

Curtis P Van Tassell

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6422786/curtis-p-van-tassell-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

165
papers

12,682
citations

50
h-index

110
g-index

167
ext. papers

15,383
ext. citations

5.2
avg, IF

5.66
L-index

#	Paper	IF	Citations
165	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
164	Towards the detection of copy number variation from single sperm sequencing in cattle.. <i>BMC Genomics</i> , 2022 , 23, 215	4.5	
163	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
162	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021 , 22, 398	4.5	0
161	Functional Variants Surrounding Endothelin 2 Are Associated With Subspecies Infection. <i>Frontiers in Veterinary Science</i> , 2021 , 8, 625323	3.1	1
160	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
159	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. <i>Genomics</i> , 2021 , 113, 2045-2055	4.3	3
158	Genomic evaluation of dairy heifer livability. <i>Journal of Dairy Science</i> , 2021 , 104, 8959-8965	4	0
157	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
156	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
155	Tangible and intangible benefits of local goats rearing in smallholder farms in Malawi. <i>Small Ruminant Research</i> , 2020 , 187, 106095	1.7	11
154	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. <i>Genomics</i> , 2020 , 112, 1477-1480	4.3	4
153	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020 , 9,	7.6	140
152	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
151	Timing and Extent of Inbreeding in African Goats. <i>Frontiers in Genetics</i> , 2019 , 10, 537	4.5	8
150	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
149	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

148	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
147	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
146	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019 , 122, 636-646	3.6	29
145	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
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	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
142	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018 , 50, 57	4.9	69
141	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
140	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
139	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
138	Systematic Profiling of Short Tandem Repeats in the Cattle Genome. <i>Genome Biology and Evolution</i> , 2017 , 9, 20-31	3.9	8
137	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
136	Population-genetic properties of differentiated copy number variations in cattle. <i>Scientific Reports</i> , 2016 , 6, 23161	4.9	52
135	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
134	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
133	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
132	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
131	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

130	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
129	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
128	Genomic Regions Associated with Sheep Resistance to Gastrointestinal Nematodes. <i>Trends in Parasitology</i> , 2016 , 32, 470-480	6.4	27
127	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
126	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
125	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
124	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
123	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
122	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
121	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
120	The Relationship between Runs of Homozygosity and Inbreeding in Jersey Cattle under Selection. <i>PLoS ONE</i> , 2015 , 10, e0129967	3.7	45
119	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014 , 15, 683	4.5	63
118	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
117	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
116	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	1.7	49
115	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
114	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
113	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

112	Accuracy of genotype imputation in Nelore cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 69	4.9	51
111	Genome-wide detection of signatures of selection in Korean Hanwoo cattle. <i>Animal Genetics</i> , 2014 , 45, 180-90	2.5	25
110	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
109	Accuracy of genomic predictions in <i>Bos indicus</i> (Nelore) cattle. <i>Genetics Selection Evolution</i> , 2014 , 46, 17	4.9	60
108	Genome-wide mapping of loci explaining variance in scrotal circumference in Nelore cattle. <i>PLoS ONE</i> , 2014 , 9, e88561	3.7	29
107	High density LD-based structural variations analysis in cattle genome. <i>PLoS ONE</i> , 2014 , 9, e103046	3.7	5
106	Genome-wide association study for birth weight in Nelore cattle points to previously described orthologous genes affecting human and bovine height. <i>BMC Genetics</i> , 2013 , 14, 52	2.6	83
105	Genomic divergence of zebu and taurine cattle identified through high-density SNP genotyping. <i>BMC Genomics</i> , 2013 , 14, 876	4.5	93
104	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
103	Quantitative trait loci for resistance to <i>Haemonchus contortus</i> artificial challenge in Red Maasai and Dorper sheep of East Africa. <i>Animal Genetics</i> , 2013 , 44, 285-95	2.5	24
102	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
101	Methods of tagSNP selection and other variables affecting imputation accuracy in swine. <i>BMC Genetics</i> , 2013 , 14, 8	2.6	33
100	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
99	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
98	Effect of artificial selection on runs of homozygosity in u.s. Holstein cattle. <i>PLoS ONE</i> , 2013 , 8, e80813	3.7	114
97	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
96	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
95	Whole genome SNP discovery and analysis of genetic diversity in Turkey (<i>Meleagris gallopavo</i>). <i>BMC Genomics</i> , 2012 , 13, 391	4.5	49

94	Effect of sample stratification on dairy GWAS results. <i>BMC Genomics</i> , 2012 , 13, 536	4.5	28
93	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012 , 22, 778-90	9.7	204
92	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
91	Imputation of microsatellite alleles from dense SNP genotypes for parental verification. <i>Frontiers in Genetics</i> , 2012 , 3, 140	4.5	15
90	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
89	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
88	Design of a bovine low-density SNP array optimized for imputation. <i>PLoS ONE</i> , 2012 , 7, e34130	3.7	132
87	How Bioinformatics Enables Livestock Applied Sciences in the Genomic Era. <i>Lecture Notes in Computer Science</i> , 2012 , 192-201	0.9	0
86	Box-Cox Transformation and Random Regression Models for Fecal egg Count Data. <i>Frontiers in Genetics</i> , 2011 , 2, 112	4.5	5
85	Genomic characteristics of cattle copy number variations. <i>BMC Genomics</i> , 2011 , 12, 127	4.5	156
84	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
83	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
82	Analysis of copy number variations among diverse cattle breeds. <i>Genome Research</i> , 2010 , 20, 693-703	9.7	214
81	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	4.1	51
80	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
79	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
78	Characterization of DGAT1 allelic effects in a sample of North American Holstein cattle. <i>Animal Biotechnology</i> , 2010 , 21, 88-99	1.4	12
77	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

76	Development and characterization of a high density SNP genotyping assay for cattle. <i>PLoS ONE</i> , 2009 , 4, e5350	3.7	666
75	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
74	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
73	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
72	High-resolution haplotype block structure in the cattle genome. <i>BMC Genetics</i> , 2009 , 10, 19	2.6	117
71	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , 2009 , 324, 522-8	33.3	863
70	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
69	A whole-genome assembly of the domestic cow, <i>Bos taurus</i> . <i>Genome Biology</i> , 2009 , 10, R42	18.3	798
68	Invited review: reliability of genomic predictions for North American Holstein bulls. <i>Journal of Dairy Science</i> , 2009 , 92, 16-24	4	815
67	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
66	Distribution and location of genetic effects for dairy traits. <i>Journal of Dairy Science</i> , 2009 , 92, 2931-46	4	186
65	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. <i>Nature Methods</i> , 2008 , 5, 247-52	21.6	458
64	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
63	Characterization of a novel microdeletion polymorphism on BTA5 in cattle. <i>Animal Genetics</i> , 2008 , 39, 655-8	2.5	3
62	Effects of increased milking frequency on gene expression in the bovine mammary gland. <i>BMC Genomics</i> , 2008 , 9, 362	4.5	44
61	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
60	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
59	Prevalence of the prion protein gene E211K variant in U.S. cattle. <i>BMC Veterinary Research</i> , 2008 , 4, 25	2.7	39

58	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
57	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
56	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
55	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
54	Whole genome linkage disequilibrium maps in cattle. <i>BMC Genetics</i> , 2007 , 8, 74	2.6	165
53	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
52	A soybean transcript map: gene distribution, haplotype and single-nucleotide polymorphism analysis. <i>Genetics</i> , 2007 , 176, 685-96	4	258
51	Discovery and profiling of bovine microRNAs from immune-related and embryonic tissues. <i>Physiological Genomics</i> , 2007 , 29, 35-43	3.6	87
50	A physical map of the bovine genome. <i>Genome Biology</i> , 2007 , 8, R165	18.3	67
49	Application of machine learning in SNP discovery. <i>BMC Bioinformatics</i> , 2006 , 7, 4	3.6	25
48	SNP-PHAGE--High throughput SNP discovery pipeline. <i>BMC Bioinformatics</i> , 2006 , 7, 468	3.6	23
47	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
46	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
45	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
44	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
43	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
42	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
41	Expressed sequence tag analysis of Eimeria-stimulated intestinal intraepithelial lymphocytes in chickens. <i>Molecular Biotechnology</i> , 2005 , 30, 143-50	3	30

40	Characterization of 954 bovine full-CDS cDNA sequences. <i>BMC Genomics</i> , 2005 , 6, 166	4.5	21
39	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
38	Characterization of a normalized cDNA library from bovine intestinal muscle and epithelial tissues. <i>Animal Biotechnology</i> , 2005 , 16, 17-29	1.4	2
37	EST-PAGE--managing and analyzing EST data. <i>Bioinformatics</i> , 2004 , 20, 286-8	7.2	23
36	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, 213-9	2.5	5
35	Physical and linkage mapping of mammary-derived expressed sequence tags in cattle. <i>Genomics</i> , 2004 , 83, 148-52	4.3	3
34	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
33	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
32	Bovine genomics update: making a cow jump over the moon. <i>Genetical Research</i> , 2004 , 84, 3-9	1.1	11
31	Calving ease (Co)variance components for a sire-maternal grandsire threshold model. <i>Journal of Dairy Science</i> , 2003 , 86, 1845-8	4	33
30	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
29	Mapping quantitative trait loci associated with resistance to coccidiosis and growth. <i>Poultry Science</i> , 2003 , 82, 9-16	3.9	45
28	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
27	Single-nucleotide polymorphisms in soybean. <i>Genetics</i> , 2003 , 163, 1123-34	4	332
26	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
25	Consensus and comprehensive linkage maps of bovine chromosome 17. <i>Animal Genetics</i> , 2001 , 32, 112-32.5		1
24	Consensus and comprehensive linkage maps of bovine chromosome 25. <i>Animal Genetics</i> , 2001 , 32, 114-52.5		1
23	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

22	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
21	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
20	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
19	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
18	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
17	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
16	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
15	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
14	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
13	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
12	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
11	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
10	Effects of exogenous somatotropin on whole-body glycemic response to insulin in young preruminant and ruminant lambs. <i>Domestic Animal Endocrinology</i> , 1995 , 12, 143-56	2.3	8
9	Production evaluation techniques based on lactation curves. <i>Journal of Dairy Science</i> , 1995 , 78, 457-65	4	6
8	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
7	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
6	Inheritance of renal amyloidosis in Chinese Shar-pei dogs. <i>Journal of Heredity</i> , 1993 , 84, 438-42	2.4	21
5	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

4	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
3	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
2	Single-molecule sequencing and conformational capture enable de novo mammalian reference genomes		12
1	A comprehensive catalogue of regulatory variants in the cattle transcriptome		6