

Curtis P Van Tassell

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165
papers

12,682
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50
h-index

110
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167
ext. papers

15,383
ext. citations

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avg, IF

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L-index

#	Paper	IF	Citations
165	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
164	Invited review: reliability of genomic predictions for North American Holstein bulls. <i>Journal of Dairy Science</i> , 2009 , 92, 16-24	4	815
163	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009 , 10, R42	18.3	798
162	Development and characterization of a high density SNP genotyping assay for cattle. <i>PLoS ONE</i> , 2009 , 4, e5350	3.7	666
161	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
160	Design of a high density SNP genotyping assay in the pig using SNPs identified and characterized by next generation sequencing technology. <i>PLoS ONE</i> , 2009 , 4, e6524	3.7	486
159	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. <i>Nature Methods</i> , 2008 , 5, 247-52	21.6	458
158	Single-nucleotide polymorphisms in soybean. <i>Genetics</i> , 2003 , 163, 1123-34	4	332
157	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. <i>Nature Genetics</i> , 2017 , 49, 643-650	36.3	323
156	Multi-platform next-generation sequencing of the domestic turkey (<i>Meleagris gallopavo</i>): genome assembly and analysis. <i>PLoS Biology</i> , 2010 , 8, e1000475	9.7	311
155	Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E3995-4004	11.5	259
154	A soybean transcript map: gene distribution, haplotype and single-nucleotide polymorphism analysis. <i>Genetics</i> , 2007 , 176, 685-96	4	258
153	Genome-wide association analysis of thirty one production, health, reproduction and body conformation traits in contemporary U.S. Holstein cows. <i>BMC Genomics</i> , 2011 , 12, 408	4.5	245
152	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010 , 20, 693-703	9.7	214
151	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012 , 22, 778-90	9.7	204
150	Distribution and location of genetic effects for dairy traits. <i>Journal of Dairy Science</i> , 2009 , 92, 2931-46	4	186
149	Whole genome linkage disequilibrium maps in cattle. <i>BMC Genetics</i> , 2007 , 8, 74	2.6	165

148	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 18644-9	11.5	159
147	Detection of quantitative trait loci affecting milk production, health, and reproductive traits in Holstein cattle. <i>Journal of Dairy Science</i> , 2004 , 87, 468-75	4	158
146	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011 , 12, 127	4.5	156
145	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	140
144	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	36.3	139
143	Design of a bovine low-density SNP array optimized for imputation. <i>PLoS ONE</i> , 2012 , 7, e34130	3.7	132
142	High-resolution haplotype block structure in the cattle genome. <i>BMC Genetics</i> , 2009 , 10, 19	2.6	117
141	Effect of artificial selection on runs of homozygosity in u.s. Holstein cattle. <i>PLoS ONE</i> , 2013 , 8, e80813	3.7	114
140	Selection of single-nucleotide polymorphisms and quality of genotypes used in genomic evaluation of dairy cattle in the United States and Canada. <i>Journal of Dairy Science</i> , 2009 , 92, 3431-6	4	112
139	A validated genome wide association study to breed cattle adapted to an environment altered by climate change. <i>PLoS ONE</i> , 2009 , 4, e6676	3.7	99
138	Genomic signatures reveal new evidences for selection of important traits in domestic cattle. <i>Molecular Biology and Evolution</i> , 2015 , 32, 711-25	8.3	93
137	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013 , 14, 876	4.5	93
136	Discovery and profiling of bovine microRNAs from immune-related and embryonic tissues. <i>Physiological Genomics</i> , 2007 , 29, 35-43	3.6	87
135	Genome-wide association study for birth weight in Nellore cattle points to previously described orthologous genes affecting human and bovine height. <i>BMC Genetics</i> , 2013 , 14, 52	2.6	83
134	Fine-mapping milk production quantitative trait loci on BTA6: analysis of the bovine osteopontin gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 6896-901	11.5	82
133	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. <i>BMC Genetics</i> , 2008 , 9, 37	2.6	74
132	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. <i>BMC Genomics</i> , 2012 , 13, 376	4.5	71
131	Genomic regions showing copy number variations associate with resistance or susceptibility to gastrointestinal nematodes in Angus cattle. <i>Functional and Integrative Genomics</i> , 2012 , 12, 81-92	3.8	71

130	Identification of a nonsense mutation in CWC15 associated with decreased reproductive efficiency in Jersey cattle. <i>PLoS ONE</i> , 2013 , 8, e54872	3.7	71
129	Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. <i>Journal of Dairy Science</i> , 2010 , 93, 5423-35	4	69
128	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018 , 50, 57	4.9	69
127	A physical map of the bovine genome. <i>Genome Biology</i> , 2007 , 8, R165	18.3	67
126	Detecting loci under recent positive selection in dairy and beef cattle by combining different genome-wide scan methods. <i>PLoS ONE</i> , 2013 , 8, e64280	3.7	65
125	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014 , 15, 683	4.5	63
124	Use of residual feed intake in Holsteins during early lactation shows potential to improve feed efficiency through genetic selection. <i>Journal of Animal Science</i> , 2013 , 91, 3978-88	0.7	63
123	Accuracy of genomic predictions in Bos indicus (Nelore) cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 17	4.9	60
122	Serial analysis of gene expression during elongation of the peri-implantation porcine trophectoderm (conceptus). <i>Physiological Genomics</i> , 2005 , 20, 188-94	3.6	57
121	Bovine exome sequence analysis and targeted SNP genotyping of recessive fertility defects BH1, HH2, and HH3 reveal a putative causative mutation in SMC2 for HH3. <i>PLoS ONE</i> , 2014 , 9, e92769	3.7	55
120	Enhanced mitochondrial complex gene function and reduced liver size may mediate improved feed efficiency of beef cattle during compensatory growth. <i>Functional and Integrative Genomics</i> , 2010 , 10, 39-51	3.8	55
119	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016 , 6, 23161	4.9	52
118	Identification of estrogen-responsive genes in the parenchyma and fat pad of the bovine mammary gland by microarray analysis. <i>Physiological Genomics</i> , 2006 , 27, 42-53	3.6	52
117	Accuracy of genotype imputation in Nelore cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 69	4.9	51
116	Prediction of unobserved single nucleotide polymorphism genotypes of Jersey cattle using reference panels and population-based imputation algorithms. <i>Journal of Dairy Science</i> , 2010 , 93, 2229-38	4	51
115	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 19	4.9	50
114	Linkage disequilibrium levels in Bos indicus and Bos taurus cattle using medium and high density SNP chip data and different minor allele frequency distributions. <i>Livestock Science</i> , 2014 , 166, 121-132	1.7	49
113	Whole genome SNP discovery and analysis of genetic diversity in Turkey (Meleagris gallopavo). <i>BMC Genomics</i> , 2012 , 13, 391	4.5	49

112	Estimates of Genetic Selection Differentials and Generation Intervals for Four Paths of Selection. <i>Journal of Dairy Science</i> , 1991 , 74, 1078-1086	4	48
111	Identification of a nonsense mutation in APAF1 that is likely causal for a decrease in reproductive efficiency in Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2016 , 99, 6693-6701	4	47
110	Genome to Phenome: Improving Animal Health, Production, and Well-Being - A New USDA Blueprint for Animal Genome Research 2018-2027. <i>Frontiers in Genetics</i> , 2019 , 10, 327	4.5	47
109	Signatures of positive selection in East African Shorthorn Zebu: A genome-wide single nucleotide polymorphism analysis. <i>Scientific Reports</i> , 2015 , 5, 11729	4.9	46
108	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016 , 23, 253-62	4.5	46
107	Mapping quantitative trait loci associated with resistance to coccidiosis and growth. <i>Poultry Science</i> , 2003 , 82, 9-16	3.9	45
106	The Relationship between Runs of Homozygosity and Inbreeding in Jersey Cattle under Selection. <i>PLoS ONE</i> , 2015 , 10, e0129967	3.7	45
105	Design and validation of a 90K SNP genotyping assay for the water buffalo (<i>Bubalus bubalis</i>). <i>PLoS ONE</i> , 2017 , 12, e0185220	3.7	44
104	Effects of increased milking frequency on gene expression in the bovine mammary gland. <i>BMC Genomics</i> , 2008 , 9, 362	4.5	44
103	Genome-wide CNV analysis reveals variants associated with growth traits in <i>Bos indicus</i> . <i>BMC Genomics</i> , 2016 , 17, 419	4.5	44
102	Assessment of autozygosity in Nellore cows (<i>Bos indicus</i>) through high-density SNP genotypes. <i>Frontiers in Genetics</i> , 2015 , 6, 5	4.5	43
101	Comparative map alignment of BTA27 and HSA4 and 8 to identify conserved segments of genome containing fat deposition QTL. <i>Mammalian Genome</i> , 2000 , 11, 682-8	3.2	43
100	Detection of quantitative trait loci influencing conformation traits and calving ease in Holstein-Friesian cattle. <i>Journal of Dairy Science</i> , 2005 , 88, 4111-9	4	42
99	A genome scan to identify quantitative trait loci affecting economically important traits in a US Holstein population. <i>Journal of Dairy Science</i> , 2001 , 84, 2535-42	4	42
98	Circulating concentrations of estradiol, luteinizing hormone, and follicle-stimulating hormone during waves of ovarian follicular development in prepubertal cattle. <i>Biology of Reproduction</i> , 1999 , 60, 405-12	3.9	42
97	Analysis of bovine mammary gland EST and functional annotation of the <i>Bos taurus</i> gene index. <i>Mammalian Genome</i> , 2002 , 13, 373-9	3.2	41
96	Identification of novel loci associated with gastrointestinal parasite resistance in a Red Maasai x Dorper backcross population. <i>PLoS ONE</i> , 2015 , 10, e0122797	3.7	41
95	Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. <i>Genetics Selection Evolution</i> , 2018 , 50, 58	4.9	41

94	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. <i>Genome Research</i> , 2020 , 30, 790-801	9.7	40
93	Signatures of Selection for Environmental Adaptation and Zebu \times Taurine Hybrid Fitness in East African Shorthorn Zebu. <i>Frontiers in Genetics</i> , 2017 , 8, 68	4.5	40
92	Prevalence of the prion protein gene E211K variant in U.S. cattle. <i>BMC Veterinary Research</i> , 2008 , 4, 25	2.7	39
91	Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation. <i>Genome Biology</i> , 2019 , 20, 153	18.3	38
90	An atlas of bovine gene expression reveals novel distinctive tissue characteristics and evidence for improving genome annotation. <i>Genome Biology</i> , 2010 , 11, R102	18.3	38
89	Transcriptome profiling of the tubular porcine conceptus identifies the differential regulation of growth and developmentally associated genes. <i>Molecular Reproduction and Development</i> , 2006 , 73, 1491-502	2.6	38
88	Genome-wide association study and ancestral origins of the slick-hair coat in tropically adapted cattle. <i>Frontiers in Genetics</i> , 2014 , 5, 101	4.5	37
87	Local inflammation as a possible mechanism of resistance to gastrointestinal nematodes in Angus heifers. <i>Veterinary Parasitology</i> , 2007 , 145, 100-7	2.8	37
86	Serial analysis of gene expression in turkey sperm storage tubules in the presence and absence of resident sperm. <i>Biology of Reproduction</i> , 2003 , 69, 469-74	3.9	37
85	Implementation of a sire-maternal grandsire model for evaluation of calving ease in the United States. <i>Journal of Dairy Science</i> , 2003 , 86, 3366-73	4	36
84	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. <i>GigaScience</i> , 2018 , 7,	7.6	34
83	Identification of quantitative trait loci affecting resistance to gastrointestinal parasites in a double backcross population of Red Maasai and Dorper sheep. <i>Animal Genetics</i> , 2012 , 43, 63-71	2.5	33
82	Methods of tagSNP selection and other variables affecting imputation accuracy in swine. <i>BMC Genetics</i> , 2013 , 14, 8	2.6	33
81	Construction of bovine whole-genome radiation hybrid and linkage maps using high-throughput genotyping. <i>Animal Genetics</i> , 2007 , 38, 120-5	2.5	33
80	Calving ease (Co)variance components for a sire-maternal grandsire threshold model. <i>Journal of Dairy Science</i> , 2003 , 86, 1845-8	4	33
79	Fate of dietary perchlorate in lactating dairy cows: Relevance to animal health and levels in the milk supply. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 16152-7	11.5	33
78	Detection of putative loci affecting milk production and composition, health, and type traits in a United States Holstein population. <i>Journal of Dairy Science</i> , 1998 , 81, 3309-14	4	31
77	Multiple-trait Gibbs sampler for animal models: flexible programs for Bayesian and likelihood-based (co)variance component inference. <i>Journal of Animal Science</i> , 1996 , 74, 2586-97	0.7	31

76	Expressed sequence tag analysis of Eimeria-stimulated intestinal intraepithelial lymphocytes in chickens. <i>Molecular Biotechnology</i> , 2005 , 30, 143-50	3	30
75	Effects of Selection on Estimates of Variance Components Using Gibbs Sampling and Restricted Maximum Likelihood. <i>Journal of Dairy Science</i> , 1995 , 78, 678-692	4	29
74	Genome-wide mapping of loci explaining variance in scrotal circumference in Nellore cattle. <i>PLoS ONE</i> , 2014 , 9, e88561	3.7	29
73	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019 , 122, 636-646	3.6	29
72	Effect of sample stratification on dairy GWAS results. <i>BMC Genomics</i> , 2012 , 13, 536	4.5	28
71	Genomic divergences among cattle, dog and human estimated from large-scale alignments of genomic sequences. <i>BMC Genomics</i> , 2006 , 7, 140	4.5	28
70	Effect of somatotropin on thyroid hormones and cytokines in lactating dairy cows during ad libitum and restricted feed intake. <i>Journal of Dairy Science</i> , 2001 , 84, 2430-9	4	28
69	Increasing the number of single nucleotide polymorphisms used in genomic evaluation of dairy cattle. <i>Journal of Dairy Science</i> , 2016 , 99, 4504-4511	4	28
68	Environmental sampling to predict fecal prevalence of Salmonella in an intensively monitored dairy herd. <i>Journal of Food Protection</i> , 2008 , 71, 1967-73	2.5	27
67	Genomic Regions Associated with Sheep Resistance to Gastrointestinal Nematodes. <i>Trends in Parasitology</i> , 2016 , 32, 470-480	6.4	27
66	Use of (Co)Variance Functions to Describe (Co)Variances for Test Day Yield. <i>Journal of Dairy Science</i> , 1999 , 82, 226.e1-226.e14	4	26
65	Genome-wide detection of signatures of selection in Korean Hanwoo cattle. <i>Animal Genetics</i> , 2014 , 45, 180-90	2.5	25
64	Comparative transcriptome analysis of in vivo- and in vitro-produced porcine blastocysts by small amplified RNA-serial analysis of gene expression (SAR-SAGE). <i>Molecular Reproduction and Development</i> , 2008 , 75, 976-88	2.6	25
63	Application of machine learning in SNP discovery. <i>BMC Bioinformatics</i> , 2006 , 7, 4	3.6	25
62	Quantitative trait loci for resistance to Haemonchus contortus artificial challenge in Red Maasai and Dorper sheep of East Africa. <i>Animal Genetics</i> , 2013 , 44, 285-95	2.5	24
61	Method R estimates of additive genetic, dominance genetic, and permanent environmental fraction of variance for yield and health traits of Holsteins. <i>Journal of Dairy Science</i> , 2000 , 83, 1873-7	4	24
60	Method R estimates of heritability for milk, fat, and protein yields of United States dairy cattle. <i>Journal of Dairy Science</i> , 1999 , 82, 2231-7	4	24
59	SNP-PHAGE--High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006 , 7, 468	3.6	23

58	EST-PAGE--managing and analyzing EST data. <i>Bioinformatics</i> , 2004 , 20, 286-8	7.2	23
57	A genome-wide survey reveals a deletion polymorphism associated with resistance to gastrointestinal nematodes in Angus cattle. <i>Functional and Integrative Genomics</i> , 2014 , 14, 333-9	3.8	22
56	Characterization of 954 bovine full-CDS cDNA sequences. <i>BMC Genomics</i> , 2005 , 6, 166	4.5	21
55	Detection of putative loci affecting milk, health, and type traits in a US Holstein population using 70 microsatellite markers in a genome scan. <i>Journal of Dairy Science</i> , 1999 , 82, 2497-502	4	21
54	Inheritance of renal amyloidosis in Chinese Shar-pei dogs. <i>Journal of Heredity</i> , 1993 , 84, 438-42	2.4	21
53	Detection of putative loci affecting milk, health, and conformation traits in a US Holstein population using 105 microsatellite markers. <i>Journal of Dairy Science</i> , 2000 , 83, 1865-72	4	20
52	Reduced representation bisulphite sequencing of ten bovine somatic tissues reveals DNA methylation patterns and their impacts on gene expression. <i>BMC Genomics</i> , 2016 , 17, 779	4.5	20
51	Predicting perchlorate exposure in milk from concentrations in dairy feed. <i>Journal of Agricultural and Food Chemistry</i> , 2007 , 55, 8806-13	5.7	16
50	Comparative analyses across cattle genders and breeds reveal the pitfalls caused by false positive and lineage-differential copy number variations. <i>Scientific Reports</i> , 2016 , 6, 29219	4.9	16
49	Imputation of microsatellite alleles from dense SNP genotypes for parental verification. <i>Frontiers in Genetics</i> , 2012 , 3, 140	4.5	15
48	Comparative analyses of sperm DNA methylomes among human, mouse and cattle provide insights into epigenomic evolution and complex traits. <i>Epigenetics</i> , 2019 , 14, 260-276	5.7	14
47	Whole genome structural analysis of Caribbean hair sheep reveals quantitative link to West African ancestry. <i>PLoS ONE</i> , 2017 , 12, e0179021	3.7	13
46	Estimation of genetic variance and covariance components for weaning weight in Simmental cattle. <i>Journal of Animal Science</i> , 1997 , 75, 325-30	0.7	13
45	Fine mapping for Weaver syndrome in Brown Swiss cattle and the identification of 41 concordant mutations across NRCAM, PNPLA8 and CTTNBP2. <i>PLoS ONE</i> , 2013 , 8, e59251	3.7	12
44	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple <i>Bos taurus</i> and <i>Bos indicus</i> breeds. <i>Frontiers in Genetics</i> , 2013 , 4, 176	4.5	12
43	Characterization of DGAT1 allelic effects in a sample of North American Holstein cattle. <i>Animal Biotechnology</i> , 2010 , 21, 88-99	1.4	12
42	Single-molecule sequencing and conformational capture enable de novo mammalian reference genomes		12
41	Bayesian analysis of twinning and ovulation rates using a multiple-trait threshold model and Gibbs sampling. <i>Journal of Animal Science</i> , 1998 , 76, 2048-61	0.7	12

40	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. <i>BMC Biology</i> , 2020 , 18, 85	7.3	11
39	Tangible and intangible benefits of local goats rearing in smallholder farms in Malawi. <i>Small Ruminant Research</i> , 2020 , 187, 106095	1.7	11
38	Genome-wide scan of gastrointestinal nematode resistance in closed Angus population selected for minimized influence of MHC. <i>PLoS ONE</i> , 2015 , 10, e0119380	3.7	11
37	Identification of quantitative trait loci affecting gastrointestinal parasite resistance in an experimental Angus population. <i>Animal Genetics</i> , 2014 , 45, 117-21	2.5	11
36	Bovine genomics update: making a cow jump over the moon. <i>Genetical Research</i> , 2004 , 84, 3-9	1.1	11
35	Integrating Signals from Sperm Methylome Analysis and Genome-Wide Association Study for a Better Understanding of Male Fertility in Cattle.. <i>Epigenomes</i> , 2019 , 3,	2.3	9
34	Timing and Extent of Inbreeding in African Goats. <i>Frontiers in Genetics</i> , 2019 , 10, 537	4.5	8
33	Systematic Profiling of Short Tandem Repeats in the Cattle Genome. <i>Genome Biology and Evolution</i> , 2017 , 9, 20-31	3.9	8
32	Technical note: Characteristics and use of the Illumina BovineLD and GeneSeek Genomic Profiler low-density bead chips for genomic evaluation. <i>Journal of Dairy Science</i> , 2013 , 96, 1258-63	4	8
31	Identification of conserved regulatory elements in mammalian promoter regions: a case study using the PCK1 promoter. <i>Genomics, Proteomics and Bioinformatics</i> , 2008 , 6, 129-43	6.5	8
30	Effects of exogenous somatotropin on whole-body glycemc response to insulin in young preruminant and ruminant lambs. <i>Domestic Animal Endocrinology</i> , 1995 , 12, 143-56	2.3	8
29	Effect of reference population size and available ancestor genotypes on imputation of Mexican Holstein genotypes. <i>Journal of Dairy Science</i> , 2015 , 98, 3478-84	4	7
28	Production evaluation techniques based on lactation curves. <i>Journal of Dairy Science</i> , 1995 , 78, 457-65	4	6
27	Consideration of Sire Relationships for Estimation of Variance Components with Interaction of Herd and Sire. <i>Journal of Dairy Science</i> , 1994 , 77, 313-324	4	6
26	A comprehensive catalogue of regulatory variants in the cattle transcriptome		6
25	Genome-wide candidate regions for selective sweeps revealed through massive parallel sequencing of DNA across ten turkey populations. <i>BMC Genetics</i> , 2014 , 15, 117	2.6	5
24	Box-Cox Transformation and Random Regression Models for Fecal egg Count Data. <i>Frontiers in Genetics</i> , 2011 , 2, 112	4.5	5
23	Characterization of open reading frame-expressed sequence tags generated from Bos indicus and B. taurus mammary gland cDNA libraries. <i>Animal Genetics</i> , 2004 , 35, 213-9	2.5	5

22	Mapping quantitative trait loci affecting dairy conformation to chromosome 27 in two Holstein grandsire families. <i>Journal of Dairy Science</i> , 2004 , 87, 450-7	4	5
21	High density LD-based structural variations analysis in cattle genome. <i>PLoS ONE</i> , 2014 , 9, e103046	3.7	5
20	VarGoats project: a dataset of 1159 whole-genome sequences to dissect <i>Capra hircus</i> global diversity. <i>Genetics Selection Evolution</i> , 2021 , 53, 86	4.9	4
19	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. <i>Genomics</i> , 2020 , 112, 1477-1480	4.3	4
18	Computational detection and experimental validation of segmental duplications and associated copy number variations in water buffalo (<i>Bubalus bubalis</i>). <i>Functional and Integrative Genomics</i> , 2019 , 19, 409-419	3.8	3
17	Characterization of a novel microdeletion polymorphism on BTA5 in cattle. <i>Animal Genetics</i> , 2008 , 39, 655-8	2.5	3
16	Physical and linkage mapping of mammary-derived expressed sequence tags in cattle. <i>Genomics</i> , 2004 , 83, 148-52	4.3	3
15	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. <i>Genomics</i> , 2021 , 113, 2045-2055	4.3	3
14	Characterization of a normalized cDNA library from bovine intestinal muscle and epithelial tissues. <i>Animal Biotechnology</i> , 2005 , 16, 17-29	1.4	2
13	Prediction of Progeny Genetic Evaluations from Simultaneous Genetic Evaluations of the Dam, Sire, and Maternal Grandsire with an Animal Model. <i>Journal of Dairy Science</i> , 1989 , 72, 1578-1582	4	2
12	Experiences from the Implementation of Community-Based Goat Breeding Programs in Malawi and Uganda: A Potential Approach for Conservation and Improvement of Indigenous Small Ruminants in Smallholder Farms. <i>Sustainability</i> , 2021 , 13, 1494	3.6	2
11	Genetic differentiation of Mexican Holstein cattle and its relationship with Canadian and U.S. Holsteins. <i>Frontiers in Genetics</i> , 2015 , 6, 7	4.5	1
10	Association analysis of bovine bactericidal/permeability-increasing protein gene polymorphisms with somatic cell score in Holstein cattle. <i>Animal Genetics</i> , 2008 , 39, 456-7	2.5	1
9	Consensus and comprehensive linkage maps of bovine chromosome 17. <i>Animal Genetics</i> , 2001 , 32, 112-32.5		1
8	Consensus and comprehensive linkage maps of bovine chromosome 25. <i>Animal Genetics</i> , 2001 , 32, 114-52.5		1
7	Comparison of Heritability and Variation for Milk Yield of Registered and Nonregistered Holstein Cows. <i>Journal of Dairy Science</i> , 1988 , 71, 2271-2277	4	1
6	Functional Variants Surrounding Endothelin 2 Are Associated With Subspecies Infection. <i>Frontiers in Veterinary Science</i> , 2021 , 8, 625323	3.1	1
5	Variants Within Genes and are Associated With Divergent Fecal Egg Counts in Katahdin Sheep at Weaning.. <i>Frontiers in Genetics</i> , 2022 , 13, 817319	4.5	1

4	How Bioinformatics Enables Livestock Applied Sciences in the Genomic Era. <i>Lecture Notes in Computer Science</i> , 2012 , 192-201	0.9	o
3	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021 , 22, 398	4.5	o
2	Genomic evaluation of dairy heifer livability. <i>Journal of Dairy Science</i> , 2021 , 104, 8959-8965	4	o
1	Towards the detection of copy number variation from single sperm sequencing in cattle.. <i>BMC Genomics</i> , 2022 , 23, 215	4.5	