

Jared E Decker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/328064/publications.pdf>

Version: 2024-02-01

52
papers

2,610
citations

236925

25
h-index

206112

48
g-index

68
all docs

68
docs citations

68
times ranked

3349
citing authors

#	ARTICLE	IF	CITATIONS
1	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. <i>PLoS Genetics</i> , 2014, 10, e1004254.	3.5	391
2	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
3	Accuracies of genomic breeding values in American Angus beef cattle using K-means clustering for cross-validation. <i>Genetics Selection Evolution</i> , 2011, 43, 40.	3.0	174
4	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
5	New World cattle show ancestry from multiple independent domestication events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1398-406.	7.1	126
6	Genome scan for meat quality traits in Nelore beef cattle. <i>Physiological Genomics</i> , 2013, 45, 1012-1020.	2.3	123
7	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. <i>BMC Genomics</i> , 2015, 16, 242.	2.8	109
8	Detection of selective sweeps in cattle using genome-wide SNP data. <i>BMC Genomics</i> , 2013, 14, 382.	2.8	102
9	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
10	Diversity and evolution of 11 innate immune genes in <i>Bos taurus taurus</i> and <i>Bos taurus indicus</i> cattle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 151-156.	7.1	81
11	Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016, 7, 13158.	12.8	81
12	Genome-wide association analysis for quantitative trait loci influencing <i>W</i> and <i>B</i> ratzler shear force in five taurine cattle breeds. <i>Animal Genetics</i> , 2012, 43, 662-673.	1.7	76
13	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
14	The Evolutionary History of Wild, Domesticated, and Feral <i>Brassica oleracea</i> (Brassicaceae). <i>Molecular Biology and Evolution</i> , 2021, 38, 4419-4434.	8.9	49
15	Candidate lethal haplotypes and causal mutations in Angus cattle. <i>BMC Genomics</i> , 2017, 18, 799.	2.8	42
16	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
17	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. <i>Genetics Selection Evolution</i> , 2015, 47, 15.	3.0	40
18	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

#	ARTICLE	IF	CITATIONS
19	Applications and efficiencies of the first cat 63K DNA array. <i>Scientific Reports</i> , 2018, 8, 7024.	3.3	38
20	A novel analytical method, Birth Date Selection Mapping, detects response of the Angus (<i>Bos taurus</i>) genome to selection on complex traits. <i>BMC Genomics</i> , 2012, 13, 606.	2.8	37
21	Genome-wide association and genotype by environment interactions for growth traits in U.S. Gelbvieh cattle. <i>BMC Genomics</i> , 2019, 20, 926.	2.8	37
22	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
23	A Truncated Retrotransposon Disrupts the <i>GRM1</i> Coding Sequence in Coton de Tulear Dogs with Bandera's Neonatal Ataxia. <i>Journal of Veterinary Internal Medicine</i> , 2011, 25, 267-272.	1.6	34
24	Insight into the genetic composition of South African Sanga cattle using SNP data from cattle breeds worldwide. <i>Genetics Selection Evolution</i> , 2016, 48, 88.	3.0	34
25	A Draft De Novo Genome Assembly for the Northern Bobwhite (<i>Colinus virginianus</i>) Reveals Evidence for a Rapid Decline in Effective Population Size Beginning in the Late Pleistocene. <i>PLoS ONE</i> , 2014, 9, e90240.	2.5	34
26	What'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
27	GM2 gangliosidosis associated with a HEXA missense mutation in Japanese Chin dogs: A potential model for Tay Sachs disease. <i>Molecular Genetics and Metabolism</i> , 2013, 108, 70-75.	1.1	25
28	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
29	Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. <i>PLoS Genetics</i> , 2021, 17, e1009652.	3.5	23
30	Agricultural Genomics: Commercial Applications Bring Increased Basic Research Power. <i>PLoS Genetics</i> , 2015, 11, e1005621.	3.5	23
31	Genome-wide association analyses identify genotype-by-environment interactions of growth traits in Simmental cattle. <i>Scientific Reports</i> , 2021, 11, 13335.	3.3	22
32	Annotated Draft Genome Assemblies for the Northern Bobwhite (<i>Colinus virginianus</i>) and the Scaled Quail (<i>Callipepla squamata</i>) Reveal Disparate Estimates of Modern Genome Diversity and Historic Effective Population Size. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3047-3058.	1.8	20
33	Genetic ancestry, admixture, and population structure in rural Dominica. <i>PLoS ONE</i> , 2021, 16, e0258735.	2.5	19
34	Genomics in the United States beef industry. <i>Livestock Science</i> , 2014, 166, 84-93.	1.6	17
35	Origins of cattle on Chirikof Island, Alaska, elucidated from genome-wide SNP genotypes. <i>Heredity</i> , 2016, 116, 502-505.	2.6	16
36	Elucidating the genetic basis of an oligogenic birth defect using whole genome sequence data in a non-model organism, <i>Bubalus bubalis</i> . <i>Scientific Reports</i> , 2017, 7, 39719.	3.3	15

#	ARTICLE	IF	CITATIONS
37	Feralization: Confronting the Complexity of Domestication and Evolution. Trends in Genetics, 2021, 37, 302-305.	6.7	14
38	Nested association mapping of important agronomic traits in three interspecific soybean populations. Theoretical and Applied Genetics, 2020, 133, 1039-1054.	3.6	12
39	Genome-wide association and genotype by environment interactions for growth traits in U.S. Red Angus cattle. BMC Genomics, 2022, 23, .	2.8	11
40	Genetic diversity and population structure of South African smallholder farmer sheep breeds determined using the OvineSNP50 beadchip. Tropical Animal Health and Production, 2017, 49, 1771-1777.	1.4	10
41	Development of a genetic evaluation for hair shedding in American Angus cattle to improve thermotolerance. Genetics Selection Evolution, 2020, 52, 63.	3.0	10
42	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. Genomics, 2021, 113, 1491-1503.	2.9	10
43	Results of the BRD CAP project: progress toward identifying genetic markers associated with BRD susceptibility. Animal Health Research Reviews, 2014, 15, 157-160.	3.1	8
44	Genetic Basis of Blood-Based Traits and Their Relationship With Performance and Environment in Beef Cattle at Weaning. Frontiers in Genetics, 2020, 11, 717.	2.3	8
45	CRUMBLER: A tool for the prediction of ancestry in cattle. PLoS ONE, 2019, 14, e0221471.	2.5	7
46	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
47	Preliminary genome-wide association study for wet-dry phenotype in smallholder ovine populations in South Africa. South African Journal of Animal Sciences, 2017, 47, 327.	0.5	4
48	Case Study: Scrotal Circumference in Beef Bullsâ€”Prediction of Measures at 365 Days of Age from Measures at 240 Days of Age with Data from the Tucumcari Bull Test. The Professional Animal Scientist, 2008, 24, 488-493.	0.7	3
49	Polymorphism analysis in genes associated with meat tenderness in Nelore cattle. Meta Gene, 2018, 18, 73-78.	0.6	3
50	Management Strategies for Adding Value to Replacement Beef Heifers. Veterinary Clinics of North America - Food Animal Practice, 2013, 29, 653-666.	1.2	2
51	Taurine and Indicine Haplotype Representation in Advanced Generation Individuals From Three American Breeds. Frontiers in Genetics, 2021, 12, 758394.	2.3	1
52	Exploring genetic variation and population structure in a threatened species, <i>Noturus placidus</i> , with whole-genome sequence data. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	1