Jeremy F Taylor

List of Publications by Year
in descending order

89 papers	10,182 citations	76326 40 h-index	53230 85 g-index
93 all docs	93 docs citations	93 times ranked	8520 citing authors

#	Article	IF	Citations
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
2	Invited Review: Reliability of genomic predictions for North American Holstein bulls. Journal of Dairy Science, 2009, 92, 16-24.	3.4	1,008
3	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. PLoS ONE, 2009, 4, e5350.	2.5	813
4	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	12.6	746
5	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. Nature Methods, 2008, 5, 247-252.	19.0	534
6	Deregressing estimated breeding values and weighting information for genomic regression analyses. Genetics Selection Evolution, 2009, 41, 55.	3.0	500
7	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. PLoS Genetics, 2014, 10, e1004254.	3.5	391
8	Consumer evaluation of beef of known categories of tenderness.. Journal of Animal Science, 1997, 75, 1521.	0.5	315
9	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	21.4	286
10	Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 152-157.	7.1	265
11	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	5.5	259
12	Distribution and location of genetic effects for dairy traits. Journal of Dairy Science, 2009, 92, 2931-2946.	3.4	210
13	Whole genome linkage disequilibrium maps in cattle. BMC Genetics, 2007, 8, 74.	2.7	201
14	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
15	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. BMC Genomics, 2014, 15, 442.	2.8	191
16	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. Genetics Selection Evolution, 2011, 43, 40.	3.0	174
17	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
18	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. BMC Genomics, 2017, 18, 386.	2.8	159

#	ARTICLE	IF	CITATIONS
19	Genome scan for meat quality traits in Nelore beef cattle. Physiological Genomics, 2013, 45, 1012-1020.	2.3	123
20	A mutation in the cathepsin D gene (CTSD) in American Bulldogs with neuronal ceroid lipofuscinosis. Molecular Genetics and Metabolism, 2006, 87, 341-348.	1.1	110
21	Genome‐wide association analysis for feed efficiency in Angus cattle. Animal Genetics, 2012, 43, 367-374.	1.7	110
22	A truncating mutation in ATP13A2 is responsible for adult-onset neuronal ceroid lipofuscinosis in Tibetan terriers. Neurobiology of Disease, 2011, 42, 468-474.	4.4	109
23	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. BMC Genomics, 2015, 16, 242.	2.8	109
24	Detection of selective sweeps in cattle using genome-wide SNP data. BMC Genomics, 2013, 14, 382.	2.8	102
25	QTLs associated with dry matter intake, metabolic mid-test weight, growth and feed efficiency have little overlap across 4 beef cattle studies. BMC Genomics, 2014, 15, 1004.	2.8	97
26	Susceptibility loci revealed for bovine respiratory disease complex in pre-weaned holstein calves. BMC Genomics, 2014, 15, 1164.	2.8	85
27	Scans for signatures of selection in Russian cattle breed genomes reveal new candidate genes for environmental adaptation and acclimation. Scientific Reports, 2018, 8, 12984.	3.3	85
28	Genome‐wide association analysis for quantitative trait loci influencing Warner‐Bratzler shear force in five taurine cattle breeds. Animal Genetics, 2012, 43, 662-673.	1.7	76
29	Accuracy of direct genomic breeding values for nationally evaluated traits in US Limousin and Simmental beef cattle. Genetics Selection Evolution, 2012, 44, 38.	3.0	63
30	Review: Genomics of bull fertility. Animal, 2018, 12, s172-s183.	3.3	63
31	A Homozygous KCNJ10 Mutation in Jack Russell Terriers and Related Breeds with Spinocerebellar Ataxia with Myokymia, Seizures, or Both. Journal of Veterinary Internal Medicine, 2014, 28, 871-877.	1.6	60
32	Implementation and accuracy of genomic selection. Aquaculture, 2014, 420-421, S8-S14.	3.5	60
33	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. Scientific Reports, 2016, 6, 39493.	3.3	57
34	BOARD-INVITED REVIEW: Applications of genomic information in livestock1. Journal of Animal Science, 2007, 85, 3148-3158.	0.5	56
35	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. Genetics Selection Evolution, 2013, 45, 30.	3.0	56
36	Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex. PLoS ONE, 2015, 10, e0142479.	2.5	56

#	Article	IF	Citations
37	AnADAMTS17Splice Donor Site Mutation in Dogs with Primary Lens Luxation. , 2010, 51, 4716.		55
38	A Novel Mutation in the Maternally Imprinted PEG3 Domain Results in a Loss of MIMT1 Expression and Causes Abortions and Stillbirths in Cattle (Bos taurus). PLoS ONE, 2010, 5, e15116.	2.5	55
39	Sliding window haplotype approaches overcome single SNP analysis limitations in identifying genes for meat tenderness in Nelore cattle. BMC Genetics, 2019, 20, 8.	2.7	53
40	Immunological Response to Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex: An RNA-Sequence Analysis of the Bronchial Lymph Node Transcriptome. PLoS ONE, 2015, 10, e0131459.	2.5	51
41	Impact of reduced marker set estimation of genomic relationship matrices on genomic selection for feed efficiency in Angus cattle. BMC Genetics, 2010, 11, 24.	2.7	50
42	Candidate lethal haplotypes and causal mutations in Angus cattle. BMC Genomics, 2017, 18, 799.	2.8	42
43	A multi-breed reference panel and additional rare variants maximize imputation accuracy in cattle. Genetics Selection Evolution, 2019, 51, 77.	3.0	42
44	Systematic Environmental, Direct, and Service Sire Effects on Conception Rate in Artificially Inseminated Holstein Cows. Journal of Dairy Science, 1985, 68, 3004-3022.	3.4	40
45	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. Genetics Selection Evolution, 2015, 47, 15.	3.0	40
46	A CLN8 nonsense mutation in the whole genome sequence of a mixed breed dog with neuronal ceroid lipofuscinosis and Australian Shepherd ancestry. Molecular Genetics and Metabolism, 2014, 112, 302-309.	1.1	38
47	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. Genetics Selection Evolution, 2015, 47, 23.	3.0	38
48	Genetic Mapping of Canine Multiple System Degeneration and Ectodermal Dysplasia Loci. Journal of Heredity, 2005, 96, 727-734.	2.4	37
49	A novel analytical method, Birth Date Selection Mapping, detects response of the Angus (Bos taurus) genome to selection on complex traits. BMC Genomics, 2012, 13, 606.	2.8	37
50	Golden Retriever dogs with neuronal ceroid lipofuscinosis have a two-base-pair deletion and frameshift in CLN5. Molecular Genetics and Metabolism, 2015, 115, 101-109.	1.1	36
51	A rare homozygous MFSD8 single-base-pair deletion and frameshift in the whole genome sequence of a Chinese Crested dog with neuronal ceroid lipofuscinosis. BMC Veterinary Research, 2014, 10, 960.	1.9	35
52	Holsteins are the genomic selection poster cows. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7690-7692.	7.1	35
53	A Truncated Retrotransposon Disrupts the *GRM1* Coding Sequence in Coton de Tulear Dogs with Bandera's Neonatal Ataxia. Journal of Veterinary Internal Medicine, 2011, 25, 267-272.	1.6	34
54	Australian Cattle Dogs with Neuronal Ceroid Lipofuscinosis are Homozygous for a *CLN5* Nonsense Mutation Previously Identified in Border Collies. Journal of Veterinary Internal Medicine, 2016, 30, 1149-1158.	1.6	34

#	Article	IF	Citations
55	What's in your next-generation sequence data? An exploration of unmapped DNA and RNA sequence reads from the bovine reference individual. BMC Genomics, 2015, 16, 1114.	2.8	32
56	Identification of genomic variants causing sperm abnormalities and reduced male fertility. Animal Reproduction Science, 2018, 194, 57-62.	1.5	32
57	Mapping of fertility traits in Finnish Ayrshire by genome-wide association analysis. Animal Genetics, 2011, 42, 263-269.	1.7	28
58	Tissue Tropism in Host Transcriptional Response to Members of the Bovine Respiratory Disease Complex. Scientific Reports, 2017, 7, 17938.	3.3	28
59	Lessons for livestock genomics from genome and transcriptome sequencing in cattle and other mammals. Genetics Selection Evolution, 2016, 48, 59.	3.0	25
60	Homozygous *PPT1* Splice Donor Mutation in a Cane Corso Dog With Neuronal Ceroid Lipofuscinosis. Journal of Veterinary Internal Medicine, 2017, 31, 149-157.	1.6	24
61	A homozygous PIGN missense mutation in Soft-Coated Wheaten Terriers with a canine paroxysmal dyskinesia. Neurogenetics, 2017, 18, 39-47.	1.4	23
62	Experimental challenge with bovine respiratory syncytial virus in dairy calves: bronchial lymph node transcriptome response. Scientific Reports, 2019, 9, 14736.	3.3	23
63	A mutation in the Warburg syndrome gene, RAB3GAP1, causes a similar syndrome with polyneuropathy and neuronal vacuolation in Black Russian Terrier dogs. Neurobiology of Disease, 2016, 86, 75-85.	4.4	22
64	Identification of loci associated with susceptibility to Mycobacterium avium subspecies paratuberculosis (Map) tissue infection in cattle. Journal of Animal Science, 2017, 95, 1080-1091.	0.5	22
65	Characterization of the rat developmental liver transcriptome. Physiological Genomics, 2013, 45, 301-311.	2.3	21
66	Spliced genes in muscle from Nelore Cattle and their association with carcass and meat quality. Scientific Reports, 2020, 10, 14701.	3.3	21
67	Genetic ancestry, admixture, and population structure in rural Dominica. PLoS ONE, 2021, 16, e0258735.	2.5	19
68	RAPTR-SV: a hybrid method for the detection of structural variants. Bioinformatics, 2015, 31, 2084-2090.	4.1	18
69	A comprehensive manually-curated compendium of bovine transcription factors. Scientific Reports, 2018, 8, 13747.	3.3	18
70	Genomics in the United States beef industry. Livestock Science, 2014, 166, 84-93.	1.6	17
71	GM2 Gangliosidosis in Shiba Inu Dogs with an In-Frame Deletion in *HEXB*. Journal of Veterinary Internal Medicine, 2017, 31, 1520-1526.	1.6	16
72	Expression of the Bovine NK-Lysin Gene Family and Activity against Respiratory Pathogens. PLoS ONE, 2016, 11, e0158882.	2.5	15

#	Article	IF	Citations
73	Messenger RNA biomarkers of Bovine Respiratory Syncytial Virus infection in the whole blood of dairy calves. Scientific Reports, 2021, 11, 9392.	3.3	13
74	Rapid Communication: Subclinical bovine respiratory disease â€" loci and pathogens associated with lung lesions in feedlot cattle1. Journal of Animal Science, 2017, 95, 2726-2731.	0.5	12
75	ATAC-Seq identifies regions of open chromatin in the bronchial lymph nodes of dairy calves experimentally challenged with bovine respiratory syncytial virus. BMC Genomics, 2021, 22, 14.	2.8	11
76	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. Genomics, 2021, 113, 1491-1503.	2.9	10
77	Variation in<i>myogenic differentiation 1</i>mRNA abundance isÂassociated with beef tenderness in Nelore cattle. Animal Genetics, 2016, 47, 491-494.	1.7	8
78	Identification of bovine CpG SNPs as potential targets for epigenetic regulation via DNA methylation. PLoS ONE, 2019, 14, e0222329.	2.5	8
79	CRUMBLER: A tool for the prediction of ancestry in cattle. PLoS ONE, 2019, 14, e0221471.	2.5	7
80	QTL-mapping and genomic prediction for bovine respiratory disease in U.S. Holsteins using sequence imputation and feature selection. BMC Genomics, 2019, 20, 555.	2.8	6
81	Elucidation of the Host Bronchial Lymph Node miRNA Transcriptome Response to Bovine Respiratory Syncytial Virus. Frontiers in Genetics, 2021, 12, 633125.	2.3	5
82	Short communication: Characterization of the milk protein expression profiles in dairy buffaloes with and without subclinical mastitis. Journal of Dairy Science, 2020, 103, 2677-2684.	3.4	4
83	Impaired collagen chaperone results in preterm PROM. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13267-13268.	7.1	3
84	A Non-Synonymous Point Mutation in a WD-40 Domain Repeat of EML5 Leads to Decreased Bovine Sperm Quality and Fertility. Frontiers in Cell and Developmental Biology, 2022, 10, 872740.	3.7	3
85	A simple procedure for directly obtaining haplotype sequences of diploid genomes. BMC Genomics, 2015, 16, 642.	2.8	2
86	Using online tools at the Bovine Genome Database to manually annotate genes in the new reference genome. Animal Genetics, 2020, 51, 675-682.	1.7	2
87	Taurine and Indicine Haplotype Representation in Advanced Generation Individuals From Three American Breeds. Frontiers in Genetics, 2021, 12, 758394.	2.3	1
88	Validating loci associated with bovine respiratory disease complex in preâ€weaned Holstein calves. Animal Genetics, 2020, 51, 91-94.	1.7	0
89	Genomic tools for characterizing monogenic and polygenic traits in ruminants--using the bovine as an example. Society of Reproduction and Fertility Supplement, 2010, 67, 13-28.	0.2	0