

Curtis P Van Tassell

List of Publications by Year in descending order

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165
papers

17,096
citations

20817

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167
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times ranked

11901
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#	ARTICLE	IF	CITATIONS
1	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
2	Towards the detection of copy number variation from single sperm sequencing in cattle. <i>BMC Genomics</i> , 2022, 23, 215.	2.8	2
3	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
4	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	2.8	4
5	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
6	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. <i>Genomics</i> , 2021, 113, 2045-2055.	2.9	16
7	Genomic evaluation of dairy heifer livability. <i>Journal of Dairy Science</i> , 2021, 104, 8959-8965.	3.4	7
8	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.	3.0	16
9	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. <i>Genomics</i> , 2020, 112, 1477-1480.	2.9	14
10	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
11	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
12	Tangible and intangible benefits of local goats rearing in smallholder farms in Malawi. <i>Small Ruminant Research</i> , 2020, 187, 106095.	1.2	27
13	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
14	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
15	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
16	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, 10.	1.8	12
17	Timing and Extent of Inbreeding in African Goats. <i>Frontiers in Genetics</i> , 2019, 10, 537.	2.3	15
18	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

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19	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
20	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019, 122, 636-646.	2.6	42
21	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
22	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
23	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
24	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018, 50, 57.	3.0	114
25	AdaptMap: exploring goat diversity and adaptation. <i>Genetics Selection Evolution</i> , 2018, 50, 61.	3.0	70
26	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
27	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
28	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
29	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
30	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
31	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
32	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
33	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
34	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.	3.3	44
35	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
36	Genomic Regions Associated with Sheep Resistance to Gastrointestinal Nematodes. <i>Trends in Parasitology</i> , 2016, 32, 470-480.	3.3	43

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37	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	2.5	20
38	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016, 6, 23161.	3.3	91
39	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
40	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
41	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
42	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
43	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
44	Effect of reference population size and available ancestor genotypes on imputation of Mexican Holstein genotypes. <i>Journal of Dairy Science</i> , 2015, 98, 3478-3484.	3.4	12
45	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
46	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
47	The Relationship between Runs of Homozygosity and Inbreeding in Jersey Cattle under Selection. <i>PLoS ONE</i> , 2015, 10, e0129967.	2.5	80
48	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
49	Genome-wide association study and ancestral origins of the slick-hair coat in tropically adapted cattle. <i>Frontiers in Genetics</i> , 2014, 5, 101.	2.3	51
50	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
51	Accuracy of genotype imputation in Nellore cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 69.	3.0	86
52	Genome-wide detection of signatures of selection in Korean Hanwoo cattle. <i>Animal Genetics</i> , 2014, 45, 180-190.	1.7	40
53	Identification of quantitative trait loci affecting gastrointestinal parasite resistance in an experimental Angus population. <i>Animal Genetics</i> , 2014, 45, 117-121.	1.7	11
54	Accuracy of genomic predictions in <i>Bos indicus</i> (Nellore) cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 17.	3.0	77

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55	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. BMC Genomics, 2014, 15, 683.	2.8	89
56	A genome-wide survey reveals a deletion polymorphism associated with resistance to gastrointestinal nematodes in Angus cattle. Functional and Integrative Genomics, 2014, 14, 333-339.	3.5	24
57	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. Genetics Selection Evolution, 2014, 46, 19.	3.0	79
58	Linkage disequilibrium levels in Bos indicus and Bos taurus cattle using medium and high density SNP chip data and different minor allele frequency distributions. Livestock Science, 2014, 166, 121-132.	1.6	69
59	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. PLoS ONE, 2014, 9, e88561.	2.5	33
60	High Density LD-Based Structural Variations Analysis in Cattle Genome. PLoS ONE, 2014, 9, e103046.	2.5	6
61	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
62	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. BMC Genomics, 2013, 14, 876.	2.8	142
63	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
64	Quantitative trait loci for resistance to <i>Hemonchus contortus</i> artificial challenge in Red Maaasai and Dorper sheep of East Africa. Animal Genetics, 2013, 44, 285-295.	1.7	30
65	Use of residual feed intake in Holsteins during early lactation shows potential to improve feed efficiency through genetic selection. Journal of Animal Science, 2013, 91, 3978-3988.	0.5	90
66	Methods of tagSNP selection and other variables affecting imputation accuracy in swine. BMC Genetics, 2013, 14, 8.	2.7	36
67	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
68	Detecting Loci under Recent Positive Selection in Dairy and Beef Cattle by Combining Different Genome-Wide Scan Methods. PLoS ONE, 2013, 8, e64280.	2.5	84
69	Effect of Artificial Selection on Runs of Homozygosity in U.S. Holstein Cattle. PLoS ONE, 2013, 8, e80813.	2.5	165
70	Imputation of microsatellite alleles from dense SNP genotypes for parentage verification across multiple Bos taurus and Bos indicus breeds. Frontiers in Genetics, 2013, 4, 176.	2.3	29
71	Identification of a Nonsense Mutation in CWC15 Associated with Decreased Reproductive Efficiency in Jersey Cattle. PLoS ONE, 2013, 8, e54872.	2.5	88
72	Whole genome SNP discovery and analysis of genetic diversity in Turkey (Meleagris gallopavo). BMC Genomics, 2012, 13, 391.	2.8	63

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73	Effect of sample stratification on dairy GWAS results. BMC Genomics, 2012, 13, 536.	2.8	33
74	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	5.5	259
75	Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. BMC Genomics, 2012, 13, 376.	2.8	90
76	Box-Cox Transformation and Random Regression Models for Fecal egg Count Data. Frontiers in Genetics, 2012, 2, 112.	2.3	8
77	Imputation of Microsatellite Alleles from Dense SNP Genotypes for Parental Verification. Frontiers in Genetics, 2012, 3, 140.	2.3	26
78	Genomic regions showing copy number variations associate with resistance or susceptibility to gastrointestinal nematodes in Angus cattle. Functional and Integrative Genomics, 2012, 12, 81-92.	3.5	87
79	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
80	Design of a Bovine Low-Density SNP Array Optimized for Imputation. PLoS ONE, 2012, 7, e34130.	2.5	159
81	How Bioinformatics Enables Livestock Applied Sciences in the Genomic Era. Lecture Notes in Computer Science, 2012, , 192-201.	1.3	1
82	Genomic characteristics of cattle copy number variations. BMC Genomics, 2011, 12, 127.	2.8	201
83	Genome-wide association analysis of thirty one production, health, reproduction and body conformation traits in contemporary U.S. Holstein cows. BMC Genomics, 2011, 12, 408.	2.8	349
84	Enhanced mitochondrial complex gene function and reduced liver size may mediate improved feed efficiency of beef cattle during compensatory growth. Functional and Integrative Genomics, 2010, 10, 39-51.	3.5	99
85	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	5.6	348
86	Analysis of copy number variations among diverse cattle breeds. Genome Research, 2010, 20, 693-703.	5.5	280
87	Prediction of unobserved single nucleotide polymorphism genotypes of Jersey cattle using reference panels and population-based imputation algorithms. Journal of Dairy Science, 2010, 93, 2229-2238.	3.4	58
88	Accuracy of direct genomic values derived from imputed single nucleotide polymorphism genotypes in Jersey cattle. Journal of Dairy Science, 2010, 93, 5423-5435.	3.4	85
89	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
90	Characterization of DGAT1 Allelic Effects in a Sample of North American Holstein Cattle. Animal Biotechnology, 2010, 21, 88-99.	1.5	17

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91	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. PLoS ONE, 2009, 4, e5350.	2.5	813
92	Design of a High Density SNP Genotyping Assay in the Pig Using SNPs Identified and Characterized by Next Generation Sequencing Technology. PLoS ONE, 2009, 4, e6524.	2.5	568
93	A Validated Genome Wide Association Study to Breed Cattle Adapted to an Environment Altered by Climate Change. PLoS ONE, 2009, 4, e6676.	2.5	122
94	Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 18644-18649.	7.1	196
95	Unlocking the bovine genome. BMC Genomics, 2009, 10, 193.	2.8	46
96	High-resolution haplotype block structure in the cattle genome. BMC Genetics, 2009, 10, 19.	2.7	141
97	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
98	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	12.6	746
99	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . Genome Biology, 2009, 10, R42.	9.6	1,005
100	Invited Review: Reliability of genomic predictions for North American Holstein bulls. Journal of Dairy Science, 2009, 92, 16-24.	3.4	1,008
101	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
102	Distribution and location of genetic effects for dairy traits. Journal of Dairy Science, 2009, 92, 2931-2946.	3.4	210
103	Prevalence of the prion protein gene E211K variant in U.S. cattle. BMC Veterinary Research, 2008, 4, 25.	1.9	46
104	An assessment of population structure in eight breeds of cattle using a whole genome SNP panel. BMC Genetics, 2008, 9, 37.	2.7	95
105	Comparative transcriptome analysis of in vivo and in vitro produced porcine blastocysts by small amplified RNA Serial analysis of gene expression (SAR-SAGE). Molecular Reproduction and Development, 2008, 75, 976-988.	2.0	30
106	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. Nature Methods, 2008, 5, 247-252.	19.0	534
107	Association analysis of bovine bactericidal/permeability-increasing protein gene polymorphisms with somatic cell score in Holstein cattle. Animal Genetics, 2008, 39, 456-457.	1.7	1
108	Characterization of a novel microdeletion polymorphism on BTA5 in cattle. Animal Genetics, 2008, 39, 655-658.	1.7	3

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109	Effects of increased milking frequency on gene expression in the bovine mammary gland. BMC Genomics, 2008, 9, 362.	2.8	53
110	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
111	Environmental Sampling To Predict Fecal Prevalence of Salmonella in an Intensively Monitored Dairy Herd. Journal of Food Protection, 2008, 71, 1967-1973.	1.7	32
112	A Soybean Transcript Map: Gene Distribution, Haplotype and Single-Nucleotide Polymorphism Analysis. Genetics, 2007, 176, 685-696.	2.9	285
113	Discovery and profiling of bovine microRNAs from immune-related and embryonic tissues. Physiological Genomics, 2007, 29, 35-43.	2.3	104
114	A physical map of the bovine genome. Genome Biology, 2007, 8, R165.	9.6	73
115	Predicting Perchlorate Exposure in Milk from Concentrations in Dairy Feed. Journal of Agricultural and Food Chemistry, 2007, 55, 8806-8813.	5.2	17
116	Local inflammation as a possible mechanism of resistance to gastrointestinal nematodes in Angus heifers. Veterinary Parasitology, 2007, 145, 100-107.	1.8	42
117	Whole genome linkage disequilibrium maps in cattle. BMC Genetics, 2007, 8, 74.	2.7	201
118	Construction of bovine whole-genome radiation hybrid and linkage maps using high-throughput genotyping. Animal Genetics, 2007, 38, 120-125.	1.7	36
119	Identification of estrogen-responsive genes in the parenchyma and fat pad of the bovine mammary gland by microarray analysis. Physiological Genomics, 2006, 27, 42-53.	2.3	61
120	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
121	Application of machine learning in SNP discovery. BMC Bioinformatics, 2006, 7, 4.	2.6	43
122	SNP-PHAGE-High throughput SNP discovery pipeline. BMC Bioinformatics, 2006, 7, 468.	2.6	29
123	Genomic divergences among cattle, dog and human estimated from large-scale alignments of genomic sequences. BMC Genomics, 2006, 7, 140.	2.8	33
124	Serial analysis of gene expression during elongation of the peri-implantation porcine trophectoderm (conceptus). Physiological Genomics, 2005, 20, 188-194.	2.3	65
125	Expressed Sequence Tag Analysis of <i>Eimeria</i> -Stimulated Intestinal Intraepithelial Lymphocytes in Chickens. Molecular Biotechnology, 2005, 30, 143-150.	2.4	34
126	Characterization of 954 bovine full-CDS cDNA sequences. BMC Genomics, 2005, 6, 166.	2.8	26

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127	Fate of dietary perchlorate in lactating dairy cows: Relevance to animal health and levels in the milk supply. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16152-16157.	7.1	36
128	CHARACTERIZATION OF A NORMALIZED CDNA LIBRARY FROM BOVINE INTESTINAL MUSCLE AND EPITHELIAL TISSUES. Animal Biotechnology, 2005, 16, 17-29.	1.5	5
129	Detection of Quantitative Trait Loci Influencing Conformation Traits and Calving Ease in Holstein-Friesian Cattle. Journal of Dairy Science, 2005, 88, 4111-4119.	3.4	56
130	Fine-mapping milk production quantitative trait loci on BTA6: Analysis of the bovine osteopontin gene. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6896-6901.	7.1	95
131	EST-PAGE--managing and analyzing EST data. Bioinformatics, 2004, 20, 286-288.	4.1	26
132	Characterization of open reading frame-expressed sequence tags generated from Bos indicus and B. taurus mammary gland cDNA libraries. Animal Genetics, 2004, 35, 213-219.	1.7	5
133	Physical and linkage mapping of mammary-derived expressed sequence tags in cattle. Genomics, 2004, 83, 148-152.	2.9	3
134	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
135	Detection of Quantitative Trait Loci Affecting Milk Production, Health, and Reproductive Traits in Holstein Cattle. Journal of Dairy Science, 2004, 87, 468-475.	3.4	189
136	Bovine genomics update: making a cow jump over the moon. Genetical Research, 2004, 84, 3-9.	0.9	12
137	Calving Ease (Co)Variance Components for a Sire-Maternal Grandsire Threshold Model. Journal of Dairy Science, 2003, 86, 1845-1848.	3.4	38
138	Implementation of a Sire-Maternal Grandsire Model for Evaluation of Calving Ease in the United States. Journal of Dairy Science, 2003, 86, 3366-3373.	3.4	38
139	Mapping quantitative trait loci associated with resistance to coccidiosis and growth. Poultry Science, 2003, 82, 9-16.	3.4	57
140	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
141	Single-Nucleotide Polymorphisms in Soybean. Genetics, 2003, 163, 1123-1134.	2.9	367
142	Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index. Mammalian Genome, 2002, 13, 373-379.	2.2	48
143	Effect of Somatotropin on Thyroid Hormones and Cytokines in Lactating Dairy Cows During Ad Libitum and Restricted Feed Intake. Journal of Dairy Science, 2001, 84, 2430-2439.	3.4	38
144	A Genome Scan To Identify Quantitative Trait Loci Affecting Economically Important Traits in a US Holstein Population. Journal of Dairy Science, 2001, 84, 2535-2542.	3.4	58

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145	Consensus and comprehensive linkage maps of bovine chromosome 17. <i>Animal Genetics</i> , 2001, 32, 112-113.	1.7	2
146	Consensus and comprehensive linkage maps of bovine chromosome 25. <i>Animal Genetics</i> , 2001, 32, 114-115.	1.7	1
147	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, 682-688.	2.2	47
148	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
149	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
150	Circulating Concentrations of Estradiol, Luteinizing Hormone, and Follicle-Stimulating Hormone during Waves of Ovarian Follicular Development in Prepubertal Cattle ¹ . <i>Biology of Reproduction</i> , 1999, 60, 405-412.	2.7	49
151	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
152	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
153	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
154	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
155	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.	0.5	13
156	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
157	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.	0.5	43
158	Effects of exogenous somatotropin on whole-body glycemic response to insulin in young preruminant and ruminant lambs. <i>Domestic Animal Endocrinology</i> , 1995, 12, 143-156.	1.6	9
159	Production Evaluation Techniques Based on Lactation Curves. <i>Journal of Dairy Science</i> , 1995, 78, 457-465.	3.4	7
160	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.	3.4	41
161	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.	3.4	7
162	Inheritance of Renal Amyloidosis in Chinese Shar-pei Dogs. <i>Journal of Heredity</i> , 1993, 84, 438-442.	2.4	29

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163	Estimates of Genetic Selection Differentials and Generation Intervals for Four Paths of Selection. Journal of Dairy Science, 1991, 74, 1078-1086.	3.4	59
164	Prediction of Progeny Genetic Evaluations from Simultaneous Genetic Evaluations of the Dam, Sire, and Maternal Grandsire with an Animal Model. Journal of Dairy Science, 1989, 72, 1578-1582.	3.4	2
165	Comparison of Heritability and Variation for Milk Yield of Registered and Nonregistered Holstein Cows. Journal of Dairy Science, 1988, 71, 2271-2277.	3.4	1