start sites in <i>Bos taurus indicus</i> . <i>Communications Biology</i> , 2021, 4, 829.	4.4	2
24	Prowler: a novel trimming algorithm for Oxford Nanopore sequence data. <i>Bioinformatics</i> , 2021, 37, 3936-3937.	4.1	11
25	A linkage disequilibrium-based approach to position unmapped SNPs in crop species. <i>BMC Genomics</i> , 2021, 22, 773.	2.8	7
26	Feed Preference Response of Weaner Bull Calves to <i>Bacillus amyloliquefaciens</i> H57 Probiotic and Associated Volatile Organic Compounds in High Concentrate Feed Pellets. <i>Animals</i> , 2021, 11, 51.	2.3	6
27	An Epigenetic Aging Clock for Cattle Using Portable Sequencing Technology. <i>Frontiers in Genetics</i> , 2021, 12, 760450.	2.3	11
28	Challenges and Opportunities in Applying Genomic Selection to Ruminants Owned by Smallholder Farmers. <i>Agriculture (Switzerland)</i> , 2021, 11, 1172.	3.1	8
29	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	106
30	Genomic prediction using low-coverage portable Nanopore sequencing. <i>PLoS ONE</i> , 2021, 16, e0261274.	2.5	10
31	Across-breed validation study confirms and identifies new loci associated with sexual precocity in Brahman and Nellore cattle. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 139-154.	2.0	2
32	Multi-environment analysis of sorghum breeding trials using additive and dominance genomic relationships. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1009-1018.	3.6	13
33	The impact of reduced sleep on school related outcomes for typically developing children aged 11-19: A systematic review. <i>School Psychology International</i> , 2020, 41, 569-594.	1.9	10
34	Optimized Genetic Testing for Polledness in Multiple Breeds of Cattle. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 539-544.	1.8	12
35	Genetic control of temperament traits across species: association of autism spectrum disorder risk genes with cattle temperament. <i>Genetics Selection Evolution</i> , 2020, 52, 51.	3.0	25
36	Using prior information from humans to prioritize genes and gene-associated variants for complex traits in livestock. <i>PLoS Genetics</i> , 2020, 16, e1008780.	3.5	10

#	ARTICLE	IF	CITATIONS
37	X chromosome variants are associated with male fertility traits in two bovine populations. <i>Genetics Selection Evolution</i> , 2020, 52, 46.	3.0	16
38	Genomic predictions for enteric methane production are improved by metabolome and microbiome data in sheep (<i>Ovis aries</i>). <i>Journal of Animal Science</i> , 2020, 98, .	0.5	4
39	The Future of Livestock Management: A Review of Real-Time Portable Sequencing Applied to Livestock. <i>Genes</i> , 2020, 11, 1478.	2.4	9
40	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
41	Selection signatures in tropical cattle are enriched for promoter and coding regions and reveal missense mutations in the damage response gene HELB. <i>Genetics Selection Evolution</i> , 2020, 52, 27.	3.0	17
42	Use of whole-genome sequence data and novel genomic selection strategies to improve selection for age at puberty in tropically-adapted beef heifers. <i>Genetics Selection Evolution</i> , 2020, 52, 28.	3.0	22
43	What are the experiences of education for unaccompanied asylum-seeking minors in the UK?. <i>Child: Care, Health and Development</i> , 2020, 46, 414-421.	1.7	6
44	Genome-wide association studies for yield component traits in a macadamia breeding population. <i>BMC Genomics</i> , 2020, 21, 199.	2.8	25
45	Accelerating Genetic Gain in Sugarcane Breeding Using Genomic Selection. <i>Agronomy</i> , 2020, 10, 585.	3.0	60
46	Characterization of the poll allele in Brahman cattle using long-read Oxford Nanopore sequencing. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	10
47	Title is missing!. , 2020, 16, e1008780.		0
48	Title is missing!. , 2020, 16, e1008780.		0
49	Title is missing!. , 2020, 16, e1008780.		0
50	Title is missing!. , 2020, 16, e1008780.		0
51	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
52	Unraveling genetic sensitivity of beef cattle to environmental variation under tropical conditions. <i>Genetics Selection Evolution</i> , 2019, 51, 29.	3.0	35
53	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
54	The Impact of Genomic and Traditional Selection on the Contribution of Mutational Variance to Long-Term Selection Response and Genetic Variance. <i>Genetics</i> , 2019, 213, 361-378.	2.9	8

#	ARTICLE	IF	CITATIONS
55	Quantifying the contribution of sequence variants with regulatory and evolutionary significance to 34 bovine complex traits. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19398-19408.	7.1	99
56	â€œSpeedGSâ€•to Accelerate Genetic Gain in Spring Wheat. , 2019, , 303-327.		35
57	Breeding crops to feed 10 billion. Nature Biotechnology, 2019, 37, 744-754.	17.5	577
58	Breeding improves wheat productivity under contrasting agrochemical input levels. Nature Plants, 2019, 5, 706-714.	9.3	194
59	A real-world application of Social Stories as an intervention for children with communication and behaviour difficulties. Emotional and Behavioural Difficulties, 2019, 24, 323-338.	1.2	3
60	Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome. Nature Genetics, 2019, 51, 896-904.	21.4	225
61	Overlap between eQTL and QTL associated with production traits and fertility in dairy cattle. BMC Genomics, 2019, 20, 291.	2.8	25
62	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans. Genetics, 2019, 211, 1131-1141.	2.9	99
63	Population structure, genetic diversity and linkage disequilibrium in a macadamia breeding population using SNP and silicoDArT markers. Tree Genetics and Genomes, 2019, 15, 1.	1.6	19
64	Fine-mapping sequence mutations with a major effect on oligosaccharide content in bovine milk. Scientific Reports, 2019, 9, 2137.	3.3	13
65	Boosting Genetic Gain in Allogamous Crops via Speed Breeding and Genomic Selection. Frontiers in Plant Science, 2019, 10, 1364.	3.6	35
66	Accelerating crop genetic gains with genomic selection. Theoretical and Applied Genetics, 2019, 132, 669-686.	3.6	218
67	Prediction of genetic value for sweet cherry fruit maturity among environments using a 6K SNP array. Horticulture Research, 2019, 6, 6.	6.3	25
68	Towards multi-breed genomic evaluations for female fertility of tropical beef cattle1. Journal of Animal Science, 2019, 97, 55-62.	0.5	32
69	1000 Bull Genomes Project to Map Simple and Complex Genetic Traits in Cattle: Applications and Outcomes. Annual Review of Animal Biosciences, 2019, 7, 89-102.	7.4	241
70	Harnessing genomic information for livestock improvement. Nature Reviews Genetics, 2019, 20, 135-156.	16.3	262
71	Multivariate genomic predictions for age at puberty in tropically adapted beef heifers1. Journal of Animal Science, 2019, 97, 90-100.	0.5	10
72	Selecting for Nut Characteristics in Macadamia Using a Genome-wide Association Study. Hortscience: A Publication of the American Society for Horticultural Science, 2019, 54, 629-632.	1.0	12

#	ARTICLE	IF	CITATIONS
73	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
74	Mammalian genomic regulatory regions predicted by utilizing human genomics, transcriptomics, and epigenetics data. <i>GigaScience</i> , 2018, 7, 1-17.	6.4	27
75	Prospects for increasing yield in macadamia using component traits and genomics. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	21
76	Variance explained by whole genome sequence variants in coding and regulatory genome annotations for six dairy traits. <i>BMC Genomics</i> , 2018, 19, 237.	2.8	19
77	Insights into population genetics and evolution of polyploids and their ancestors. <i>Molecular Ecology Resources</i> , 2018, 18, 1157-1172.	4.8	16
78	The cost-benefit of genomic testing of heifers and using sexed semen in pasture-based dairy herds. <i>Journal of Dairy Science</i> , 2018, 101, 6159-6173.	3.4	13
79	Responses of dairy cows with divergent residual feed intake as calves to metabolic challenges during midlactation and the nonlactating period. <i>Journal of Dairy Science</i> , 2018, 101, 6474-6485.	3.4	9
80	Benchmarking Bayesian genome enabled-prediction models for age at first calving in Nellore cows. <i>Livestock Science</i> , 2018, 211, 75-79.	1.6	9
81	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
82	Variation in floral and growth traits in a macadamia breeding population. <i>Acta Horticulturae</i> , 2018, , 623-630.	0.2	0
83	Candidate mutations used to aid the prediction of genetic merit for female reproductive traits in tropical beef cattle. <i>Revista Brasileira De Zootecnia</i> , 2018, 47, .	0.8	4
84	Sequencing the mosaic genome of Brahman cattle identifies historic and recent introgression including polled. <i>Scientific Reports</i> , 2018, 8, 17761.	3.3	39
85	An initiator codon mutation in SDE2 causes recessive embryonic lethality in Holstein cattle. <i>Journal of Dairy Science</i> , 2018, 101, 6220-6231.	3.4	23
86	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
87	Genome variants associated with RNA splicing variations in bovine are extensively shared between tissues. <i>BMC Genomics</i> , 2018, 19, 521.	2.8	34
88	A multi-trait Bayesian method for mapping QTL and genomic prediction. <i>Genetics Selection Evolution</i> , 2018, 50, 10.	3.0	32
89	Development of Genomic Prediction in Sorghum. <i>Crop Science</i> , 2018, 58, 690-700.	1.8	31
90	Genomic prediction of reproduction traits for Merino sheep. <i>Animal Genetics</i> , 2017, 48, 338-348.	1.7	11

#	ARTICLE	IF	CITATIONS
91	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
92	Detection and assessment of copy number variation using PacBio long-read and Illumina sequencing in New Zealand dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 5472-5478.	3.4	17
93	Exome sequence genotype imputation in globally diverse hexaploid wheat accessions. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1393-1404.	3.6	25
94	Responses of dairy cows to short-term heat stress in controlled-climate chambers. <i>Animal Production Science</i> , 2017, 57, 1233.	1.3	67
95	Partitioning of energy and nitrogen in lactating primiparous and multiparous Holstein-Friesian cows with divergent residual feed intake. <i>Animal Production Science</i> , 2017, 57, 1499.	1.3	7
96	Optimizing Resource Allocation in a Genomic Breeding Program for Perennial Ryegrass to Balance Genetic Gain, Cost, and Inbreeding. <i>Crop Science</i> , 2017, 57, 243-252.	1.8	27
97	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
98	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
99	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
100	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
101	Detection and validation of structural variations in bovine whole-genome sequence data. <i>Genetics Selection Evolution</i> , 2017, 49, 13.	3.0	27
102	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
103	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
104	Multi-breed genomic prediction using Bayes R with sequence data and dropping variants with a small effect. <i>Genetics Selection Evolution</i> , 2017, 49, 70.	3.0	29
105	Exploring and Harnessing Haplotype Diversity to Improve Yield Stability in Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 1534.	3.6	86
106	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.	2.8	17
107	Breeding Differently—the Digital Revolution: High-Throughput Phenotyping and Genotyping. <i>Potato Research</i> , 2017, 60, 337-352.	2.7	11
108	A practical future-scenarios selection tool to breed for heat tolerance in Australian dairy cattle. <i>Animal Production Science</i> , 2017, 57, 1488.	1.3	7

#	ARTICLE	IF	CITATIONS
109	Evaluating the ability of a lifetime nutrient-partitioning model for simulating the performance of Australian Holstein dairy cows. <i>Animal Production Science</i> , 2017, 57, 1563.	1.3	0
110	Estimated allele substitution effects underlying genomic evaluation models depend on the scaling of allele counts. <i>Genetics Selection Evolution</i> , 2017, 49, 79.	3.0	9
111	Leveraging genetically simple traits to identify small-effect variants for complex phenotypes. <i>BMC Genomics</i> , 2016, 17, 858.	2.8	42
112	Genomic selection: A paradigm shift in animal breeding. <i>Animal Frontiers</i> , 2016, 6, 6-14.	1.7	332
113	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
114	Genomewide association study of methane emissions in Angus beef cattle with validation in dairy cattle1. <i>Journal of Animal Science</i> , 2016, 94, 4151-4166.	0.5	41
115	Improving the selection efficiency in potato breeding. <i>Acta Horticulturae</i> , 2016, , 237-242.	0.2	4
116	Models for Genome Ã— Environment Interaction: Examples in Livestock. <i>Crop Science</i> , 2016, 56, 2251-2259.	1.8	43
117	Improving Genetic Gain with Genomic Selection in Autotetraploid Potato. <i>Plant Genome</i> , 2016, 9, plantgenome2016.02.0021.	2.8	115
118	Genomic Selection Improves Heat Tolerance in Dairy Cattle. <i>Scientific Reports</i> , 2016, 6, 34114.	3.3	112
119	Genomic heritabilities and genomic estimated breeding values for methane traits in Angus cattle1. <i>Journal of Animal Science</i> , 2016, 94, 902-908.	0.5	43
120	Genomic selection for tolerance to heat stress in Australian dairy cattle. <i>Journal of Dairy Science</i> , 2016, 99, 2849-2862.	3.4	143
121	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
122	Genetics of complex traits: prediction of phenotype, identification of causal polymorphisms and genetic architecture. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2016, 283, 20160569.	2.6	118
123	Polyceraty (multiâ€œhorns) in Damara sheep maps to ovine chromosome 2. <i>Animal Genetics</i> , 2016, 47, 263-266.	1.7	15
124	<sc>GO</sc>â€œ<sc>FAANG</sc> meeting: a Gathering On Functional Annotation of <sc>An</sc>imal Genomes. <i>Animal Genetics</i> , 2016, 47, 528-533.	1.7	65
125	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
126	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

#	ARTICLE	IF	CITATIONS
127	Detailed phenotyping identifies genes with pleiotropic effects on body composition. BMC Genomics, 2016, 17, 224.	2.8	52
128	Technical note: Equivalent genomic models with a residual polygenic effect. Journal of Dairy Science, 2016, 99, 2016-2025.	3.4	24
129	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. Biology of Reproduction, 2016, 94, 19.	2.7	53
130	Reducing the carbon footprint of Australian milk production by mitigation of enteric methane emissions. Animal Production Science, 2016, 56, 1017.	1.3	42
131	Targeted imputation of sequence variants and gene expression profiling identifies twelve candidate genes associated with lactation volume, composition and calving interval in dairy cattle. Mammalian Genome, 2016, 27, 81-97.	2.2	75
132	Animal board invited review: genetic possibilities to reduce enteric methane emissions from ruminants. Animal, 2015, 9, 1431-1440.	3.3	119
133	Design of a low-density SNP chip for the main Australian sheep breeds and its effect on imputation and genomic prediction accuracy. Animal Genetics, 2015, 46, 544-556.	1.7	38
134	A computationally efficient algorithm for genomic prediction using a Bayesian model. Genetics Selection Evolution, 2015, 47, 34.	3.0	23
135	Accuracy of genotype imputation based on random and selected reference sets in purebred and crossbred sheep populations and its effect on accuracy of genomic prediction. Genetics Selection Evolution, 2015, 47, 97.	3.0	28
136	Extensive variation between tissues in allele specific expression in an outbred mammal. BMC Genomics, 2015, 16, 993.	2.8	86
137	A catalogue of novel bovine long noncoding RNA across 18 tissues. PLoS ONE, 2015, 10, e0141225.	2.5	130
138	Rare Variants in Transcript and Potential Regulatory Regions Explain a Small Percentage of the Missing Heritability of Complex Traits in Cattle. PLoS ONE, 2015, 10, e0143945.	2.5	16
139	Simultaneous Discovery, Estimation and Prediction Analysis of Complex Traits Using a Bayesian Mixture Model. PLoS Genetics, 2015, 11, e1004969.	3.5	339
140	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
141	Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. Genetics Selection Evolution, 2015, 47, 26.	3.0	56
142	Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project. Genome Biology, 2015, 16, 57.	8.8	331
143	Impact of QTL properties on the accuracy of multi-breed genomic prediction. Genetics Selection Evolution, 2015, 47, 42.	3.0	49
144	Including overseas performance information in genomic evaluations of Australian dairy cattle. Journal of Dairy Science, 2015, 98, 3443-3459.	3.4	21

#	ARTICLE	IF	CITATIONS
145	Two-Variance-Component Model Improves Genetic Prediction in Family Datasets. <i>American Journal of Human Genetics</i> , 2015, 97, 677-690.	6.2	26
146	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
147	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
148	How old are quantitative trait loci and how widely do they segregate?. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 121-134.	2.0	31
149	Validation of markers with non-additive effects on milk yield and fertility in Holstein and Jersey cows. <i>BMC Genetics</i> , 2015, 16, 89.	2.7	17
150	Characterizing homozygosity across United States, New Zealand and Australian Jersey cow and bull populations. <i>BMC Genomics</i> , 2015, 16, 187.	2.8	22
151	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
152	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
153	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.	3.4	6
154	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
155	Thermoregulatory differences in lactating dairy cattle classed as efficient or inefficient based on residual feed intake. <i>Animal Production Science</i> , 2014, 54, 1877.	1.3	20
156	Linkage disequilibrium over short physical distances measured in sheep using a high-density SNP chip. <i>Animal Genetics</i> , 2014, 45, 754-757.	1.7	113
157	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
158	Accuracy of imputation to whole-genome sequence data in Holstein Friesian cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 41.	3.0	128
159	Selection Signatures in Worldwide Sheep Populations. <i>PLoS ONE</i> , 2014, 9, e103813.	2.5	197
160	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
161	An independent validation association study of carcass quality, shear force, intramuscular fat percentage and omega-3 polyunsaturated fatty acid content with gene markers in Australian lamb. <i>Meat Science</i> , 2014, 96, 1025-1033.	5.5	18
162	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

#	ARTICLE	IF	CITATIONS
163	Genomic selection in crops, trees and forages: a review. <i>Crop and Pasture Science</i> , 2014, 65, 1177.	1.5	128
164	Genomic selection for feed efficiency in dairy cattle. <i>Animal</i> , 2014, 8, 1-10.	3.3	98
165	Improving breeding efficiency in potato using molecular and quantitative genetics. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2279-2292.	3.6	74
166	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
167	Multibreed genome wide association can improve precision of mapping causative variants underlying milk production in dairy cattle. <i>BMC Genomics</i> , 2014, 15, 62.	2.8	105
168	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
169	Genomic prediction for rust resistance in diverse wheat landraces. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1795-1803.	3.6	114
170	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
171	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
172	Selection for complex traits leaves little or no classic signatures of selection. <i>BMC Genomics</i> , 2014, 15, 246.	2.8	124
173	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
174	Short communication: Validation of genomic breeding value predictions for feed intake and feed efficiency traits. <i>Journal of Dairy Science</i> , 2014, 97, 537-542.	3.4	18
175	Imputation of genotypes from low density (50,000 markers) to high density (700,000 markers) of cows from research herds in Europe, North America, and Australasia using 2 reference populations. <i>Journal of Dairy Science</i> , 2014, 97, 1799-1811.	3.4	29
176	Incorporating heifer feed efficiency in the Australian selection index using genomic selection. <i>Journal of Dairy Science</i> , 2014, 97, 3883-3893.	3.4	31
177	Whole-tract dry matter and nitrogen digestibility of lactating dairy cows selected for phenotypic divergence in residual feed intake. <i>Animal Production Science</i> , 2014, 54, 1460.	1.3	6
178	Resources and strategies for implementation of genomic selection in breeding of forage species. <i>Crop and Pasture Science</i> , 2014, 65, 1238.	1.5	17
179	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
180	Use of molecular technologies for the advancement of animal breeding: genomic selection in dairy cattle populations in Australia, Ireland and New Zealand. <i>Animal Production Science</i> , 2013, 53, 869.	1.3	30

#	ARTICLE	IF	CITATIONS
181	The symbiotic rumen microbiome and cattle performance: a brief review. <i>Animal Production Science</i> , 2013, 53, 876.	1.3	13
182	Author reply to A commentary on Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 894-894.	16.3	6
183	Genes of the RNASE5 pathway contain SNP associated with milk production traits in dairy cattle. <i>Genetics Selection Evolution</i> , 2013, 45, 25.	3.0	21
184	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
185	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
186	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013, 14, 507-515.	16.3	617
187	Prospects for genomic selection in forage plant species. <i>Plant Breeding</i> , 2013, 132, 133-143.	1.9	125
188	Accelerating Improvement of Livestock with Genomic Selection. <i>Annual Review of Animal Biosciences</i> , 2013, 1, 221-237.	7.4	258
189	Overview of Statistical Methods for Genome-Wide Association Studies (GWAS). <i>Methods in Molecular Biology</i> , 2013, 1019, 149-169.	0.9	127
190	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
191	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
192	Latent Biochemical Relationships in the Bloodâ€™Milk Metabolic Axis of Dairy Cows Revealed by Statistical Integration of ¹ H NMR Spectroscopic Data. <i>Journal of Proteome Research</i> , 2013, 12, 1428-1435.	3.7	23
193	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
194	Metagenomics of rumen bacteriophage from thirteen lactating dairy cattle. <i>BMC Microbiology</i> , 2013, 13, 242.	3.3	51
195	Metagenomic Predictions: From Microbiome to Complex Health and Environmental Phenotypes in Humans and Cattle. <i>PLoS ONE</i> , 2013, 8, e73056.	2.5	103
196	A review of how dairy farmers can use and profit from genomic technologies. <i>Animal Production Science</i> , 2012, 52, 180.	1.3	31
197	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
198	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

#	ARTICLE	IF	CITATIONS
199	Design and phenotyping procedures for recording wool, skin, parasite resistance, growth, carcass yield and quality traits of the SheepGENOMICS mapping flock. <i>Animal Production Science</i> , 2012, 52, 157.	1.3	24
200	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
201	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
202	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
203	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
204	Discovery and trait association of single nucleotide polymorphisms from gene regions of influence on meat tenderness and long-chain omega-3 fatty acid content in Australian lamb. <i>Animal Production Science</i> , 2012, 52, 591.	1.3	11
205	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
206	High throughput whole rumen metagenome profiling using untargeted massively parallel sequencing. <i>BMC Genetics</i> , 2012, 13, 53.	2.7	68
207	Strategies and utility of imputed SNP genotypes for genomic analysis in dairy cattle. <i>BMC Genomics</i> , 2012, 13, 538.	2.8	68
208	Genome position specific priors for genomic prediction. <i>BMC Genomics</i> , 2012, 13, 543.	2.8	38
209	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
210	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
211	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
212	Accuracy of genotype imputation in sheep breeds. <i>Animal Genetics</i> , 2012, 43, 72-80.	1.7	98
213	A single nucleotide polymorphism on chromosome 10 is highly predictive for the polled phenotype in Australian Merino sheep. <i>Animal Genetics</i> , 2012, 43, 468-470.	1.7	31
214	Design of a Bovine Low-Density SNP Array Optimized for Imputation. <i>PLoS ONE</i> , 2012, 7, e34130.	2.5	159
215	Polymorphic Regions Affecting Human Height Also Control Stature in Cattle. <i>Genetics</i> , 2011, 187, 981-984.	2.9	154
216	Molecular characterization of a long range haplotype affecting protein yield and mastitis susceptibility in Norwegian Red cattle. <i>BMC Genetics</i> , 2011, 12, 70.	2.7	19

#	ARTICLE	IF	CITATIONS
217	Genetic parameters for growth and survival in <i>Penaeus monodon</i> cultured in India. <i>Aquaculture</i> , 2011, 318, 74-78.	3.5	37
218	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
219	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
220	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
221	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
222	Use of a microsatellite-based pedigree in estimation of heritabilities for economic traits in Australian blue mussel, <i>Mytilus galloprovincialis</i> . <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 482-490.	2.0	25
223	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
224	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
225	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
226	Impacts of stock enhancement strategies on the effective population size of Murray cod, <i>Maccullochella peelii</i> , a threatened Australian fish. <i>Fisheries Management and Ecology</i> , 2011, 18, 467-481.	2.0	17
227	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. <i>BMC Genomics</i> , 2011, 12, 318.	2.8	135
228	Recent and historical recombination in the admixed Norwegian Red cattle breed. <i>BMC Genomics</i> , 2011, 12, 33.	2.8	10
229	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
230	Genome-wide association studies for feedlot and growth traits in cattle. <i>Journal of Animal Science</i> , 2011, 89, 1684-1697.	0.5	156
231	Imputation of Missing Genotypes From Sparse to High Density Using Long-Range Phasing. <i>Genetics</i> , 2011, 189, 317-327.	2.9	79
232	Genotype calling and mapping of multisite variants using an Atlantic salmon iSelect SNP array. <i>Bioinformatics</i> , 2011, 27, 303-310.	4.1	66
233	Detection of chromosome segments of zebu and taurine origin and their effect on beef production and growth. <i>Journal of Animal Science</i> , 2011, 89, 2050-2060.	0.5	41
234	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

#	ARTICLE	IF	CITATIONS
235	A genome wide association study for QTL affecting direct and maternal effects of stillbirth and dystocia in cattle. <i>Animal Genetics</i> , 2010, 41, 273-280.	1.7	32
236	Testing options for the commercialization of abalone selective breeding using bioeconomic simulation modelling. <i>Aquaculture Research</i> , 2010, 41, e268-e288.	1.8	13
237	Limited evidence for genetic variation for resistance to the white spot syndrome virus in Indian populations of <i>Penaeus monodon</i> . <i>Aquaculture Research</i> , 2010, 41, e872-e877.	1.8	11
238	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
239	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
240	Genomic selection in livestock populations. <i>Genetical Research</i> , 2010, 92, 413-421.	0.9	90
241	Sensitivity of genomic selection to using different prior distributions. <i>BMC Proceedings</i> , 2010, 4, S5.	1.6	33
242	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
243	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
244	Genetic markers for lactation persistency in primiparous Australian dairy cows. <i>Journal of Dairy Science</i> , 2010, 93, 2202-2214.	3.4	23
245	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
246	Multivariate analysis of a genome-wide association study in dairy cattle. <i>Journal of Dairy Science</i> , 2010, 93, 3818-3833.	3.4	72
247	Deterministic models of breeding scheme designs that incorporate genomic selection. <i>Journal of Dairy Science</i> , 2010, 93, 5455-5466.	3.4	64
248	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
249	Using LASSO to estimate marker effects for Genomic Selection. <i>Italian Journal of Animal Science</i> , 2009, 8, 168-170.	1.9	0
250	A Validated Genome Wide Association Study to Breed Cattle Adapted to an Environment Altered by Climate Change. <i>PLoS ONE</i> , 2009, 4, e6676.	2.5	122
251	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
252	Reliability of Genomic Predictions Across Multiple Populations. <i>Genetics</i> , 2009, 183, 1545-1553.	2.9	280

#	ARTICLE	IF	CITATIONS
253	Sampling strategies for whole genome association studies in aquaculture and outcrossing plant species. <i>Genetical Research</i> , 2009, 91, 367-371.	0.9	5
254	A novel predictor of multilocus haplotype homozygosity: comparison with existing predictors. <i>Genetical Research</i> , 2009, 91, 413-426.	0.9	31
255	Casein haplotypes and their association with milk production traits in Norwegian Red cattle. <i>Genetics Selection Evolution</i> , 2009, 41, 24.	3.0	68
256	Accuracy of genomic breeding values in multi-breed dairy cattle populations. <i>Genetics Selection Evolution</i> , 2009, 41, 51.	3.0	371
257	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
258	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
259	Characterization of a QTL region affecting clinical mastitis and protein yield on BTA6. <i>Animal Genetics</i> , 2009, 40, 701-712.	1.7	19
260	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
261	LASSO with cross-validation for genomic selection. <i>Genetical Research</i> , 2009, 91, 427-436.	0.9	137
262	Increased accuracy of artificial selection by using the realized relationship matrix. <i>Genetical Research</i> , 2009, 91, 47-60.	0.9	544
263	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
264	Gene by environment interactions for production traits in Australian dairy cattle. <i>Journal of Dairy Science</i> , 2009, 92, 4008-4017.	3.4	33
265	Invited review: Genomic selection in dairy cattle: Progress and challenges. <i>Journal of Dairy Science</i> , 2009, 92, 433-443.	3.4	1,359
266	Increased accuracy of artificial selection by using the realized relationship matrix: Erratum. <i>Genetical Research</i> , 2009, 91, 143-143.	0.9	4
267	Identification and characterisation of novel SNP markers in Atlantic cod: Evidence for directional selection. <i>BMC Genetics</i> , 2008, 9, 18.	2.7	112
268	Comparison of casein haplotypes between two geographically distant European dairy goat breeds. <i>Journal of Animal Breeding and Genetics</i> , 2008, 125, 68-72.	2.0	8
269	The origin of selection signatures on bovine chromosome 6. <i>Animal Genetics</i> , 2008, 39, 105-111.	1.7	67
270	Construction of a dense SNP map for bovine chromosome 6 to assist the assembly of the bovine genome sequence. <i>Animal Genetics</i> , 2008, 39, 97-104.	1.7	17

#	ARTICLE	IF	CITATIONS
271	Detection of QTL for growth rate in the blacklip abalone (<i>Haliotis rubra</i> Leach) using selective DNA pooling. <i>Animal Genetics</i> , 2008, 39, 606-614.	1.7	19
272	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
273	Modelling the use of gene expression profiles with selective breeding for improved disease resistance in Atlantic salmon (<i>Salmo salar</i>). <i>Aquaculture</i> , 2008, 285, 38-46.	3.5	19
274	Linkage Disequilibrium and Persistence of Phase in Holstein-Friesian, Jersey and Angus Cattle. <i>Genetics</i> , 2008, 179, 1503-1512.	2.9	439
275	Predicting Unobserved Phenotypes for Complex Traits from Whole-Genome SNP Data. <i>PLoS Genetics</i> , 2008, 4, e1000231.	3.5	175
276	Use of gene expression data for predicting continuous phenotypes for animal production and breeding. <i>Animal</i> , 2008, 2, 1413-1420.	3.3	15
277	Technical note: Prediction of breeding values using marker-derived relationship matrices. <i>Journal of Animal Science</i> , 2008, 86, 2089-2092.	0.5	106
278	SNP detection exploiting multiple sources of redundancy in large EST collections improves validation rates. <i>Bioinformatics</i> , 2007, 23, 1692-1693.	4.1	38
279	Statistical Epistasis Is a Generic Feature of Gene Regulatory Networks. <i>Genetics</i> , 2007, 175, 411-420.	2.9	99
280	Accuracy of marker-assisted selection with single markers and marker haplotypes in cattle. <i>Genetical Research</i> , 2007, 89, 215-220.	0.9	87
281	An extensive resource of single nucleotide polymorphism markers associated with Atlantic salmon (<i>Salmo salar</i>) expressed sequences. <i>Aquaculture</i> , 2007, 265, 82-90.	3.5	110
282	Optimisation of marker assisted selection for abalone breeding programs. <i>Aquaculture</i> , 2007, 265, 61-69.	3.5	32
283	Recent human effective population size estimated from linkage disequilibrium. <i>Genome Research</i> , 2007, 17, 520-526.	5.5	381
284	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
285	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
286	Genomic selection. <i>Journal of Animal Breeding and Genetics</i> , 2007, 124, 323-330.	2.0	595
287	Nonlinear regulation enhances the phenotypic expression of trans-acting genetic polymorphisms. <i>BMC Systems Biology</i> , 2007, 1, 32.	3.0	12
288	Use of molecular markers to maximise diversity of founder populations for aquaculture breeding programs. <i>Aquaculture</i> , 2006, 255, 573-578.	3.5	24

#	ARTICLE	IF	CITATIONS
289	Genomic organization and transcript profiling of the bovine toll-like receptor gene cluster TLR6-TLR1-TLR10. <i>Gene</i> , 2006, 384, 45-50.	2.2	32
290	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
291	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
292	Evaluation of three strategies using DNA markers for traceability in aquaculture species. <i>Aquaculture</i> , 2005, 250, 70-81.	3.5	46
293	Modern Biotechnology and Aquaculture. , 2005, , 301-317.		2
294	Break-even cost of genotyping genetic mutations affecting economic traits in Australian pig enterprises. <i>Livestock Science</i> , 2004, 89, 235-242.	1.2	5
295	Evaluation of marker assisted selection in pig enterprises. <i>Livestock Science</i> , 2003, 81, 197-211.	1.2	32
296	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
297	Novel Multilocus Measure of Linkage Disequilibrium to Estimate Past Effective Population Size. <i>Genome Research</i> , 2003, 13, 635-643.	5.5	398
298	Look ahead mate selection schemes for multi-breed beef populations. <i>Animal Science</i> , 2002, 74, 13-23.	1.3	10
299	The distribution of the effects of genes affecting quantitative traits in livestock. <i>Genetics Selection Evolution</i> , 2001, 33, 209-29.	3.0	301
300	Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. <i>Genetics</i> , 2001, 157, 1819-1829.	2.9	5,963
301	Mate selection strategies to exploit across- and within-breed dominance variation. <i>Journal of Animal Breeding and Genetics</i> , 2000, 117, 347-359.	2.0	16