

# Jeremy F Taylor

## List of Publications by Year in descending order

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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	A Non-Synonymous Point Mutation in a WD-40 Domain Repeat of EML5 Leads to Decreased Bovine Sperm Quality and Fertility. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 872740.	3.7	3
2	Messenger RNA biomarkers of Bovine Respiratory Syncytial Virus infection in the whole blood of dairy calves. <i>Scientific Reports</i> , 2021, 11, 9392.	3.3	13
3	Elucidation of the Host Bronchial Lymph Node miRNA Transcriptome Response to Bovine Respiratory Syncytial Virus. <i>Frontiers in Genetics</i> , 2021, 12, 633125.	2.3	5
4	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. <i>Genomics</i> , 2021, 113, 1491-1503.	2.9	10
5	ATAC-Seq identifies regions of open chromatin in the bronchial lymph nodes of dairy calves experimentally challenged with bovine respiratory syncytial virus. <i>BMC Genomics</i> , 2021, 22, 14.	2.8	11
6	Taurine and Indicine Haplotype Representation in Advanced Generation Individuals From Three American Breeds. <i>Frontiers in Genetics</i> , 2021, 12, 758394.	2.3	1
7	Genetic ancestry, admixture, and population structure in rural Dominica. <i>PLoS ONE</i> , 2021, 16, e0258735.	2.5	19
8	Validating loci associated with bovine respiratory disease complex in pre-weaned Holstein calves. <i>Animal Genetics</i> , 2020, 51, 91-94.	1.7	0
9	Spliced genes in muscle from Nelore Cattle and their association with carcass and meat quality. <i>Scientific Reports</i> , 2020, 10, 14701.	3.3	21
10	Using online tools at the Bovine Genome Database to manually annotate genes in the new reference genome. <i>Animal Genetics</i> , 2020, 51, 675-682.	1.7	2
11	Short communication: Characterization of the milk protein expression profiles in dairy buffaloes with and without subclinical mastitis. <i>Journal of Dairy Science</i> , 2020, 103, 2677-2684.	3.4	4
12	QTL-mapping and genomic prediction for bovine respiratory disease in U.S. Holsteins using sequence imputation and feature selection. <i>BMC Genomics</i> , 2019, 20, 555.	2.8	6
13	Experimental challenge with bovine respiratory syncytial virus in dairy calves: bronchial lymph node transcriptome response. <i>Scientific Reports</i> , 2019, 9, 14736.	3.3	23
14	CRUMBLER: A tool for the prediction of ancestry in cattle. <i>PLoS ONE</i> , 2019, 14, e0221471.	2.5	7
15	Identification of bovine CpG SNPs as potential targets for epigenetic regulation via DNA methylation. <i>PLoS ONE</i> , 2019, 14, e0222329.	2.5	8
16	Sliding window haplotype approaches overcome single SNP analysis limitations in identifying genes for meat tenderness in Nelore cattle. <i>BMC Genetics</i> , 2019, 20, 8.	2.7	53
17	A multi-breed reference panel and additional rare variants maximize imputation accuracy in cattle. <i>Genetics Selection Evolution</i> , 2019, 51, 77.	3.0	42
18	Review: Genomics of bull fertility. <i>Animal</i> , 2018, 12, s172-s183.	3.3	63

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19	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
20	Identification of genomic variants causing sperm abnormalities and reduced male fertility. <i>Animal Reproduction Science</i> , 2018, 194, 57-62.	1.5	32
21	A comprehensive manually-curated compendium of bovine transcription factors. <i>Scientific Reports</i> , 2018, 8, 13747.	3.3	18
22	Scans for signatures of selection in Russian cattle breed genomes reveal new candidate genes for environmental adaptation and acclimation. <i>Scientific Reports</i> , 2018, 8, 12984.	3.3	85
23	A homozygous PIGN missense mutation in Soft-Coated Wheaten Terriers with a canine paroxysmal dyskinesia. <i>Neurogenetics</i> , 2017, 18, 39-47.	1.4	23
24	Homozygous <i>PPT1</i> Splice Donor Mutation in a Cane Corso Dog With Neuronal Ceroid Lipofuscinosis. <i>Journal of Veterinary Internal Medicine</i> , 2017, 31, 149-157.	1.6	24
25	<i>GM2</i> Gangliosidosis in Shiba Inu Dogs with an In-frame Deletion in <i>HEXB</i> . <i>Journal of Veterinary Internal Medicine</i> , 2017, 31, 1520-1526.	1.6	16
26	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. <i>BMC Genomics</i> , 2017, 18, 386.	2.8	159
27	Tissue Tropism in Host Transcriptional Response to Members of the Bovine Respiratory Disease Complex. <i>Scientific Reports</i> , 2017, 7, 17938.	3.3	28
28	Rapid Communication: Subclinical bovine respiratory disease " loci and pathogens associated with lung lesions in feedlot cattle1. <i>Journal of Animal Science</i> , 2017, 95, 2726-2731.	0.5	12
29	Candidate lethal haplotypes and causal mutations in Angus cattle. <i>BMC Genomics</i> , 2017, 18, 799.	2.8	42
30	Identification of loci associated with susceptibility to <i>Mycobacterium avium</i> subspecies paratuberculosis (Map) tissue infection in cattle. <i>Journal of Animal Science</i> , 2017, 95, 1080-1091.	0.5	22
31	Variation in <i>myogenic differentiation 1</i> mRNA abundance is associated with beef tenderness in Nelore cattle. <i>Animal Genetics</i> , 2016, 47, 491-494.	1.7	8
32	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. <i>Scientific Reports</i> , 2016, 6, 39493.	3.3	57
33	Lessons for livestock genomics from genome and transcriptome sequencing in cattle and other mammals. <i>Genetics Selection Evolution</i> , 2016, 48, 59.	3.0	25
34	Australian Cattle Dogs with Neuronal Ceroid Lipofuscinosis are Homozygous for a <i>CLN5</i> Nonsense Mutation Previously Identified in Border Collies. <i>Journal of Veterinary Internal Medicine</i> , 2016, 30, 1149-1158.	1.6	34
35	Holsteins are the genomic selection poster cows. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7690-7692.	7.1	35
36	A mutation in the Warburg syndrome gene, <i>RAB3GAP1</i> , causes a similar syndrome with polyneuropathy and neuronal vacuolation in Black Russian Terrier dogs. <i>Neurobiology of Disease</i> , 2016, 86, 75-85.	4.4	22

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37	Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 152-157.	7.1	265
38	Expression of the Bovine NK-Lysin Gene Family and Activity against Respiratory Pathogens. <i>PLoS ONE</i> , 2016, 11, e0158882.	2.5	15
39	Whatâ€™s in your next-generation sequence data? An exploration of unmapped DNA and RNA sequence reads from the bovine reference individual. <i>BMC Genomics</i> , 2015, 16, 1114.	2.8	32
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. <i>PLoS ONE</i> , 2015, 10, e0131459.	2.5	51
41	RAPTR-SV: a hybrid method for the detection of structural variants. <i>Bioinformatics</i> , 2015, 31, 2084-2090.	4.1	18
42	Golden Retriever dogs with neuronal ceroid lipofuscinosis have a two-base-pair deletion and frameshift in CLN5. <i>Molecular Genetics and Metabolism</i> , 2015, 115, 101-109.	1.1	36
43	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. <i>Genetics Selection Evolution</i> , 2015, 47, 15.	3.0	40
44	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 23.	3.0	38
45	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	2.8	109
46	A simple procedure for directly obtaining haplotype sequences of diploid genomes. <i>BMC Genomics</i> , 2015, 16, 642.	2.8	2
47	Single Pathogen Challenge with Agents of the Bovine Respiratory Disease Complex. <i>PLoS ONE</i> , 2015, 10, e0142479.	2.5	56
48	QTLs associated with dry matter intake, metabolic mid-test weight, growth and feed efficiency have little overlap across 4 beef cattle studies. <i>BMC Genomics</i> , 2014, 15, 1004.	2.8	97
49	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	3.5	391
50	A Homozygous <i>KCNJ10</i> Mutation in Jack Russell Terriers and Related Breeds with Spinocerebellar Ataxia with Myokymia, Seizures, or Both. <i>Journal of Veterinary Internal Medicine</i> , 2014, 28, 871-877.	1.6	60
51	Genomics in the United States beef industry. <i>Livestock Science</i> , 2014, 166, 84-93.	1.6	17
52	Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds. <i>BMC Genomics</i> , 2014, 15, 442.	2.8	191
53	Implementation and accuracy of genomic selection. <i>Aquaculture</i> , 2014, 420-421, S8-S14.	3.5	60
54	A CLN8 nonsense mutation in the whole genome sequence of a mixed breed dog with neuronal ceroid lipofuscinosis and Australian Shepherd ancestry. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 302-309.	1.1	38

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55	Susceptibility loci revealed for bovine respiratory disease complex in pre-weaned holstein calves. BMC Genomics, 2014, 15, 1164.	2.8	85
56	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
57	Detection of selective sweeps in cattle using genome-wide SNP data. BMC Genomics, 2013, 14, 382.	2.8	102
58	Comparison of molecular breeding values based on within- and across-breed training in beef cattle. Genetics Selection Evolution, 2013, 45, 30.	3.0	56
59	Characterization of the rat developmental liver transcriptome. Physiological Genomics, 2013, 45, 301-311.	2.3	21
60	Genome scan for meat quality traits in Nelore beef cattle. Physiological Genomics, 2013, 45, 1012-1020.	2.3	123
61	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
62	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	5.5	259
63	A novel analytical method, Birth Date Selection Mapping, detects response of the Angus ( <i>Bos taurus</i> ) genome to selection on complex traits. BMC Genomics, 2012, 13, 606.	2.8	37
64	Genome-wide association analysis for feed efficiency in Angus cattle. Animal Genetics, 2012, 43, 367-374.	1.7	110
65	Genome-wide association analysis for quantitative trait loci influencing <i>W</i> and <i>B</i> ratzler shear force in five taurine cattle breeds. Animal Genetics, 2012, 43, 662-673.	1.7	76
66	A Truncated Retrotransposon Disrupts the <i>GRM1</i> Coding Sequence in Coton de Tulear Dogs with Bandera's Neonatal Ataxia. Journal of Veterinary Internal Medicine, 2011, 25, 267-272.	1.6	34
67	Mapping of fertility traits in Finnish Ayrshire by genome-wide association analysis. Animal Genetics, 2011, 42, 263-269.	1.7	28
68	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
69	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
70	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
71	AnADAMTS17Splice Donor Site Mutation in Dogs with Primary Lens Luxation. , 2010, 51, 4716.		55
72	A Novel Mutation in the Maternally Imprinted PEG3 Domain Results in a Loss of MIMT1 Expression and Causes Abortions and Stillbirths in Cattle ( <i>Bos taurus</i> ). PLoS ONE, 2010, 5, e15116.	2.5	55

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73	Genomic tools for characterizing monogenic and polygenic traits in ruminants—using the bovine as an example. <i>Society of Reproduction and Fertility Supplement</i> , 2010, 67, 13-28.	0.2	0
74	Development and Characterization of a High Density SNP Genotyping Assay for Cattle. <i>PLoS ONE</i> , 2009, 4, e5350.	2.5	813
75	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, 18644-18649.	7.1	196
76	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
77	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
78	Invited Review: Reliability of genomic predictions for North American Holstein bulls. <i>Journal of Dairy Science</i> , 2009, 92, 16-24.	3.4	1,008
79	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, 3431-3436.	3.4	163
80	Distribution and location of genetic effects for dairy traits. <i>Journal of Dairy Science</i> , 2009, 92, 2931-2946.	3.4	210
81	Deregressing estimated breeding values and weighting information for genomic regression analyses. <i>Genetics Selection Evolution</i> , 2009, 41, 55.	3.0	500
82	SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. <i>Nature Methods</i> , 2008, 5, 247-252.	19.0	534
83	BOARD-INVITED REVIEW: Applications of genomic information in livestock1. <i>Journal of Animal Science</i> , 2007, 85, 3148-3158.	0.5	56
84	Whole genome linkage disequilibrium maps in cattle. <i>BMC Genetics</i> , 2007, 8, 74.	2.7	201
85	A mutation in the cathepsin D gene (CTSD) in American Bulldogs with neuronal ceroid lipofuscinosis. <i>Molecular Genetics and Metabolism</i> , 2006, 87, 341-348.	1.1	110
86	Impaired collagen chaperone results in preterm PROM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13267-13268.	7.1	3
87	Genetic Mapping of Canine Multiple System Degeneration and Ectodermal Dysplasia Loci. <i>Journal of Heredity</i> , 2005, 96, 727-734.	2.4	37
88	Consumer evaluation of beef of known categories of tenderness.. <i>Journal of Animal Science</i> , 1997, 75, 1521.	0.5	315
89	Systematic Environmental, Direct, and Service Sire Effects on Conception Rate in Artificially Inseminated Holstein Cows. <i>Journal of Dairy Science</i> , 1985, 68, 3004-3022.	3.4	40