John B Cole

List of Publications by Citations

140 papers	**4,922** citations	**39** h-index	**65** g-index
150 ext. papers	**6,512** ext. citations	**3.8** avg, IF	**5.89** L-index

#	Paper	IF	Citations
140	Temperature-humidity indices as indicators of milk production losses due to heat stress. *Journal of Dairy Science*, **2007**, 90, 1947-56	4	319
139	Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E3995-4004	11.5	259
138	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	4.5	245
137	Distribution and location of genetic effects for dairy traits. *Journal of Dairy Science*, **2009**, 92, 2931-46	4	186
136	Genomic Selection in Dairy Cattle: The USDA Experience. *Annual Review of Animal Biosciences*, **2017**, 5, 309-327	13.7	154
135	De novo assembly of the cattle reference genome with single-molecule sequencing. *GigaScience*, **2020**, 9,	7.6	140
134	Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. *Animal*, **2015**, 9, 191-207	3.1	139
133	Genomic imputation and evaluation using high-density Holstein genotypes. *Journal of Dairy Science*, **2013**, 96, 668-78	4	125
132	Effect of artificial selection on runs of homozygosity in u.s. Holstein cattle. *PLoS ONE*, **2013**, 8, e80813	3.7	114
131	Cattle Sex-Specific Recombination and Genetic Control from a Large Pedigree Analysis. *PLoS Genetics*, **2015**, 11, e1005387	6	112
130	Genomic signatures reveal new evidences for selection of important traits in domestic cattle. *Molecular Biology and Evolution*, **2015**, 32, 711-25	8.3	93
129	Discovery of single nucleotide polymorphisms in candidate genes associated with fertility and production traits in Holstein cattle. *BMC Genetics*, **2013**, 14, 49	2.6	91
128	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	2.6	83
127	Genomic inbreeding and relationships among Holsteins, Jerseys, and Brown Swiss. *Journal of Dairy Science*, **2011**, 94, 5673-82	4	82
126	Genetic and environmental factors that affect gestation length in dairy cattle. *Journal of Dairy Science*, **2009**, 92, 2259-69	4	78
125	Identification of a nonsense mutation in CWC15 associated with decreased reproductive efficiency in Jersey cattle. *PLoS ONE*, **2013**, 8, e54872	3.7	71
124	Genomic selection for producer-recorded health event data in US dairy cattle. *Journal of Dairy Science*, **2014**, 97, 3190-9	4	70

123	Symposium review: Possibilities in an age of genomics: The future of selection indices. *Journal of Dairy Science*, **2018**, 101, 3686-3701	4	69
122	Genome-wide association mapping for identification of quantitative trait loci for rectal temperature during heat stress in Holstein cattle. *PLoS ONE*, **2013**, 8, e69202	3.7	64
121	Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. *BMC Genomics*, **2014**, 15, 683	4.5	63
120	Selecting sequence variants to improve genomic predictions for dairy cattle. *Genetics Selection Evolution*, **2017**, 49, 32	4.9	61
119	Accuracy of genomic predictions in Bos indicus (Nellore) cattle. *Genetics Selection Evolution*, **2014**, 46, 17	4.9	60
118	Heritability of rectal temperature and genetic correlations with production and reproduction traits in dairy cattle. *Journal of Dairy Science*, **2012**, 95, 3401-5	4	56
117	A genome-wide association study for clinical mastitis in first parity US Holstein cows using single-step approach and genomic matrix re-weighting procedure. *PLoS ONE*, **2015**, 10, e0114919	3.7	55
116	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. *PLoS ONE*, **2014**, 9, e92769	3.7	55
115	A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. *Frontiers in Genetics*, **2019**, 10, 412	4.5	54
114	Improvement of prediction ability for genomic selection of dairy cattle by including dominance effects. *PLoS ONE*, **2014**, 9, e103934	3.7	54
113	Genomewide Association Study of African Children Identifies Association of SCHIP1 and PDE8A with Facial Size and Shape. *PLoS Genetics*, **2016**, 12, e1006174	6	53
112	Technical note: adjustment of traditional cow evaluations to improve accuracy of genomic predictions. *Journal of Dairy Science*, **2011**, 94, 6188-93	4	51
111	Productive life and reasons for disposal of Holstein cows selected for large versus small body size. *Journal of Dairy Science*, **1999**, 82, 795-801	4	48
110	Invited review: Opportunities for genetic improvement of metabolic diseases. *Journal of Dairy Science*, **2016**, 99, 6855-6873	4	46
109	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. *DNA Research*, **2016**, 23, 253-62	4.5	46
108	Phenotypic and genetic effects of recessive haplotypes on yield, longevity, and fertility. *Journal of Dairy Science*, **2016**, 99, 7274-7288	4	44
107	Use of single nucleotide polymorphisms in candidate genes associated with daughter pregnancy rate for prediction of genetic merit for reproduction in Holstein cows. *Animal Genetics*, **2016**, 47, 288-97	2.5	44
106	Assessment of autozygosity in Nellore cows (Bos indicus) through high-density SNP genotypes. *Frontiers in Genetics*, **2015**, 6, 5	4.5	43

105	Invited review: Genetics and claw health: Opportunities to enhance claw health by genetic selection. *Journal of Dairy Science*, **2018**, 101, 4801-4821	4	43
104	A simple strategy for managing many recessive disorders in a dairy cattle breeding program. *Genetics Selection Evolution*, **2015**, 47, 94	4.9	43
103	Genetic evaluation and best prediction of lactation persistency. *Journal of Dairy Science*, **2006**, 89, 2722-8	4	41
102	Comprehensive analyses of 723 transcriptomes enhance genetic and biological interpretations for complex traits in cattle. *Genome Research*, **2020**, 30, 790-801	9.7	40
101	Symposium review: Genetics, genome-wide association study, and genetic improvement of dairy fertility traits. *Journal of Dairy Science*, **2019**, 102, 3735-3743	4	37
100	Single nucleotide polymorphisms in candidate genes associated with fertilizing ability of sperm and subsequent embryonic development in cattle. *Biology of Reproduction*, **2013**, 89, 69	3.9	36
99	Genetic evaluation of lactation persistency for five breeds of dairy cattle. *Journal of Dairy Science*, **2009**, 92, 2248-58	4	36
98	A Vision for Development and Utilization of High-Throughput Phenotyping and Big Data Analytics in Livestock. *Frontiers in Genetics*, **2019**, 10, 1197	4.5	35
97	Genetic evaluations for mixed-breed populations. *Journal of Dairy Science*, **2007**, 90, 2434-41	4	34
96	Phenotypic and genetic relationships of common health disorders with milk and fat yield persistencies from producer-recorded health data and test-day yields. *Journal of Dairy Science*, **2009**, 92, 1785-95	4	33
95	Explorations in genome-wide association studies and network analyses with dairy cattle fertility traits. *Journal of Dairy Science*, **2016**, 99, 6420-6435	4	33
94	Convergent Evolution of Slick Coat in Cattle through Truncation Mutations in the Prolactin Receptor. *Frontiers in Genetics*, **2018**, 9, 57	4.5	32
93	Dissection of additive, dominance, and imprinting effects for production and reproduction traits in Holstein cattle. *BMC Genomics*, **2017**, 18, 425	4.5	30
92	Stillbirth (co)variance components for a sire-maternal grandsire threshold model and development of a calving ability index for sire selection. *Journal of Dairy Science*, **2007**, 90, 2489-96	4	30
91	Incidence validation and relationship analysis of producer-recorded health event data from on-farm computer systems in the United States. *Journal of Dairy Science*, **2012**, 95, 5422-5435	4	29
90	Genome-wide mapping of loci explaining variance in scrotal circumference in Nellore cattle. *PLoS ONE*, **2014**, 9, e88561	3.7	29
89	Functional annotation and Bayesian fine-mapping reveals candidate genes for important agronomic traits in Holstein bulls. *Communications Biology*, **2019**, 2, 212	6.7	28
88	Single nucleotide polymorphisms associated with thermoregulation in lactating dairy cows exposed to heat stress. *Journal of Animal Breeding and Genetics*, **2015**, 132, 409-19	2.9	28

87	Effect of sample stratification on dairy GWAS results. *BMC Genomics*, **2012**, 13, 536	4.5	28
86	Genomic evaluation of age at first calving. *Journal of Dairy Science*, **2017**, 100, 6853-6861	4	27
85	Comparison of gene editing versus conventional breeding to introgress the POLLED allele into the US dairy cattle population. *Journal of Dairy Science*, **2019**, 102, 4215-4226	4	27
84	Genetic parameters of milk ELISA scores for Johne's disease. *Journal of Dairy Science*, **2010**, 93, 1729-35	4	27
83	GWAS and fine-mapping of livability and six disease traits in Holstein cattle. *BMC Genomics*, **2020**, 21, 41	4.5	26
82	A genome-wide association study of calf birth weight in Holstein cattle using single nucleotide polymorphisms and phenotypes predicted from auxiliary traits. *Journal of Dairy Science*, **2014**, 97, 3156-72	4	25
81	Genetic evaluation of stillbirth in United States Holsteins using a sire-maternal grandsire threshold model. *Journal of Dairy Science*, **2007**, 90, 2480-8	4	25
80	Genetic evaluation of calving ease for Brown Swiss and Jersey bulls from purebred and crossbred calvings. *Journal of Dairy Science*, **2005**, 88, 1529-39	4	25
79	Single nucleotide variants and InDels identified from whole-genome re-sequencing of Guzerat, Gyr, Girolando and Holstein cattle breeds. *PLoS ONE*, **2017**, 12, e0173954	3.7	24
78	A single nucleotide polymorphism in COQ9 affects mitochondrial and ovarian function and fertility in Holstein cows. *Biology of Reproduction*, **2017**, 96, 652-663	3.9	23
77	Short communication: Use of young bulls in the United States. *Journal of Dairy Science*, **2014**, 97, 3213-20	4	23
76	Genomic evaluation, breed identification, and discovery of a haplotype affecting fertility for Ayrshire dairy cattle. *Journal of Dairy Science*, **2014**, 97, 3878-82	4	23
75	Use of haplotypes to estimate Mendelian sampling effects and selection limits. *Journal of Animal Breeding and Genetics*, **2011**, 128, 446-55	2.9	23
74	Genomewide association study of reproductive efficiency in female cattle. *Journal of Animal Science*, **2014**, 92, 1945-57	0.7	22
73	Breeding and Genetics Symposium: really big data: processing and analysis of very large data sets. *Journal of Animal Science*, **2012**, 90, 723-33	0.7	22
72	Best prediction of yields for long lactations. *Journal of Dairy Science*, **2009**, 92, 1796-810	4	22
71	PyPedal: A computer program for pedigree analysis. *Computers and Electronics in Agriculture*, **2007**, 57, 107-113	6.5	22
70	Association of single nucleotide polymorphisms in candidate genes previously related to genetic variation in fertility with phenotypic measurements of reproductive function in Holstein cows. *Journal of Dairy Science*, **2017**, 100, 3725-3734	4	21

69	Genetic and epigenetic architecture of paternal origin contribute to gestation length in cattle. *Communications Biology*, **2019**, 2, 100	6.7	21
68	Phenotypic relationships of common health disorders in dairy cows to lactation persistency estimated from daily milk weights. *Journal of Dairy Science*, **2007**, 90, 4424-34	4	21
67	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers. *Journal of Animal Science*, **2017**, 95, 4796-4812	0.7	20
66	Population structure of a colony of dog guides. *Journal of Animal Science*, **2004**, 82, 2906-12	0.7	20
65	Evaluation of genetic components in traits related to superovulation, in vitro fertilization, and embryo transfer in Holstein cattle. *Journal of Dairy Science*, **2017**, 100, 2877-2891	4	19
64	High-density genome-wide association study for residual feed intake in Holstein dairy cattle. *Journal of Dairy Science*, **2019**, 102, 11067-11080	4	19
63	Defining the optimal period length and stage of growth or lactation to estimate residual feed intake in dairy cows. *Journal of Dairy Science*, **2019**, 102, 6131-6143	4	18
62	Genome changes due to artificial selection in U.S. Holstein cattle. *BMC Genomics*, **2019**, 20, 128	4.5	18
61	Symposium review: Exploiting homozygosity in the era of genomics-Selection, inbreeding, and mating programs. *Journal of Dairy Science*, **2020**, 103, 5302-5313	4	17
60	Economic considerations of breeding for polled dairy cows versus dehorning in the United States. *Journal of Dairy Science*, **2017**, 100, 4941-4952	4	16
59	Stochastic dynamic simulation modeling including multitrait genetics to estimate genetic, technical, and financial consequences of dairy farm reproduction and selection strategies. *Journal of Dairy Science*, **2016**, 99, 8187-8202	4	15
58	Comparative analyses of sperm DNA methylomes among human, mouse and cattle provide insights into epigenomic evolution and complex traits. *Epigenetics*, **2019**, 14, 260-276	5.7	14
57	The future of phenomics in dairy cattle breeding. *Animal Frontiers*, **2020**, 10, 37-44	5.5	14
56	Reducing animal sequencing redundancy by preferentially selecting animals with low-frequency haplotypes. *Journal of Dairy Science*, **2016**, 99, 5526-5534	4	14
55	Genomic prediction of residual feed intake in US Holstein dairy cattle. *Journal of Dairy Science*, **2020**, 103, 2477-2486	4	13
54	Visualization of results from genomic evaluations. *Journal of Dairy Science*, **2010**, 93, 2727-40	4	13
53	Analyses of inter-individual variations of sperm DNA methylation and their potential implications in cattle. *BMC Genomics*, **2019**, 20, 888	4.5	13
52	Variance of gametic diversity and its application in selection programs. *Journal of Dairy Science*, **2019**, 102, 5279-5294	4	12

No.	Reference	IF	Citations
51	Epigenomics and genotype-phenotype association analyses reveal conserved genetic architecture of complex traits in cattle and human. *BMC Biology*, **2020**, 18, 80	7.3	12
50	Short communication: genetic evaluation of stillbirth in US Brown Swiss and Jersey cattle. *Journal of Dairy Science*, **2014**, 97, 2474-80	4	12
49	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	3.7	12
48	Array CGH-based detection of CNV regions and their potential association with reproduction and other economic traits in Holsteins. *BMC Genomics*, **2019**, 20, 181	4.5	11
47	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. *BMC Biology*, **2020**, 18, 85	7.3	11
46	The development of genomics applied to dairy breeding. *Livestock Science*, **2014**, 166, 66-75	1.7	11
45	Integrating Signals from Sperm Methylome Analysis and Genome-Wide Association Study for a Better Understanding of Male Fertility in Cattle.. *Epigenomes*, **2019**, 3,	2.3	9
44	Dissection of genomic correlation matrices of US Holsteins using multivariate factor analysis. *Journal of Animal Breeding and Genetics*, **2015**, 132, 9-20	2.9	9
43	Tropospheric Ozone in Louisiana and Synoptic Circulation. *Journal of Applied Meteorology and Climatology*, **2004**, 43, 1438-1451		9
42	Estimating the effect of the deleterious recessive haplotypes AH1 and AH2 on reproduction performance of Ayrshire cattle. *Journal of Dairy Science*, **2019**, 102, 5315-5322	4	8
41	Short communication: best prediction of 305-day lactation yields with regional and seasonal effects. *Journal of Dairy Science*, **2011**, 94, 1601-4	4	8
40	Construction of PRDM9 allele-specific recombination maps in cattle using large-scale pedigree analysis and genome-wide single sperm genomics. *DNA Research*, **2018**, 25, 183-194	4.5	7
39	Short communication: Projecting milk yield using best prediction and the MilkBot lactation model. *Journal of Dairy Science*, **2012**, 95, 4041-4	4	7
38	Investigating conception rate for beef service sires bred to dairy cows and heifers. *Journal of Dairy Science*, **2020**, 103, 10374-10382	4	7
37	Genotype imputation in a tropical crossbred dairy cattle population. *Journal of Dairy Science*, **2017**, 100, 9623-9634	4	6
36	Development of a Lifetime Merit-based selection index for US dairy grazing systems. *Journal of Dairy Science*, **2014**, 97, 4568-78	4	6
35	A comprehensive catalogue of regulatory variants in the cattle transcriptome		6
34	Fast Bayesian fine-mapping of 35 production, reproduction and body conformation traits in dairy cattle		6

33	Symposium review: Development, implementation, and perspectives of health evaluations in the United States. *Journal of Dairy Science*, **2020**, 103, 5354-5365	4	5
32	Visualization of the transmission of direct genomic values for paternal and maternal chromosomes for 15 traits in US Brown Swiss, Holstein, and Jersey cattle. *Journal of Dairy Science*, **2013**, 96, 2713-2726	4	5
31	Multiparity evaluation of calving ease and stillbirth with separate genetic effects by parity. *Journal of Dairy Science*, **2008**, 91, 3173-8	4	5
30	Genomic selection in multi-breed dairy cattle populations. *Revista Brasileira De Zootecnia*, **2016**, 45, 195-202	1.2	5
29	Benchmarking dairy herd health status using routinely recorded herd summary data. *Journal of Dairy Science*, **2016**, 99, 1298-1314	4	4
28	Including gene networks to predict calving difficulty in Holstein, Brown Swiss and Jersey cattle. *BMC Genetics*, **2018**, 19, 20	2.6	4
27	Discovering ancestors and connecting relatives in large genomic databases. *Journal of Dairy Science* , **2020**, 103, 1729-1734	4	4
26	Modeling pedigree accuracy and uncertain parentage in single-step genomic evaluations of simulated and US Holstein datasets. *Journal of Dairy Science*, **2019**, 102, 2308-2318	4	4
25	Major quantitative trait loci influencing milk production and conformation traits in Guernsey dairy cattle detected on Bos taurus autosome 19. *Journal of Dairy Science*, **2021**, 104, 550-560	4	4
24	Comparison of Gene Editing Versus Conventional Breeding to Introgress the Allele Into the Tropically Adapted Australian Beef Cattle Population. *Frontiers in Genetics*, **2021**, 12, 593154	4.5	4
23	Validating the Use of Bovine Buccal Sampling as a Proxy for the Rumen Microbiota by Using a Time Course and Random Forest Classification Approach. *Applied and Environmental Microbiology*, **2020**, 86,	4.8	3
22	BREEDING AND GENETICS SYMPOSIUM: Resilience of livestock to changing environments. *Journal of Animal Science*, **2017**, 95, 1777-1779	0.7	3
21	Genomic prediction of disease occurrence using producer-recorded health data: a comparison of methods. *Genetics Selection Evolution*, **2015**, 47, 41	4.9	3
20	Breeding and Genetics Symposium: systems biology in animal breeding: Identifying relationships among markers, genes, and phenotypes. *Journal of Animal Science*, **2013**, 91, 521-2	0.7	3
19	Impact of genetic merit for milk somatic cell score of sires and maternal grandsires on herd life of their daughters. *Journal of Dairy Science*, **2009**, 92, 2224-8	4	3
18	Management of Mendelian Traits in Breeding Programs by Gene Editing: A Simulation Study		3
17	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	0.7	3
16	Simulation of introgression of the allele into the Jersey breed via conventional breeding vs. gene editing. *Translational Animal Science*, **2018**, 2, S57-S60	1.4	3

List of Publications

#	Publication		
15	Genetic and nongenetic profiling of milk pregnancy-associated glycoproteins in Holstein cattle. *Journal of Dairy Science*, **2018**, 101, 9987-10000	4	3
14	Single-cell transcriptomic analyses of dairy cattle ruminal epithelial cells during weaning. *Genomics*, **2021**, 113, 2045-2055	4.3	3
13	Application of the a posteriori granddaughter design to the Holstein genome. *Animal*, **2014**, 8, 511-9	3.1	2
12	Short communication: Phenotypic and genetic effects of the polled haplotype on yield, longevity, and fertility in US Brown Swiss, Holstein, and Jersey cattle. *Journal of Dairy Science*, **2019**, 102, 8247-8250	4	2
11	Invited review: The future of selection decisions and breeding programs: What are we breeding for, and who decides?. *Journal of Dairy Science*, **2021**, 104, 5111-5124	4	2
10	Truncation of IFT80 causes early embryonic loss in cattle		2
9	0379 Genetic analysis of superovulation and embryo transfer traits in Holstein cattle. *Journal of Animal Science*, **2016**, 94, 183-184	0.7	1
8	Technical note: Changes to herd cutoff date in conception rate evaluations. *Journal of Dairy Science* , **2013**, 96, 1264-8	4	1
7	Development of polymorphic markers in the immune gene complex loci of cattle. *Journal of Dairy Science*, **2021**, 104, 6897-6908	4	1
6	Genome-wide recombination map construction from single sperm sequencing in cattle.. *BMC Genomics*, **2022**, 23, 181	4.5	1
5	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.. *Genomics*, **2022**, 114, 110296	4.3	0
4	Trends in genetic diversity and the effect of inbreeding in American Angus cattle under genomic selection. *Genetics Selection Evolution*, **2021**, 53, 50	4.9	0
3	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	0.7	
2	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	0.7	
1	Effect of Temperature and Maternal Age on Recombination Rate in Cattle. *Frontiers in Genetics*, **2021**, 12, 682718	4.5	