

Curtis P Van Tassell

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6422786/publications.pdf>

Version: 2024-02-01

165
papers

17,096
citations

20817

60
h-index

15732

125
g-index

167
all docs

167
docs citations

167
times ranked

11901
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
2	Invited Review: Reliability of genomic predictions for North American Holstein bulls. <i>Journal of Dairy Science</i> , 2009, 92, 16-24.	3.4	1,008
3	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009, 10, R42.	9.6	1,005
4	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. <i>PLoS ONE</i> , 2009, 4, e5350.	2.5	813
5	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
6	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.	21.4	600
7	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.	2.5	568
8	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. <i>Nature Methods</i> , 2008, 5, 247-252.	19.0	534
9	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.	7.1	395
10	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
11	Single-Nucleotide Polymorphisms in Soybean. <i>Genetics</i> , 2003, 163, 1123-1134.	2.9	367
12	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.	2.8	349
13	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (<i>Meleagris gallopavo</i>): Genome Assembly and Analysis. <i>PLoS Biology</i> , 2010, 8, e1000475.	5.6	348
14	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
15	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. <i>Genetics</i> , 2007, 176, 685-696.	2.9	285
16	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010, 20, 693-703.	5.5	280
17	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012, 22, 778-790.	5.5	259
18	Distribution and location of genetic effects for dairy traits. <i>Journal of Dairy Science</i> , 2009, 92, 2931-2946.	3.4	210

#	ARTICLE	IF	CITATIONS
19	Whole genome linkage disequilibrium maps in cattle. <i>BMC Genetics</i> , 2007, 8, 74.	2.7	201
20	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011, 12, 127.	2.8	201
21	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, 18644-18649.	7.1	196
22	Detection of Quantitative Trait Loci Affecting Milk Production, Health, and Reproductive Traits in Holstein Cattle. <i>Journal of Dairy Science</i> , 2004, 87, 468-475.	3.4	189
23	Genomic Signatures Reveal New Evidences for Selection of Important Traits in Domestic Cattle. <i>Molecular Biology and Evolution</i> , 2015, 32, 711-725.	8.9	173
24	Effect of Artificial Selection on Runs of Homozygosity in U.S. Holstein Cattle. <i>PLoS ONE</i> , 2013, 8, e80813.	2.5	165
25	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, 3431-3436.	3.4	163
26	Design of a Bovine Low-Density SNP Array Optimized for Imputation. <i>PLoS ONE</i> , 2012, 7, e34130.	2.5	159
27	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013, 14, 876.	2.8	142
28	High-resolution haplotype block structure in the cattle genome. <i>BMC Genetics</i> , 2009, 10, 19.	2.7	141
29	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.	2.3	133
30	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
31	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.	2.3	118
32	Signatures of positive selection in East African Shorthorn Zebu: A genome-wide single nucleotide polymorphism analysis. <i>Scientific Reports</i> , 2015, 5, 11729.	3.3	114
33	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018, 50, 57.	3.0	114
34	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.	2.7	111
35	Discovery and profiling of bovine microRNAs from immune-related and embryonic tissues. <i>Physiological Genomics</i> , 2007, 29, 35-43.	2.3	104
36	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.	3.5	99

#	ARTICLE	IF	CITATIONS
37	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. <i>Genome Research</i> , 2020, 30, 790-801.	5.5	97
38	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, 6896-6901.	7.1	95
39	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. <i>BMC Genetics</i> , 2008, 9, 37.	2.7	95
40	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	3.3	91
41	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. <i>BMC Genomics</i> , 2012, 13, 376.	2.8	90
42	Use of residual feed intake in Holsteins during early lactation shows potential to improve feed efficiency through genetic selection ¹ . <i>Journal of Animal Science</i> , 2013, 91, 3978-3988.	0.5	90
43	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014, 15, 683.	2.8	89
44	Identification of a Nonsense Mutation in CWC15 Associated with Decreased Reproductive Efficiency in Jersey Cattle. <i>PLoS ONE</i> , 2013, 8, e54872.	2.5	88
45	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.	3.5	87
46	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.	3.0	87
47	Accuracy of genotype imputation in Nelore cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 69.	3.0	86
48	Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. <i>Journal of Dairy Science</i> , 2010, 93, 5423-5435.	3.4	85
49	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.	2.5	84
50	The Relationship between Runs of Homozygosity and Inbreeding in Jersey Cattle under Selection. <i>PLoS ONE</i> , 2015, 10, e0129967.	2.5	80
51	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 19.	3.0	79
52	Accuracy of genomic predictions in <i>Bos indicus</i> (Nelore) cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 17.	3.0	77
53	Design and validation of a 90K SNP genotyping assay for the water buffalo (<i>Bubalus bubalis</i>). <i>PLoS ONE</i> , 2017, 12, e0185220.	2.5	76
54	A physical map of the bovine genome. <i>Genome Biology</i> , 2007, 8, R165.	9.6	73

#	ARTICLE	IF	CITATIONS
55	AdaptMap: exploring goat diversity and adaptation. <i>Genetics Selection Evolution</i> , 2018, 50, 61.	3.0	70
56	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.	2.5	69
57	Linkage disequilibrium levels in <i>Bos indicus</i> and <i>Bos taurus</i> cattle using medium and high density SNP chip data and different minor allele frequency distributions. <i>Livestock Science</i> , 2014, 166, 121-132.	1.6	69
58	Assessment of autozygosity in Nellore cows (<i>Bos indicus</i>) through high-density SNP genotypes. <i>Frontiers in Genetics</i> , 2015, 6, 5.	2.3	69
59	Genome-wide CNV analysis reveals variants associated with growth traits in <i>Bos indicus</i> . <i>BMC Genomics</i> , 2016, 17, 419.	2.8	69
60	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.	3.4	66
61	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.	8.8	66
62	Serial analysis of gene expression during elongation of the peri-implantation porcine trophectoderm (conceptus). <i>Physiological Genomics</i> , 2005, 20, 188-194.	2.3	65
63	Whole genome SNP discovery and analysis of genetic diversity in Turkey (<i>Meleagris gallopavo</i>). <i>BMC Genomics</i> , 2012, 13, 391.	2.8	63
64	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.	2.3	61
65	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. <i>GigaScience</i> , 2018, 7, .	6.4	60
66	Identification of Novel Loci Associated with Gastrointestinal Parasite Resistance in a Red Maasai x Dorper Backcross Population. <i>PLoS ONE</i> , 2015, 10, e0122797.	2.5	60
67	Estimates of Genetic Selection Differentials and Generation Intervals for Four Paths of Selection. <i>Journal of Dairy Science</i> , 1991, 74, 1078-1086.	3.4	59
68	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016, 23, 253-262.	3.4	59
69	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, 2535-2542.	3.4	58
70	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, 2229-2238.	3.4	58
71	Mapping quantitative trait loci associated with resistance to coccidiosis and growth. <i>Poultry Science</i> , 2003, 82, 9-16.	3.4	57
72	Detection of Quantitative Trait Loci Influencing Conformation Traits and Calving Ease in Holstein-Friesian Cattle. <i>Journal of Dairy Science</i> , 2005, 88, 4111-4119.	3.4	56

#	ARTICLE	IF	CITATIONS
73	Effects of increased milking frequency on gene expression in the bovine mammary gland. BMC Genomics, 2008, 9, 362.	2.8	53
74	Genome-wide association study and ancestral origins of the slick-hair coat in tropically adapted cattle. Frontiers in Genetics, 2014, 5, 101.	2.3	51
75	Circulating Concentrations of Estradiol, Luteinizing Hormone, and Follicle-Stimulating Hormone during Waves of Ovarian Follicular Development in Prepubertal Cattle ¹ . Biology of Reproduction, 1999, 60, 405-412.	2.7	49
76	Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index. Mammalian Genome, 2002, 13, 373-379.	2.2	48
77	Comparative map alignment of BTA27 and HSA4 and 8 to identify conserved segments of genome containing fat deposition QTL. Mammalian Genome, 2000, 11, 682-688.	2.2	47
78	Prevalence of the prion protein gene E211K variant in U.S. cattle. BMC Veterinary Research, 2008, 4, 25.	1.9	46
79	Unlocking the bovine genome. BMC Genomics, 2009, 10, 193.	2.8	46
80	An atlas of bovine gene expression reveals novel distinctive tissue characteristics and evidence for improving genome annotation. Genome Biology, 2010, 11, R102.	8.8	46
81	Serial Analysis of Gene Expression in Turkey Sperm Storage Tubules in the Presence and Absence of Resident Sperm. Biology of Reproduction, 2003, 69, 469-474.	2.7	45
82	Transcriptome profiling of the tubular porcine conceptus identifies the differential regulation of growth and developmentally associated genes. Molecular Reproduction and Development, 2006, 73, 1491-1502.	2.0	45
83	Identification of quantitative trait loci affecting resistance to gastrointestinal parasites in a double backcross population of Red Maasai and Dorper sheep. Animal Genetics, 2012, 43, 63-71.	1.7	44
84	Comparative analyses across cattle genders and breeds reveal the pitfalls caused by false positive and lineage-differential copy number variations. Scientific Reports, 2016, 6, 29219.	3.3	44
85	Application of machine learning in SNP discovery. BMC Bioinformatics, 2006, 7, 4.	2.6	43
86	Genomic Regions Associated with Sheep Resistance to Gastrointestinal Nematodes. Trends in Parasitology, 2016, 32, 470-480.	3.3	43
87	Multiple-trait Gibbs sampler for animal models: flexible programs for Bayesian and likelihood-based (co)variance component inference. Journal of Animal Science, 1996, 74, 2586-97.	0.5	43
88	Local inflammation as a possible mechanism of resistance to gastrointestinal nematodes in Angus heifers. Veterinary Parasitology, 2007, 145, 100-107.	1.8	42
89	Diversity of copy number variation in the worldwide goat population. Heredity, 2019, 122, 636-646.	2.6	42
90	Effects of Selection on Estimates of Variance Components Using Gibbs Sampling and Restricted Maximum Likelihood. Journal of Dairy Science, 1995, 78, 678-692.	3.4	41

#	ARTICLE	IF	CITATIONS
91	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, 3309-3314.	3.4	41
92	Genome-wide detection of signatures of selection in Korean Hanwoo cattle. <i>Animal Genetics</i> , 2014, 45, 180-190.	1.7	40
93	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, 2430-2439.	3.4	38
94	Calving Ease (Co)Variance Components for a Sire-Maternal Grand sire Threshold Model. <i>Journal of Dairy Science</i> , 2003, 86, 1845-1848.	3.4	38
95	Implementation of a Sire-Maternal Grand sire Model for Evaluation of Calving Ease in the United States. <i>Journal of Dairy Science</i> , 2003, 86, 3366-3373.	3.4	38
96	Genome-Wide Scan of Gastrointestinal Nematode Resistance in Closed Angus Population Selected for Minimized Influence of MHC. <i>PLoS ONE</i> , 2015, 10, e0119380.	2.5	37
97	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, 16152-16157.	7.1	36
98	Construction of bovine whole-genome radiation hybrid and linkage maps using high-throughput genotyping. <i>Animal Genetics</i> , 2007, 38, 120-125.	1.7	36
99	Methods of tag SNP selection and other variables affecting imputation accuracy in swine. <i>BMC Genetics</i> , 2013, 14, 8.	2.7	36
100	Increasing the number of single nucleotide polymorphisms used in genomic evaluation of dairy cattle. <i>Journal of Dairy Science</i> , 2016, 99, 4504-4511.	3.4	36
101	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.	3.4	35
102	Expressed Sequence Tag Analysis of <i>Eimeria</i> -Stimulated Intestinal Intraepithelial Lymphocytes in Chickens. <i>Molecular Biotechnology</i> , 2005, 30, 143-150.	2.4	34
103	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. <i>BMC Biology</i> , 2020, 18, 85.	3.8	34
104	Method R Estimates of Heritability for Milk, Fat, and Protein Yields of United States Dairy Cattle. <i>Journal of Dairy Science</i> , 1999, 82, 2231-2237.	3.4	33
105	Genomic divergences among cattle, dog and human estimated from large-scale alignments of genomic sequences. <i>BMC Genomics</i> , 2006, 7, 140.	2.8	33
106	Effect of sample stratification on dairy GWAS results. <i>BMC Genomics</i> , 2012, 13, 536.	2.8	33
107	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. <i>PLoS ONE</i> , 2014, 9, e88561.	2.5	33
108	Environmental Sampling To Predict Fecal Prevalence of Salmonella in an Intensively Monitored Dairy Herd. <i>Journal of Food Protection</i> , 2008, 71, 1967-1973.	1.7	32

#	ARTICLE	IF	CITATIONS
109	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, 2497-2502.	3.4	31
110	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, 1873-1877.	3.4	30
111	Comparative transcriptome analysis of in vivo and in vitro produced porcine blastocysts by small amplified RNA Serial analysis of gene expression (SARAGE). <i>Molecular Reproduction and Development</i> , 2008, 75, 976-988.	2.0	30
112	Quantitative trait loci for resistance to <i>Hemonchus contortus</i> artificial challenge in Red Maaai and Dorper sheep of East Africa. <i>Animal Genetics</i> , 2013, 44, 285-295.	1.7	30
113	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.	2.8	30
114	Inheritance of Renal Amyloidosis in Chinese Shar-pei Dogs. <i>Journal of Heredity</i> , 1993, 84, 438-442.	2.4	29
115	SNP-PHAGE—High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006, 7, 468.	2.6	29
116	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.	2.3	29
117	Whole genome structural analysis of Caribbean hair sheep reveals quantitative link to West African ancestry. <i>PLoS ONE</i> , 2017, 12, e0179021.	2.5	29
118	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, 1865-1872.	3.4	28
119	Tangible and intangible benefits of local goats rearing in smallholder farms in Malawi. <i>Small Ruminant Research</i> , 2020, 187, 106095.	1.2	27
120	Estimation of genetic variance and covariance components for weaning weight in Simmental cattle.. <i>Journal of Animal Science</i> , 1997, 75, 325.	0.5	26
121	EST-PAGE—managing and analyzing EST data. <i>Bioinformatics</i> , 2004, 20, 286-288.	4.1	26
122	Characterization of 954 bovine full-CDS cDNA sequences. <i>BMC Genomics</i> , 2005, 6, 166.	2.8	26
123	Imputation of Microsatellite Alleles from Dense SNP Genotypes for Parental Verification. <i>Frontiers in Genetics</i> , 2012, 3, 140.	2.3	26
124	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.	2.7	25
125	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, 333-339.	3.5	24
126	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	2.5	20

#	ARTICLE	IF	CITATIONS
127	Fine Mapping for Weaver Syndrome in Brown Swiss Cattle and the Identification of 41 Concordant Mutations across NRCAM, PNPLA8 and CTTNBP2. PLoS ONE, 2013, 8, e59251.	2.5	18
128	Predicting Perchlorate Exposure in Milk from Concentrations in Dairy Feed. Journal of Agricultural and Food Chemistry, 2007, 55, 8806-8813.	5.2	17
129	Characterization of DGAT1 Allelic Effects in a Sample of North American Holstein Cattle. Animal Biotechnology, 2010, 21, 88-99.	1.5	17
130	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. Genomics, 2021, 113, 2045-2055.	2.9	16
131	VarGoats project: a dataset of 1159 whole-genome sequences to dissect Capra hircus global diversity. Genetics Selection Evolution, 2021, 53, 86.	3.0	16
132	Timing and Extent of Inbreeding in African Goats. Frontiers in Genetics, 2019, 10, 537.	2.3	15
133	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. Genomics, 2020, 112, 1477-1480.	2.9	14
134	Bayesian analysis of twinning and ovulation rates using a multiple-trait threshold model and Gibbs sampling. Journal of Animal Science, 1998, 76, 2048-61.	0.5	13
135	Bovine genomics update: making a cow jump over the moon. Genetical Research, 2004, 84, 3-9.	0.9	12
136	Technical note: Characteristics and use of the Illumina BovineLD and GeneSeek Genomic Profiler low-density bead chips for genomic evaluation. Journal of Dairy Science, 2013, 96, 1258-1263.	3.4	12
137	Effect of reference population size and available ancestor genotypes on imputation of Mexican Holstein genotypes. Journal of Dairy Science, 2015, 98, 3478-3484.	3.4	12
138	Integrating Signals from Sperm Methylome Analysis and Genome-Wide Association Study for a Better Understanding of Male Fertility in Cattle. Epigenomes, 2019, 3, 10.	1.8	12
139	Identification of quantitative trait loci affecting gastrointestinal parasite resistance in an experimental Angus population. Animal Genetics, 2014, 45, 117-121.	1.7	11
140	Effects of exogenous somatotropin on whole-body glycemic response to insulin in young preruminant and ruminant lambs. Domestic Animal Endocrinology, 1995, 12, 143-156.	1.6	9
141	Mapping Quantitative Trait Loci Affecting Dairy Conformation to Chromosome 27 in Two Holstein Grandsire Families. Journal of Dairy Science, 2004, 87, 450-457.	3.4	8
142	Identification of Conserved Regulatory Elements in Mammalian Promoter Regions: A Case Study Using the PCK1 Promoter. Genomics, Proteomics and Bioinformatics, 2008, 6, 129-143.	6.9	8
143	Box-Cox Transformation and Random Regression Models for Fecal egg Count Data. Frontiers in Genetics, 2012, 2, 112.	2.3	8
144	Consideration of Sire Relationships for Estimation of Variance Components with Interaction of Herd and Sire. Journal of Dairy Science, 1994, 77, 313-324.	3.4	7

#	ARTICLE	IF	CITATIONS
145	Production Evaluation Techniques Based on Lactation Curves. <i>Journal of Dairy Science</i> , 1995, 78, 457-465.	3.4	7
146	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.	2.7	7
147	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.	3.5	7
148	Genomic evaluation of dairy heifer livability. <i>Journal of Dairy Science</i> , 2021, 104, 8959-8965.	3.4	7
149	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.	3.2	6
150	Functional Variants Surrounding Endothelin 2 Are Associated With <i>Mycobacterium avium</i> Subspecies paratuberculosis Infection. <i>Frontiers in Veterinary Science</i> , 2021, 8, 625323.	2.2	6
151	High Density LD-Based Structural Variations Analysis in Cattle Genome. <i>PLoS ONE</i> , 2014, 9, e103046.	2.5	6
152	Variants Within Genes EDIL3 and ADGRB3 are Associated With Divergent Fecal Egg Counts in Katahdin Sheep at Weaning. <i>Frontiers in Genetics</i> , 2022, 13, 817319.	2.3	6
153	Characterization of open reading frame-expressed sequence tags generated from <i>Bos indicus</i> and <i>B. taurus</i> mammary gland cDNA libraries. <i>Animal Genetics</i> , 2004, 35, 213-219.	1.7	5
154	CHARACTERIZATION OF A NORMALIZED CDNA LIBRARY FROM BOVINE INTESTINAL MUSCLE AND EPITHELIAL TISSUES. <i>Animal Biotechnology</i> , 2005, 16, 17-29.	1.5	5
155	Genetic differentiation of Mexican Holstein cattle and its relationship with Canadian and U.S. Holsteins. <i>Frontiers in Genetics</i> , 2015, 6, 7.	2.3	4
156	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	2.8	4
157	Physical and linkage mapping of mammary-derived expressed sequence tags in cattle. <i>Genomics</i> , 2004, 83, 148-152.	2.9	3
158	Characterization of a novel microdeletion polymorphism on BTAS in cattle. <i>Animal Genetics</i> , 2008, 39, 655-658.	1.7	3
159	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.	3.4	2
160	Consensus and comprehensive linkage maps of bovine chromosome 17. <i>Animal Genetics</i> , 2001, 32, 112-113.	1.7	2
161	Towards the detection of copy number variation from single sperm sequencing in cattle. <i>BMC Genomics</i> , 2022, 23, 215.	2.8	2
162	Comparison of Heritability and Variation for Milk Yield of Registered and Nonregistered Holstein Cows. <i>Journal of Dairy Science</i> , 1988, 71, 2271-2277.	3.4	1

#	ARTICLE	IF	CITATIONS
163	Consensus and comprehensive linkage maps of bovine chromosome 25. <i>Animal Genetics</i> , 2001, 32, 114-115.	1.7	1
164	Association analysis of bovine <i>bactericidal/permeability-increasing protein</i> gene polymorphisms with somatic cell score in Holstein cattle. <i>Animal Genetics</i> , 2008, 39, 456-457.	1.7	1
165	How Bioinformatics Enables Livestock Applied Sciences in the Genomic Era. <i>Lecture Notes in Computer Science</i> , 2012, , 192-201.	1.3	1