

John B Cole

List of Publications by Year in descending order

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Version: 2024-02-01

144
papers

7,658
citations

53660

45
h-index

62479

80
g-index

152
all docs

152
docs citations

152
times ranked

5162
citing authors

#	ARTICLE	IF	CITATIONS
1	Temperature-Humidity Indices as Indicators of Milk Production Losses due to Heat Stress. <i>Journal of Dairy Science</i> , 2007, 90, 1947-1956.	1.4	464
2	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.	3.3	395
3	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	3.3	380
4	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.	1.2	349
5	Genomic Selection in Dairy Cattle: The USDA Experience. <i>Annual Review of Animal Biosciences</i> , 2017, 5, 309-327.	3.6	257
6	Distribution and location of genetic effects for dairy traits. <i>Journal of Dairy Science</i> , 2009, 92, 2931-2946.	1.4	210
7	Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. <i>Animal</i> , 2015, 9, 191-207.	1.3	177
8	Genomic Signatures Reveal New Evidences for Selection of Important Traits in Domestic Cattle. <i>Molecular Biology and Evolution</i> , 2015, 32, 711-725.	3.5	173
9	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. <i>PLoS Genetics</i> , 2015, 11, e1005387.	1.5	168
10	Effect of Artificial Selection on Runs of Homozygosity in U.S. Holstein Cattle. <i>PLoS ONE</i> , 2013, 8, e80813.	1.1	165
11	Genomic imputation and evaluation using high-density Holstein genotypes. <i>Journal of Dairy Science</i> , 2013, 96, 668-678.	1.4	163
12	Discovery of single nucleotide polymorphisms in candidate genes associated with fertility and production traits in Holstein cattle. <i>BMC Genetics</i> , 2013, 14, 49.	2.7	140
13	A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 412.	1.1	136
14	Symposium review: Possibilities in an age of genomics: The future of selection indices. <i>Journal of Dairy Science</i> , 2018, 101, 3686-3701.	1.4	120
15	A Genome-Wide Association Study for Clinical Mastitis in First Parity US Holstein Cows Using Single-Step Approach and Genomic Matrix Re-Weighting Procedure. <i>PLoS ONE</i> , 2015, 10, e0114919.	1.1	113
16	Selecting sequence variants to improve genomic predictions for dairy cattle. <i>Genetics Selection Evolution</i> , 2017, 49, 32.	1.2	113
17	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
18	Genetic and environmental factors that affect gestation length in dairy cattle. <i>Journal of Dairy Science</i> , 2009, 92, 2259-2269.	1.4	106

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19	Genomic inbreeding and relationships among Holsteins, Jerseys, and Brown Swiss. <i>Journal of Dairy Science</i> , 2011, 94, 5673-5682.	1.4	104
20	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. <i>Genome Research</i> , 2020, 30, 790-801.	2.4	97
21	Genomic selection for producer-recorded health event data in US dairy cattle. <i>Journal of Dairy Science</i> , 2014, 97, 3190-3199.	1.4	96
22	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. <i>BMC Genomics</i> , 2014, 15, 683.	1.2	89
23	Identification of a Nonsense Mutation in CWC15 Associated with Decreased Reproductive Efficiency in Jersey Cattle. <i>PLoS ONE</i> , 2013, 8, e54872.	1.1	88
24	Genome-Wide Association Mapping for Identification of Quantitative Trait Loci for Rectal Temperature during Heat Stress in Holstein Cattle. <i>PLoS ONE</i> , 2013, 8, e69202.	1.1	86
25	Heritability of rectal temperature and genetic correlations with production and reproduction traits in dairy cattle. <i>Journal of Dairy Science</i> , 2012, 95, 3401-3405.	1.4	84
26	Genomewide Association Study of African Children Identifies Association of SCHIP1 and PDE8A with Facial Size and Shape. <i>PLoS Genetics</i> , 2016, 12, e1006174.	1.5	81
27	Symposium review: Genetics, genome-wide association study, and genetic improvement of dairy fertility traits. <i>Journal of Dairy Science</i> , 2019, 102, 3735-3743.	1.4	78
28	Accuracy of genomic predictions in <i>Bos indicus</i> (Nellore) cattle. <i>Genetics Selection Evolution</i> , 2014, 46, 17.	1.2	77
29	Improvement of Prediction Ability for Genomic Selection of Dairy Cattle by Including Dominance Effects. <i>PLoS ONE</i> , 2014, 9, e103934.	1.1	74
30	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.	1.1	69
31	Assessment of autozygosity in Nellore cows (<i>Bos indicus</i>) through high-density SNP genotypes. <i>Frontiers in Genetics</i> , 2015, 6, 5.	1.1	69
32	Invited review: Opportunities for genetic improvement of metabolic diseases. <i>Journal of Dairy Science</i> , 2016, 99, 6855-6873.	1.4	69
33	Phenotypic and genetic effects of recessive haplotypes on yield, longevity, and fertility. <i>Journal of Dairy Science</i> , 2016, 99, 7274-7288.	1.4	67
34	Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. <i>Journal of Dairy Science</i> , 2018, 101, 4801-4821.	1.4	66
35	GWAS and fine-mapping of livability and six disease traits in Holstein cattle. <i>BMC Genomics</i> , 2020, 21, 41.	1.2	66
36	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. <i>Frontiers in Genetics</i> , 2019, 10, 1197.	1.1	64

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37	Productive Life and Reasons for Disposal of Holstein Cows Selected for Large Versus Small Body Size. <i>Journal of Dairy Science</i> , 1999, 82, 795-801.	1.4	63
38	Functional annotation and Bayesian fine-mapping reveals candidate genes for important agronomic traits in Holstein bulls. <i>Communications Biology</i> , 2019, 2, 212.	2.0	61
39	A simple strategy for managing many recessive disorders in a dairy cattle breeding program. <i>Genetics Selection Evolution</i> , 2015, 47, 94.	1.2	59
40	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016, 23, 253-262.	1.5	59
41	Explorations in genome-wide association studies and network analyses with dairy cattle fertility traits. <i>Journal of Dairy Science</i> , 2016, 99, 6420-6435.	1.4	59
42	Technical note: Adjustment of traditional cow evaluations to improve accuracy of genomic predictions. <i>Journal of Dairy Science</i> , 2011, 94, 6188-6193.	1.4	58
43	Use of single nucleotide polymorphisms in candidate genes associated with daughter pregnancy rate for prediction of genetic merit for reproduction in Holstein cows. <i>Animal Genetics</i> , 2016, 47, 288-297.	0.6	57
44	Genetic evaluation of lactation persistency for five breeds of dairy cattle. <i>Journal of Dairy Science</i> , 2009, 92, 2248-2258.	1.4	55
45	Genetic Evaluation and Best Prediction of Lactation Persistency. <i>Journal of Dairy Science</i> , 2006, 89, 2722-2728.	1.4	47
46	Single nucleotide variants and InDels identified from whole-genome re-sequencing of Guzerat, Gyr, Girolando and Holstein cattle breeds. <i>PLoS ONE</i> , 2017, 12, e0173954.	1.1	47
47	Genetic Evaluations for Mixed-Breed Populations. <i>Journal of Dairy Science</i> , 2007, 90, 2434-2441.	1.4	46
48	Dissection of additive, dominance, and imprinting effects for production and reproduction traits in Holstein cattle. <i>BMC Genomics</i> , 2017, 18, 425.	1.2	46
49	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. <i>Frontiers in Genetics</i> , 2018, 9, 57.	1.1	45
50	Comparison of gene editing versus conventional breeding to introgress the POLLED allele into the US dairy cattle population. <i>Journal of Dairy Science</i> , 2019, 102, 4215-4226.	1.4	45
51	Single Nucleotide Polymorphisms in Candidate Genes Associated with Fertilizing Ability of Sperm and Subsequent Embryonic Development in Cattle. <i>Biology of Reproduction</i> , 2013, 89, 69.	1.2	42
52	Genetic and epigenetic architecture of paternal origin contribute to gestation length in cattle. <i>Communications Biology</i> , 2019, 2, 100.	2.0	41
53	Incidence validation and relationship analysis of producer-recorded health event data from on-farm computer systems in the United States. <i>Journal of Dairy Science</i> , 2012, 95, 5422-5435.	1.4	40
54	Single nucleotide polymorphisms associated with thermoregulation in lactating dairy cows exposed to heat stress. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 409-419.	0.8	40

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55	Genomic evaluation of age at first calving. <i>Journal of Dairy Science</i> , 2017, 100, 6853-6861.	1.4	39
56	Genome changes due to artificial selection in U.S. Holstein cattle. <i>BMC Genomics</i> , 2019, 20, 128.	1.2	39
57	A genome-wide association study of calf birth weight in Holstein cattle using single nucleotide polymorphisms and phenotypes predicted from auxiliary traits. <i>Journal of Dairy Science</i> , 2014, 97, 3156-3172.	1.4	38
58	High-density genome-wide association study for residual feed intake in Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 11067-11080.	1.4	38
59	Phenotypic and genetic relationships of common health disorders with milk and fat yield persistencies from producer-recorded health data and test-day yields. <i>Journal of Dairy Science</i> , 2009, 92, 1785-1795.	1.4	37
60	Best prediction of yields for long lactations. <i>Journal of Dairy Science</i> , 2009, 92, 1796-1810.	1.4	35
61	Evaluation of genetic components in traits related to superovulation, in vitro fertilization, and embryo transfer in Holstein cattle. <i>Journal of Dairy Science</i> , 2017, 100, 2877-2891.	1.4	35
62	A single nucleotide polymorphism in COQ9 affects mitochondrial and ovarian function and fertility in Holstein cows. <i>Biology of Reproduction</i> , 2017, 96, 652-663.	1.2	35
63	Genomic prediction of residual feed intake in US Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2020, 103, 2477-2486.	1.4	35
64	BREEDING AND GENETICS SYMPOSIUM: Really big data: Processing and analysis of very large data sets1. <i>Journal of Animal Science</i> , 2012, 90, 723-733.	0.2	34
65	Array CGH-based detection of CNV regions and their potential association with reproduction and other economic traits in Holsteins. <i>BMC Genomics</i> , 2019, 20, 181.	1.2	34
66	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. <i>BMC Biology</i> , 2020, 18, 85.	1.7	34
67	Effect of sample stratification on dairy GWAS results. <i>BMC Genomics</i> , 2012, 13, 536.	1.2	33
68	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. <i>PLoS ONE</i> , 2014, 9, e88561.	1.1	33
69	Stillbirth (Co)Variance Components for a Sire-Maternal Grand sire Threshold Model and Development of a Calving Ability Index for Sire Selection. <i>Journal of Dairy Science</i> , 2007, 90, 2489-2496.	1.4	32
70	Use of haplotypes to estimate Mendelian sampling effects and selection limits. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 446-455.	0.8	32
71	Association of single nucleotide polymorphisms in candidate genes previously related to genetic variation in fertility with phenotypic measurements of reproductive function in Holstein cows. <i>Journal of Dairy Science</i> , 2017, 100, 3725-3734.	1.4	32
72	The future of phenomics in dairy cattle breeding. <i>Animal Frontiers</i> , 2020, 10, 37-44.	0.8	32

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73	PyPedal: A computer program for pedigree analysis. <i>Computers and Electronics in Agriculture</i> , 2007, 57, 107-113.	3.7	31
74	Genetic parameters of milk ELISA scores for Johne's disease. <i>Journal of Dairy Science</i> , 2010, 93, 1729-1735.	1.4	31
75	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers ^{1,2} . <i>Journal of Animal Science</i> , 2017, 95, 4796-4812.	0.2	31
76	Defining the optimal period length and stage of growth or lactation to estimate residual feed intake in dairy cows. <i>Journal of Dairy Science</i> , 2019, 102, 6131-6143.	1.4	31
77	Symposium review: Exploiting homozygosity in the era of genomics—Selection, inbreeding, and mating programs. <i>Journal of Dairy Science</i> , 2020, 103, 5302-5313.	1.4	30
78	Genomewide association study of reproductive efficiency in female cattle ^{1,2,3,4} . <i>Journal of Animal Science</i> , 2014, 92, 1945-1957.	0.2	29
79	Genetic Evaluation of Stillbirth in United States Holsteins Using a Sire-Maternal Grand sire Threshold Model. <i>Journal of Dairy Science</i> , 2007, 90, 2480-2488.	1.4	28
80	Phenotypic Relationships of Common Health Disorders in Dairy Cows to Lactation Persistency Estimated from Daily Milk Weights. <i>Journal of Dairy Science</i> , 2007, 90, 4424-4434.	1.4	28
81	Genomic evaluation, breed identification, and discovery of a haplotype affecting fertility for Ayrshire dairy cattle. <i>Journal of Dairy Science</i> , 2014, 97, 3878-3882.	1.4	28
82	Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. <i>BMC Biology</i> , 2020, 18, 80.	1.7	28
83	Invited review: The future of selection decisions and breeding programs: What are we breeding for, and who decides?. <i>Journal of Dairy Science</i> , 2021, 104, 5111-5124.	1.4	28
84	Population structure of a colony of dog guides. <i>Journal of Animal Science</i> , 2004, 82, 2906-2912.	0.2	26
85	Genetic Evaluation of Calving Ease for Brown Swiss and Jersey Bulls from Purebred and Crossbred Calvings. <i>Journal of Dairy Science</i> , 2005, 88, 1529-1539.	1.4	26
86	Short communication: Use of young bulls in the United States. <i>Journal of Dairy Science</i> , 2014, 97, 3213-3220.	1.4	25
87	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.	1.3	25
88	Investigating conception rate for beef service sires bred to dairy cows and heifers. <i>Journal of Dairy Science</i> , 2020, 103, 10374-10382.	1.4	23
89	Trends in genetic diversity and the effect of inbreeding in American Angus cattle under genomic selection. <i>Genetics Selection Evolution</i> , 2021, 53, 50.	1.2	22
90	Economic considerations of breeding for polled dairy cows versus dehorning in the United States. <i>Journal of Dairy Science</i> , 2017, 100, 4941-4952.	1.4	21

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91	Variance of gametic diversity and its application in selection programs. <i>Journal of Dairy Science</i> , 2019, 102, 5279-5294.	1.4	21
92	The development of genomics applied to dairy breeding. <i>Livestock Science</i> , 2014, 166, 66-75.	0.6	19
93	Analyses of inter-individual variations of sperm DNA methylation and their potential implications in cattle. <i>BMC Genomics</i> , 2019, 20, 888.	1.2	19
94	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.	1.1	18
95	Symposium review: Development, implementation, and perspectives of health evaluations in the United States. <i>Journal of Dairy Science</i> , 2020, 103, 5354-5365.	1.4	18
96	Stochastic dynamic simulation modeling including multitrait genetics to estimate genetic, technical, and financial consequences of dairy farm reproduction and selection strategies. <i>Journal of Dairy Science</i> , 2016, 99, 8187-8202.	1.4	17
97	Visualization of results from genomic evaluations. <i>Journal of Dairy Science</i> , 2010, 93, 2727-2740.	1.4	16
98	Reducing animal sequencing redundancy by preferentially selecting animals with low-frequency haplotypes. <i>Journal of Dairy Science</i> , 2016, 99, 5526-5534.	1.4	16
99	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. <i>Genomics</i> , 2021, 113, 2045-2055.	1.3	16
100	Short communication: Genetic evaluation of stillbirth in US Brown Swiss and Jersey cattle. <i>Journal of Dairy Science</i> , 2014, 97, 2474-2480.	1.4	15
101	Construction of PRDM9 allele-specific recombination maps in cattle using large-scale pedigree analysis and genome-wide single sperm genomics. <i>DNA Research</i> , 2018, 25, 183-194.	1.5	15
102	Genotype imputation in a tropical crossbred dairy cattle population. <i>Journal of Dairy Science</i> , 2017, 100, 9623-9634.	1.4	13
103	Short communication: Best prediction of 305-day lactation yields with regional and seasonal effects. <i>Journal of Dairy Science</i> , 2011, 94, 1601-1604.	1.4	12
104	Dissection of genomic correlation matrices of US Holsteins using multivariate factor analysis. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 9-20.	0.8	12
105	Genomic selection in multi-breed dairy cattle populations. <i>Revista Brasileira De Zootecnia</i> , 2016, 45, 195-202.	0.3	12
106	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.	0.8	12
107	Estimating the effect of the deleterious recessive haplotypes AH1 and AH2 on reproduction performance of Ayrshire cattle. <i>Journal of Dairy Science</i> , 2019, 102, 5315-5322.	1.4	12
108	Comparison of Gene Editing Versus Conventional Breeding to Introgress the POLLED Allele Into the Tropically Adapted Australian Beef Cattle Population. <i>Frontiers in Genetics</i> , 2021, 12, 593154.	1.1	12

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109	Short communication: Projecting milk yield using best prediction and the MilkBot lactation model. <i>Journal of Dairy Science</i> , 2012, 95, 4041-4044.	1.4	11
110	Tropospheric Ozone in Louisiana and Synoptic Circulation. <i>Journal of Applied Meteorology and Climatology</i> , 2004, 43, 1438-1451.	1.7	10
111	Major quantitative trait loci influencing milk production and conformation traits in Guernsey dairy cattle detected on Bos taurus autosome 19. <i>Journal of Dairy Science</i> , 2021, 104, 550-560.	1.4	10
112	Modeling pedigree accuracy and uncertain parentage in single-step genomic evaluations of simulated and US Holstein datasets. <i>Journal of Dairy Science</i> , 2019, 102, 2308-2318.	1.4	9
113	Development of a Lifetime Merit-based selection index for US dairy grazing systems. <i>Journal of Dairy Science</i> , 2014, 97, 4568-4578.	1.4	8
114	Validating the Use of Bovine Buccal Sampling as a Proxy for the Rumen Microbiota by Using a Time Course and Random Forest Classification Approach. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	8
115	Multiparity Evaluation of Calving Ease and Stillbirth with Separate Genetic Effects by Parity. <i>Journal of Dairy Science</i> , 2008, 91, 3173-3178.	1.4	7
116	Genetic and nongenetic profiling of milk pregnancy-associated glycoproteins in Holstein cattle. <i>Journal of Dairy Science</i> , 2018, 101, 9987-10000.	1.4	7
117	Discovering ancestors and connecting relatives in large genomic databases. <i>Journal of Dairy Science</i> , 2020, 103, 1729-1734.	1.4	7
118	Visualization of the transmission of direct genomic values for paternal and maternal chromosomes for 15 traits in US Brown Swiss, Holstein, and Jersey cattle. <i>Journal of Dairy Science</i> , 2013, 96, 2713-2726.	1.4	6
119	Benchmarking dairy herd health status using routinely recorded herd summary data. <i>Journal of Dairy Science</i> , 2016, 99, 1298-1314.	1.4	6
120	Simulation of introgression of the POLLED allele into the Jersey breed via conventional breeding vs. gene editing ¹ . <i>Translational Animal Science</i> , 2018, 2, S57-S60.	0.4	5
121	Impact of genetic merit for milk somatic cell score of sires and maternal grandsires on herd life of their daughters. <i>Journal of Dairy Science</i> , 2009, 92, 2224-2228.	1.4	4
122	Including gene networks to predict calving difficulty in Holstein, Brown Swiss and Jersey cattle. <i>BMC Genetics</i> , 2018, 19, 20.	2.7	4
123	An alternative interpretation of residual feed intake by phenotypic recursive relationships in dairy cattle. <i>JDS Communications</i> , 2021, 2, 371-375.	0.5	4
124	Short communication: Phenotypic and genetic effects of the polled haplotype on yield, longevity, and fertility in US Brown Swiss, Holstein, and Jersey cattle. <i>Journal of Dairy Science</i> , 2019, 102, 8247-8250.	1.4	4
125	Inheritance of a mutation causing neuropathy with splayed forelimbs in Jersey cattle. <i>Journal of Dairy Science</i> , 2022, 105, 1338-1345.	1.4	4
126	Functional annotation of regulatory elements in cattle genome reveals the roles of extracellular interaction and dynamic change of chromatin states in rumen development during weaning. <i>Genomics</i> , 2022, 114, 110296.	1.3	4

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127	Genome-wide recombination map construction from single sperm sequencing in cattle. BMC Genomics, 2022, 23, 181.	1.2	4
128	BREEDING AND GENETICS SYMPOSIUM: Systems biology in animal breeding: Identifying relationships among markers, genes, and phenotypes ¹ . Journal of Animal Science, 2013, 91, 521-522.	0.2	3
129	Application of the a posteriori granddaughter design to the Holstein genome. Animal, 2014, 8, 511-519.	1.3	3
130	Genomic prediction of disease occurrence using producer-recorded health data: a comparison of methods. Genetics Selection Evolution, 2015, 47, 41.	1.2	3
131	BREEDING AND GENETICS SYMPOSIUM: Resilience of livestock to changing environments ¹ . Journal of Animal Science, 2017, 95, 1777-1779.	0.2	3
132	The Larson Blue coat color phenotype in Holsteins: Characteristics and effects on body temperature regulation and production in lactating cows in a hot climate. Journal of Animal Science, 2017, 95, 1164.	0.2	3
133	Technical note: Changes to herd cutoff date in conception rate evaluations. Journal of Dairy Science, 2013, 96, 1264-1268.	1.4	2
134	0379 Genetic analysis of superovulation and embryo transfer traits in Holstein cattle. Journal of Animal Science, 2016, 94, 183-184.	0.2	2
135	Development of polymorphic markers in the immune gene complex loci of cattle. Journal of Dairy Science, 2021, 104, 6897-6908.	1.4	2
136	169 A dairy calf DNA biobank for the discovery of new recessive genetic disorders. Journal of Animal Science, 2017, 95, 83-83.	0.2	1
137	Effect of Temperature and Maternal Age on Recombination Rate in Cattle. Frontiers in Genetics, 2021, 12, 682718.	1.1	1
138	Improving production efficiency through genetic selection. , 0, , 331-340.		1
139	0306 Exploring the feasibility of using copy number variants as genetic markers through large-scale whole genome sequencing experiments. Journal of Animal Science, 2016, 94, 146-146.	0.2	1
140	Genome-wide association study of reproductive efficiency in female cattle, ⁵ . Journal of Animal Science, 0, , .	0.2	0
141	165 Genetic variants with potential loss of function in Gyr, Girolando, and Guzerat cattle breeds by resequencing. Journal of Animal Science, 2017, 95, 81-81.	0.2	0
142	123 CHANGES IN EXPRESSION OF GENES ASSOCIATED WITH GENETIC VARIATION IN PRE-IMPLANTATION DEVELOPMENT OF THE BOVINE EMBRYO. Reproduction, Fertility and Development, 2014, 26, 175.	0.1	0
143	256 GENOMIC EVALUATION OF FERTILITY TRAITS AND DISCOVERY OF HAPLOTYPES THAT AFFECT FERTILITY OF US DAIRY CATTLE. Reproduction, Fertility and Development, 2016, 28, 260.	0.1	0
144	5 A SINGLE NUCLEOTIDE POLYMORPHISM IN COQ9 AFFECTS MITOCHONDRIAL FUNCTION, BODY WEIGHT CHANGE AFTER CALVING, AND FERTILITY IN HOLSTEIN COWS. Reproduction, Fertility and Development, 2016, 28, 132.	0.1	0