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List of Publications by Year
in descending order

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

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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	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
2	Genome-wide association and genotype by environment interactions for growth traits in U.S. Red Angus cattle. BMC Genomics, 2022, 23, .	2.8	11
3	Feralization: Confronting the Complexity of Domestication and Evolution. Trends in Genetics, 2021, 37, 302-305.	6.7	14
4	Introgression, admixture, and selection facilitate genetic adaptation to high-altitude environments in cattle. Genomics, 2021, 113, 1491-1503.	2.9	10
5	Genome-wide association analyses identify genotype-by-environment interactions of growth traits in Simmental cattle. Scientific Reports, 2021, 11, 13335.	3.3	22
6	The Evolutionary History of Wild, Domesticated, and Feral<i>Brassica oleracea</i>(Brassicaceae). Molecular Biology and Evolution, 2021, 38, 4419-4434.	8.9	49
7	Powerful detection of polygenic selection and evidence of environmental adaptation in US beef cattle. PLoS Genetics, 2021, 17, e1009652.	3.5	23
8	Taurine and Indicine Haplotype Representation in Advanced Generation Individuals From Three American Breeds. Frontiers in Genetics, 2021, 12, 758394.	2.3	1
9	Genetic ancestry, admixture, and population structure in rural Dominica. PLoS ONE, 2021, 16, e0258735.	2.5	19
10	Development of a genetic evaluation for hair shedding in American Angus cattle to improve thermotolerance. Genetics Selection Evolution, 2020, 52, 63.	3.0	10
11	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
12	Nested association mapping of important agronomic traits in three interspecific soybean populations. Theoretical and Applied Genetics, 2020, 133, 1039-1054.	3.6	12
13	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
14	CRUMBLER: A tool for the prediction of ancestry in cattle. PLoS ONE, 2019, 14, e0221471.	2.5	7
15	Genome-wide association and genotype by environment interactions for growth traits in U.S. Gelbvieh cattle. BMC Genomics, 2019, 20, 926.	2.8	37
16	A multi-breed reference panel and additional rare variants maximize imputation accuracy in cattle. Genetics Selection Evolution, 2019, 51, 77.	3.0	42
17	Applications and efficiencies of the first cat 63K DNA array. Scientific Reports, 2018, 8, 7024.	3.3	38
18	Polymorphism analysis in genes associated with meat tenderness in Nelore cattle. Meta Gene, 2018, 18, 73-78.	0.6	3

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19	Elucidating the genetic basis of an oligogenic birth defect using whole genome sequence data in a non-model organism, Bubalus bubalis. Scientific Reports, 2017, 7, 39719.	3.3	15
20	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
21	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. G3: Genes, Genomes, Genetics, 2017, 7, 3047-3058.	1.8	20
22	Genome-wide association study for feed efficiency and growth traits in U.S. beef cattle. BMC Genomics, 2017, 18, 386.	2.8	159
23	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
24	Candidate lethal haplotypes and causal mutations in Angus cattle. BMC Genomics, 2017, 18, 799.	2.8	42
25	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. Scientific Reports, 2016, 6, 39493.	3.3	57
26	Insight into the genetic composition of South African Sanga cattle using SNP data from cattle breeds worldwide. Genetics Selection Evolution, 2016, 48, 88.	3.0	34
27	Lessons for livestock genomics from genome and transcriptome sequencing in cattle and other mammals. Genetics Selection Evolution, 2016, 48, 59.	3.0	25
28	Early cave art and ancient DNA record the origin of European bison. Nature Communications, 2016, 7, 13158.	12.8	81
29	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
30	Origins of cattle on Chirikof Island, Alaska, elucidated from genome-wide SNP genotypes. Heredity, 2016, 116, 502-505.	2.6	16
31	Whatâ€™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
32	Detection of quantitative trait loci for mineral content of Nelore longissimus dorsi muscle. Genetics Selection Evolution, 2015, 47, 15.	3.0	40
33	Comparison of Bayesian models to estimate direct genomic values in multi-breed commercial beef cattle. Genetics Selection Evolution, 2015, 47, 23.	3.0	38
34	Global liver gene expression differences in Nelore steers with divergent residual feed intake phenotypes. BMC Genomics, 2015, 16, 242.	2.8	109
35	Agricultural Genomics: Commercial Applications Bring Increased Basic Research Power. PLoS Genetics, 2015, 11, e1005621.	3.5	23
36	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

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37	Worldwide Patterns of Ancestry, Divergence, and Admixture in Domesticated Cattle. PLoS Genetics, 2014, 10, e1004254.	3.5	391
38	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
39	Genomics in the United States beef industry. Livestock Science, 2014, 166, 84-93.	1.6	17
40	A Draft De Novo Genome Assembly for the Northern Bobwhite (Colinus virginianus) Reveals Evidence for a Rapid Decline in Effective Population Size Beginning in the Late Pleistocene. PLoS ONE, 2014, 9, e90240.	2.5	34
41	Detection of selective sweeps in cattle using genome-wide SNP data. BMC Genomics, 2013, 14, 382.	2.8	102
42	Management Strategies for Adding Value to Replacement Beef Heifers. Veterinary Clinics of North America - Food Animal Practice, 2013, 29, 653-666.	1.2	2
43	GM2 gangliosidosis associated with a HEXA missense mutation in Japanese Chin dogs: A potential model for Tay Sachs disease. Molecular Genetics and Metabolism, 2013, 108, 70-75.	1.1	25
44	New World cattle show ancestry from multiple independent domestication events. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1398-406.	7.1	126
45	Genome scan for meat quality traits in Nelore beef cattle. Physiological Genomics, 2013, 45, 1012-1020.	2.3	123
46	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
47	Genomeâ€wide association analysis for quantitative trait loci influencing <scp>W</scp>arnerâ€“<scp>B</scp>ratzler shear force in five taurine cattle breeds. Animal Genetics, 2012, 43, 662-673.	1.7	76
48	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
49	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
50	Diversity and evolution of 11 innate immune genes in <i>Bos taurus taurus</i> and <i>Bos taurus indicus</i> cattle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 151-156.	7.1	81
51	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
52	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