Flavio S Schenkel

List of Publications by Year
in descending order

		71102	58581
246	8,644	41	82
papers	citations	h-index	g-index
247	247	247	5071
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Invited Review: Reliability of genomic predictions for North American Holstein bulls. Journal of Dairy Science, 2009, 92, 16-24.	3.4	1,008
2	A new approach for efficient genotype imputation using information from relatives. BMC Genomics, 2014, 15, 478.	2.8	760
3	QMSim: a large-scale genome simulator for livestock. Bioinformatics, 2009, 25, 680-681.	4.1	286
4	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	21.4	286
5	Association of single nucleotide polymorphisms in the leptin gene with carcass and meat quality traits of beef cattle1. Journal of Animal Science, 2005, 83, 2009-2020.	0.5	166
6	Genetic parameters and breed differences for feed efficiency, growth, and body composition traits of young beef bulls. Canadian Journal of Animal Science, 2004, 84, 177-185.	1.5	164
7	Selection of single-nucleotide polymorphisms and quality of genotypes used in genomic evaluation of dairy cattle in the United States and Canada. Journal of Dairy Science, 2009, 92, 3431-3436.	3.4	163
8	Extent of Linkage Disequilibrium in Holstein Cattle in North America. Journal of Dairy Science, 2008, 91, 2106-2117.	3.4	148
9	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. BMC Genomics, 2017, 18, 229.	2.8	141
10	Association of a single nucleotide polymorphism in the calpastatin gene with carcass and meat quality traits of beef cattle1. Journal of Animal Science, 2006, 84, 291-299.	0.5	140
11	Application of site and haplotype-frequency based approaches for detecting selection signatures in cattle. BMC Genomics, 2011, 12, 318.	2.8	135
12	Assessing feed efficiency in beef steers through feeding behavior, infrared thermography and glucocorticoids. Animal, 2010, 4, 692-701.	3.3	131
13	Application of infrared thermography as an indicator of heat and methane production and its use in the study of skin temperature in response to physiological events in dairy cattle (Bos taurus). Journal of Thermal Biology, 2008, 33, 468-475.	2.5	125
14	A Genome Scan to Detect Quantitative Trait Loci for Economically Important Traits in Holstein Cattle Using Two Methods and a Dense Single Nucleotide Polymorphism Map. Journal of Dairy Science, 2008, 91, 3225-3236.	3.4	120
15	Characteristics of linkage disequilibrium in North American Holsteins. BMC Genomics, 2010, 11, 421.	2.8	120
16	Genome-wide association study for birth weight in Nellore cattle points to previously described orthologous genes affecting human and bovine height. BMC Genetics, 2013, 14, 52.	2.7	111
17	Genome-wide association for milk production and female fertility traits in Canadian dairy Holstein cattle. BMC Genetics, 2016, 17, 75.	2.7	110
18	Study of whole genome linkage disequilibrium in Nellore cattle. BMC Genomics, 2013, 14, 305.	2.8	106

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19	Characterization of linkage disequilibrium, consistency of gametic phase and admixture in Australian and Canadian goats. BMC Genetics, 2015, 16, 67.	2.7	91
20	Accuracy of genotype imputation in Nelore cattle. Genetics Selection Evolution, 2014, 46, 69.	3.0	86
21	Effect of genomic selection on rate of inbreeding and coancestry and effective population size of Holstein and Jersey cattle populations. Journal of Dairy Science, 2020, 103, 5183-5199.	3.4	85
22	Health recording in Canadian Holsteins: Data and genetic parameters. Journal of Dairy Science, 2012, 95, 4099-4108.	3.4	84
23	The GATK joint genotyping workflow is appropriate for calling variants in RNA-seq experiments. Journal of Animal Science and Biotechnology, 2019, 10, 44.	5.3	83
24	Association of Toll-Like Receptor 4 Polymorphisms with Somatic Cell Score and Lactation Persistency in Holstein Bulls. Journal of Dairy Science, 2006, 89, 3626-3635.	3.4	82
25	A principal component regression based genome wide analysis approach reveals the presence of a novel QTL on BTA7 for MAP resistance in holstein cattle. Genomics, 2010, 95, 176-182.	2.9	80
26	Rates of inbreeding and genetic diversity in Canadian Holstein and Jersey cattle. Journal of Dairy Science, 2011, 94, 5160-5175.	3.4	78
27	A genome-wide association study of immune response traits in Canadian Holstein cattle. BMC Genomics, 2014, 15, 559.	2.8	78
28	Accuracy of genomic predictions in Bos indicus (Nellore) cattle. Genetics Selection Evolution, 2014, 46, 17.	3.0	77
29	Accuracy of genomic selection in simulated populations mimicking the extent of linkage disequilibrium in beef cattle. BMC Genetics, 2011, 12, 80.	2.7	66
30	Alternative somatic cell count traits to improve mastitis resistance in Canadian Holsteins. Journal of Dairy Science, 2012, 95, 432-439.	3.4	57
31	Genome-wide association studies and genomic prediction of breeding values for calving performance and body conformation traits in Holstein cattle. Genetics Selection Evolution, 2017, 49, 82.	3.0	55
32	Genetic analysis of milk β-hydroxybutyrate and its association with fat-to-protein ratio, body condition score, clinical ketosis, and displaced abomasum in early first lactation of Canadian Holsteins. Journal of Dairy Science, 2014, 97, 7286-7292.	3.4	53
33	Genome-Wide Association for Growth Traits in Canchim Beef Cattle. PLoS ONE, 2014, 9, e94802.	2.5	53
34	Accuracy of predicting genomic breeding values for residual feed intake in Angus and Charolais beef cattle1. Journal of Animal Science, 2013, 91, 4669-4678.	0.5	52
35	Genome-wide association study for lactation persistency, female fertility, longevity, and lifetime profit index traits in Holstein dairy cattle. Journal of Dairy Science, 2017, 100, 1246-1258.	3.4	51
36	Breeding for reduced methane emission and feed-efficient Holstein cows: An international response. Journal of Dairy Science, 2021, 104, 8983-9001.	3.4	49

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37	Linkage disequilibrium and haplotype block structure in a composite beef cattle breed. BMC Genomics, 2014, 15, S6.	2.8	48
38	Prediction of genomic breeding values for growth, carcass and meat quality traits in a multi-breed sheep population using a HD SNP chip. BMC Genetics, 2017, 18, 7.	2.7	48
39	Genetic diversity of a New Zealand multi-breed sheep population and composite breeds' history revealed by a high-density SNP chip. BMC Genetics, 2017, 18, 25.	2.7	47
40	Extent of linkage disequilibrium, consistency of gametic phase, and imputation accuracy within and across Canadian dairy breeds. Journal of Dairy Science, 2014, 97, 3128-3141.	3.4	46
41	Invited review: Advances and applications of random regression models: From quantitative genetics to genomics. Journal of Dairy Science, 2019, 102, 7664-7683.	3.4	46
42	Application of single-step genomic evaluation using multiple-trait random regression test-day models in dairy cattle. Journal of Dairy Science, 2019, 102, 2365-2377.	3.4	45
43	Genetics and genomics of reproductive disorders in Canadian Holstein cattle. Journal of Dairy Science, 2019, 102, 1341-1353.	3.4	44
44	Impact of Genotype Imputation on the Performance of GBLUP and Bayesian Methods for Genomic Prediction. PLoS ONE, 2014, 9, e101544.	2.5	43
45	Identification of single nucleotide polymorphisms in bovine CARD15 and their associations with health and production traits in Canadian Holsteins. BMC Genomics, 2007, 8, 421.	2.8	42
46	Genetic relationships of clinical mastitis, cystic ovaries, and lameness with milk yield and somatic cell score in first-lactation Canadian Holsteins. Journal of Dairy Science, 2014, 97, 5806-5813.	3.4	42
47	Genome-wide association for milk production traits and somatic cell score in different lactation stages of Ayrshire, Holstein, and Jersey dairy cattle. Journal of Dairy Science, 2019, 102, 8159-8174.	3.4	42
48	Identification of single nucleotide polymorphisms in the bovine CCL2, IL8, CCR2 and IL8RA genes and their association with health and production in Canadian Holsteins. Animal Genetics, 2007, 38, 198-202.	1.7	41
49	Polymorphisms in the 5â€² Upstream Region of the CXCR1 Chemokine Receptor Gene, and Their Association with Somatic Cell Score in Holstein Cattle in Canada. Journal of Dairy Science, 2008, 91, 407-417.	3.4	41
50	Effect of recent and ancient inbreeding on production and fertility traits in Canadian Holsteins. BMC Genomics, 2020, 21, 605.	2.8	39
51	Genomewide Association Analyses of Lactation Persistency and Milk Production Traits in Holstein Cattle Based on Imputed Whole-Genome Sequence Data. Genes, 2021, 12, 1830.	2.4	39
52	The relationship between feed efficiency and the circadian profile of blood plasma analytes measured in beef heifers at different physiological stages. Animal, 2014, 8, 1684-1698.	3.3	38
53	A large and diverse collection of bovine genome sequences from the Canadian Cattle Genome Project. GigaScience, 2015, 4, 49.	6.4	38
54	Genetic associations of ketosis and displaced abomasum with milk production traits in early first lactation of Canadian Holsteins. Journal of Dairy Science, 2013, 96, 4688-4696.	3.4	37

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55	Prediction of milk fatty acid content with mid-infrared spectroscopy in Canadian dairy cattle using differently distributed model development sets. Journal of Dairy Science, 2017, 100, 5073-5081.	3.4	37
56	Genetic parameters for various growth, carcass and meat quality traits in a New Zealand sheep population. Small Ruminant Research, 2017, 154, 81-91.	1.2	37
57	Polymorphisms in the gene encoding bovine interleukin-10 receptor alpha are associated with Mycobacterium avium ssp. paratuberculosis infection status. BMC Genetics, 2010, 11, 23.	2.7	36
58	Associations of rumen parameters with feed efficiency and sampling routine in beef cattle. Animal, 2018, 12, 1442-1450.	3.3	36
59	Comparison of genomic predictions for lowly heritable traits using multi-step and single-step genomic best linear unbiased predictor in Holstein cattle. Journal of Dairy Science, 2018, 101, 8076-8086.	3.4	36
60	Genetic analysis of superovulatory response of Holstein cows in Canada. Journal of Dairy Science, 2016, 99, 3612-3623.	3.4	34
61	Accuracy of genomic predictions for feed efficiency traits of beef cattle using 50K and imputed HD genotypes1. Journal of Animal Science, 2016, 94, 1342-1353.	0.5	34
62	Genetic diversity, extent of linkage disequilibrium and persistence of gametic phase in Canadian pigs. BMC Genetics, 2017, 18, 6.	2.7	34
63	Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. PLoS ONE, 2018, 13, e0205295.	2.5	33
64	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. PLoS ONE, 2014, 9, e88561.	2.5	33
65	Bovine *PGLYRP1* polymorphisms and their association with resistance to *Mycobacterium avium* ssp. *paratuberculosis*. Animal Genetics, 2011, 42, 354-360.	1.7	32
66	Genetic parameters for hoof health traits estimated with linear and threshold models using alternative cohorts. Journal of Dairy Science, 2017, 100, 2828-2836.	3.4	31
67	Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. Canadian Journal of Animal Science, 2020, 100, 587-604.	1.5	31
68	Estimated genetic parameters for all genetically evaluated traits in Canadian Holsteins. Journal of Dairy Science, 2021, 104, 9002-9015.	3.4	30
69	Degree of connectedness among groups of centrally tested beef bulls. Canadian Journal of Animal Science, 2004, 84, 37-47.	1.5	29
70	Breed predisposition and heritability of atrial fibrillation in the Standardbred horse: A retrospective case–control study. Journal of Veterinary Cardiology, 2014, 16, 173-184.	0.9	29
71	Genome-wide association analysis for β-hydroxybutyrate concentration in Milk in Holstein dairy cattle. BMC Genetics, 2019, 20, 58.	2.7	29
72	Single-step genome-wide association for longitudinal traits of Canadian Ayrshire, Holstein, and Jersey dairy cattle. Journal of Dairy Science, 2019, 102, 9995-10011.	3.4	29

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73	Genetic Diversity and Signatures of Selection for Thermal Stress in Cattle and Other Two Bos Species Adapted to Divergent Climatic Conditions. Frontiers in Genetics, 2021, 12, 604823.	2.3	29
74	Genetic parameters for methane emission traits in Australian dairy cows. Journal of Dairy Science, 2021, 104, 539-549.	3.4	29
75	Impact of reference population on accuracy of imputation from 6K to 50K single nucleotide polymorphism chips in purebred and crossbreed beef cattle1. Journal of Animal Science, 2014, 92, 1433-1444.	0.5	28
76	Variation in fat globule size in bovine milk and its prediction using mid-infrared spectroscopy. Journal of Dairy Science, 2017, 100, 1640-1649.	3.4	28
77	Accuracy of genome-wide imputation in Braford and Hereford beef cattle. BMC Genetics, 2014, 15, 157.	2.7	27
78	Estimation of genetic effects in the presence of multicollinearity in multibreed beef cattle evaluation1. Journal of Animal Science, 2005, 83, 1788-1800.	0.5	26
79	Review: Genetics of helminth resistance in sheep. Canadian Journal of Animal Science, 2014, 94, 1-9.	1.5	26
80	Genetic analysis of groups of mid-infrared predicted fatty acids in milk. Journal of Dairy Science, 2017, 100, 4731-4744.	3.4	26
81	Comparison between estimation of breeding values and fixed effects using Bayesian and empirical BLUP estimation under selection on parents and missing pedigree information. Genetics Selection Evolution, 2002, 34, 41-59.	3.0	25
82	Genome wide association study identifies novel potential candidate genes for bovine milk cholesterol content. Scientific Reports, 2018, 8, 13239.	3.3	25
83	Generalized genetic association study with samples of related individuals. Annals of Applied Statistics, 2011, 5, .	1.1	24
84	Analyses of genetic diversity in five <scp>C</scp>anadian dairy breeds using pedigree data. Journal of Animal Breeding and Genetics, 2013, 130, 476-486.	2.0	23
85	Association of <i><scp>TLR</scp>4</i> polymorphisms with <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> infection status in Canadian Holsteins. Animal Genetics, 2015, 46, 560-565.	1.7	23
86	Genomic selection for meat quality traits in Nelore cattle. Meat Science, 2019, 148, 32-37.	5.5	23
87	The dynamic behavior of feed efficiency in primiparous dairy cattle. Journal of Dairy Science, 2020, 103, 1528-1540.	3.4	23
88	Two-step and random regression analyses of weight gain of station-tested beef bulls1. Journal of Animal Science, 2002, 80, 1497-1507.	0.5	22
89	Analysis of genetic diversity in four Canadian swine breeds using pedigree data. Canadian Journal of Animal Science, 2010, 90, 331-340.	1.5	22
90	Linear and <scp>P</scp>oisson models for genetic evaluation of tick resistance in cross‐bred <scp>H</scp>ereford x <scp>N</scp>ellore cattle. Journal of Animal Breeding and Genetics, 2013, 130, 417-424.	2.0	22

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91	The genetic architecture of milk ELISA scores as an indicator of Johne's disease (paratuberculosis) in dairy cattle. Journal of Dairy Science, 2018, 101, 10062-10075.	3.4	22
92	Estimation of direct and maternal genetic parameters for individual birth weight, weaning weight, and probe weight in Yorkshire and Landrace pigs1. Journal of Animal Science, 2018, 96, 2567-2578.	0.5	22
93	Data de desmame e desempenho reprodutivo de vacas de corte. Revista Brasileira De Zootecnia, 2002, 31, 1223-1229.	0.8	21
94	Additive, dominance, and epistatic loss effects on preweaning weight gain of crossbred beef cattle from different Bos taurus breeds1. Journal of Animal Science, 2005, 83, 1780-1787.	0.5	20
95	SNPs in the bovine IL-10 receptor are associated with somatic cell score in Canadian dairy bulls. Mammalian Genome, 2009, 20, 447-454.	2.2	20
96	Assessing the value of phenotypic information from non-genotyped animals for QTL mapping of complex traits in real and simulated populations. BMC Genetics, 2016, 17, 89.	2.7	20
97	A comparison of different algorithms for phasing haplotypes using Holstein cattle genotypes and pedigree data. Journal of Dairy Science, 2017, 100, 2837-2849.	3.4	20
98	Genomic prediction of lactation curves for milk, fat, protein, and somatic cell score in Holstein cattle. Journal of Dairy Science, 2019, 102, 452-463.	3.4	20
99	Estimation of additive and non‑additive genetic effects for fertility and reproduction traits in North American Holstein cattle using genomic information. Journal of Animal Breeding and Genetics, 2020, 137, 316-330.	2.0	20
100	Genomic predictions based on haplotypes fitted as pseudo-SNP for milk production and udder type traits and SCS in French dairy goats. Journal of Dairy Science, 2020, 103, 11559-11573.	3.4	20
101	Using imputed whole-genome sequence variants to uncover candidate mutations and genes affecting milking speed and temperament in Holstein cattle. Journal of Dairy Science, 2020, 103, 10383-10398.	3.4	20
102	Efeito de duas cargas animais em campo nativo e de duas idades à desmama no desempenho de vacas de corte primíparas. Revista Brasileira De Zootecnia, 2003, 32, 1722-1731.	0.8	19
103	Analysis of Sus scrofa liver proteome and identification of proteins differentially expressed between genders, and conventional and genetically enhanced lines. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2008, 3, 234-242.	1.0	19
104	Genetic correlations of mid-infrared-predicted milk fatty acid groups with milk production traits. Journal of Dairy Science, 2018, 101, 4295-4306.	3.4	19
105	Implementation of Bayesian methods to identify SNP and haplotype regions with transmission ratio distortion across the whole genome: TRDscan v.1.0. Journal of Dairy Science, 2019, 102, 3175-3188.	3.4	19
106	Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. Journal of Dairy Science, 2021, 104, 1928-1950.	3.4	19
107	Efeitos de Ambiente e de Heterose sobre o Ganho de Peso do Nascimento ao Desmame e sobre os Escores Visuais ao Desmame de Bovinos de Corte. Revista Brasileira De Zootecnia, 2002, 31, 1350-1361.	0.8	18
108	Multi-population genomic prediction using a multi-task Bayesian learning model. BMC Genetics, 2014, 15, 53.	2.7	18

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109	Genomic predictions for economically important traits in Brazilian Braford and Hereford beef cattle using true and imputed genotypes. BMC Genetics, 2017, 18, 2.	2.7	18
110	Genotype imputation from various low-density SNP panels and its impact on accuracy of genomic breeding values in pigs. Animal, 2018, 12, 2235-2245.	3.3	18
111	Analysis of genetic diversity in Brown Swiss, Jersey and Holstein populations using genome-wide single nucleotide polymorphism markers. BMC Research Notes, 2012, 5, 161.	1.4	17
112	Short communication: Genetic parameters for mastitis and its predictors in Canadian Holsteins. Journal of Dairy Science, 2012, 95, 7363-7366.	3.4	17
113	Strategies for genotype imputation in composite beef cattle. BMC Genetics, 2015, 16, 99.	2.7	17
114	Comparing deregression methods for genomic prediction of test‑day traits in dairy cattle. Journal of Animal Breeding and Genetics, 2018, 135, 97-106.	2.0	17
115	Genetic mechanisms underlying spermatic and testicular traits within and among cattle breeds: systematic review and prioritization of GWAS results1. Journal of Animal Science, 2018, 96, 4978-4999.	0.5	17
116	Genome-Wide Association Study for Milk Fatty Acids in Holstein Cattle Accounting for the DGAT1 Gene Effect. Animals, 2019, 9, 997.	2.3	17
117	Genomic analyses for predicted milk fatty acid composition throughout lactation in North American Holstein cattle. Journal of Dairy Science, 2020, 103, 6318-6331.	3.4	17
118	Identifying pleiotropic variants and candidate genes for fertility and reproduction traits in Holstein cattle via association studies based on imputed whole-genome sequence genotypes. BMC Genomics, 2022, 23, 331.	2.8	17
119	Bovine IFNGR2, IL12RB1, IL12RB2, and IL23R polymorphisms and MAP infection status. Mammalian Genome, 2011, 22, 583-588.	2.2	16
120	Persistency of accuracy of genomic breeding values for different simulated pig breeding programs in developing countries. Journal of Animal Breeding and Genetics, 2014, 131, 367-378.	2.0	16
121	Genome-wide association study and in silico functional analysis of the number of embryos produced by Holstein donors. Journal of Dairy Science, 2018, 101, 7248-7257.	3.4	16
122	Single-Step Methodology for Genomic Evaluation in Turkeys (Meleagris gallopavo). Frontiers in Genetics, 2019, 10, 1248.	2.3	16
123	High confidence copy number variants identified in Holstein dairy cattle from whole genome sequence and genotype array data. Scientific Reports, 2020, 10, 8044.	3.3	16
124	Bovine CLEC7A genetic variants and their association with seropositivity in Johne's disease ELISA. Gene, 2014, 537, 302-307.	2.2	15
125	Effect of IGF1, GH, and PIT1 markers on the genetic parameters of growth and reproduction traits in Canchim cattle. Molecular Biology Reports, 2015, 42, 245-251.	2.3	15
126	Assessing haplotype-based models for genomic evaluation in Holstein cattle. Canadian Journal of Animal Science, 2018, 98, 750-759.	1.5	15

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127	Genome-wide association study between copy number variants and hoof health traits in Holstein dairy cattle. Journal of Dairy Science, 2021, 104, 8050-8061.	3.4	15
128	Estimates of heritability of atrial fibrillation in the Standardbred racehorse. Equine Veterinary Journal, 2017, 49, 718-722.	1.7	14
129	A landscape of the heritability of Fourier-transform infrared spectral wavelengths of milk samples by parity and lactation stage in Holstein cows. Journal of Dairy Science, 2019, 102, 1354-1363.	3.4	14
130	Comparison of genomic prediction methods for evaluation of adaptation and productive efficiency traits in Braford and Hereford cattle. Livestock Science, 2020, 231, 103864.	1.6	14
131	Using Random Regression Models to Genetically Evaluate Functional Longevity Traits in North American Angus Cattle. Animals, 2020, 10, 2410.	2.3	14
132	Genome‐wide association study and pathway analysis for fat deposition traits in Nellore cattle raised in pasture‐based systems. Journal of Animal Breeding and Genetics, 2021, 138, 360-378.	2.0	14
133	Identification of unique ROH regions with unfavorable effects on production and fertility traits in Canadian Holsteins. Genetics Selection Evolution, 2021, 53, 68.	3.0	14
134	Genome-wide association study and functional analyses for clinical and subclinical ketosis in Holstein cattle. Journal of Dairy Science, 2021, 104, 10076-10089.	3.4	14
135	Using publicly available weather station data to investigate the effects of heat stress on milk production traits in Canadian Holstein cattle. Canadian Journal of Animal Science, 2022, 102, 368-381.	1.5	14
136	Herd of origin effect on weight gain of station-tested beef bulls. Livestock Science, 2004, 86, 93-103.	1.2	13
137	In-depth pedigree analysis in a large Brazilian Nellore herd. Genetics and Molecular Research, 2013, 12, 5758-5765.	0.2	13
138	Water buffalo genome characterization by the Illumina BovineHD BeadChip. Genetics and Molecular Research, 2014, 13, 4202-4215.	0.2	13
139	Candidate gene association analyses for ketosis resistance in Holsteins. Journal of Dairy Science, 2018, 101, 5240-5249.	3.4	13
140	Use of a single-step approach for integrating foreign information into national genomic evaluation in Holstein cattle. Journal of Dairy Science, 2019, 102, 8175-8183.	3.4	13
141	Optimizing Selection of the Reference Population for Genotype Imputation From Array to Sequence Variants. Frontiers in Genetics, 2019, 10, 510.	2.3	13
142	Johne's Disease in Dairy Cattle: An Immunogenetic Perspective. Frontiers in Veterinary Science, 2021, 8, 718987.	2.2	13
143	Single-step genomic evaluation of milk production traits in Canadian Alpine and Saanen dairy goats. Journal of Dairy Science, 2022, 105, 2393-2407.	3.4	13
144	Estimating the effect of the deleterious recessive haplotypes AH1 and AH2 on reproduction performance of Ayrshire cattle. Journal of Dairy Science, 2019, 102, 5315-5322.	3.4	12

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145	A genetic evaluation of growth, ultrasound, and carcass traits at alternative slaughter endpoints in crossbred heavy lambs1. Journal of Animal Science, 2019, 97, 521-535.	0.5	12
146	Discovering lethal alleles across the turkey genome using a transmission ratio distortion approach. Animal Genetics, 2020, 51, 876-889.	1.7	12
147	Differential gene expression in dairy cows under negative energy balance and ketosis: A systematic review and meta-analysis. Journal of Dairy Science, 2021, 104, 602-615.	3.4	12
148	Genetic relationship among reproductive traits in Nellore cattle. Animal, 2015, 9, 760-765.	3.3	11
149	Study on the introgression of beef breeds in Canchim cattle using single nucleotide polymorphism markers. PLoS ONE, 2017, 12, e0171660.	2.5	11
150	A comprehensive comparison between single- and two-step GBLUP methods in a simulated beef cattle population. Canadian Journal of Animal Science, 2018, 98, 565-575.	1.5	11
151	Genetic parameters for clutch and broodiness traits in turkeys (Meleagris Gallopavo) and their relationship with body weight and egg production. Poultry Science, 2019, 98, 6263-6269.	3.4	11
152	Comprehensive RNA-Seq Profiling Reveals Temporal and Tissue-Specific Changes in Gene Expression in Sprague–Dawley Rats as Response to Heat Stress Challenges. Frontiers in Genetics, 2021, 12, 651979.	2.3	11
153	Short Communication: Genetic association of body condition score with disease resistance in first lactation Canadian Holsteins. Canadian Journal of Animal Science, 2012, 92, 285-289.	1.5	10
154	Heritability of beef tenderness at different aging times and across breed comparisons. Canadian Journal of Animal Science, 2013, 93, 307-312.	1.5	10
155	A genome-wide association study to identify chromosomal regions influencing ovine cortisol response. Livestock Science, 2016, 187, 40-47.	1.6	10
156	Genetic parameters of milk cholesterol content in Holstein cattle. Canadian Journal of Animal Science, 2018, 98, 714-722.	1.5	10
157	Comparison between haplotype–based and individual snp–based genomic predictions for beef fatty acid profile in Nelore cattle. Journal of Animal Breeding and Genetics, 2020, 137, 468-476.	2.0	10
158	Symposium review: Multiple-trait single-step genomic evaluation for hoof health. Journal of Dairy Science, 2020, 103, 5346-5353.	3.4	10
159	Genome-wide association study for beef fatty acid profile using haplotypes in Nellore cattle. Livestock Science, 2021, 245, 104396.	1.6	10
160	Use of Breed-Specific Single Nucleotide Polymorphisms to Discriminate Between Holstein and Jersey Dairy Cattle Breeds. Animal Biotechnology, 2012, 23, 1-10.	1.5	9
161	Association of Apolipoprotein B and Adiponectin Receptor 1 Genes with Carcass, Bone Integrity and Performance Traits in a Paternal Broiler Line. PLoS ONE, 2015, 10, e0136824.	2.5	9
162	Associations of acute stress and overnight heart rate with feed efficiency in beef heifers. Animal, 2017, 11, 452-460.	3.3	9

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163	Novel methods for genotype imputation to whole-genome sequence and a simple linear model to predict imputation accuracy. BMC Genetics, 2017, 18, 120.	2.7	9
164	The effect of using cow genomic information on accuracy and bias of genomic breeding values in a simulated Holstein dairy cattle population. Journal of Dairy Science, 2018, 101, 5166-5176.	3.4	9
165	Assessing genetic diversity of various Canadian sheep breeds through pedigree analyses. Canadian Journal of Animal Science, 2018, 98, 741-749.	1.5	9
166	Genetic and genomic analyses of testicular hypoplasia in Nellore cattle. PLoS ONE, 2019, 14, e0211159.	2.5	9
167	Marginal ancestral contributions to atrial fibrillation in the Standardbred racehorse: Comparison of cases and controls. PLoS ONE, 2018, 13, e0197137.	2.5	8
168	The effect of host genetics on in vitro performance of bovine monocyte-derived macrophages. Journal of Dairy Science, 2019, 102, 9107-9116.	3.4	8
169	Genetic and phenotypic associations of milk β-hydroxybutyrate with ketosis in Canadian Holsteins. Canadian Journal of Animal Science, 2016, 96, 302-305.	1.5	7
170	Genetic and genomic analyses of embryo production in dairy cattle. Reproduction, Fertility and Development, 2020, 32, 50.	0.4	7
171	Short communication: Time-dependent genetic parameters and single-step genome-wide association analyses for predicted milk fatty acid composition in Ayrshire and Jersey dairy cattle. Journal of Dairy Science, 2020, 103, 5263-5269.	3.4	7
172	Targeted genotyping to identify potential functional variants associated with cholesterol content in bovine milk. Animal Genetics, 2020, 51, 200-209.	1.7	7
173	Single- and multiple-breed genomic evaluations for conformation traits in Canadian Alpine and Saanen dairy goats. Journal of Dairy Science, 2022, 105, 5985-6000.	3.4	7
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