

Angela Canovas

List of Publications by Year in descending order

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87
papers

2,327
citations

218662

26
h-index

254170

43
g-index

89
all docs

89
docs citations

89
times ranked

2391
citing authors

#	ARTICLE	IF	CITATIONS
1	SNP discovery in the bovine milk transcriptome using RNA-Seq technology. <i>Mammalian Genome</i> , 2010, 21, 592-598.	2.2	164
2	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. <i>BMC Genomics</i> , 2017, 18, 229.	2.8	141
3	Comparison of five different RNA sources to examine the lactating bovine mammary gland transcriptome using RNA-Sequencing. <i>Scientific Reports</i> , 2014, 4, 5297.	3.3	132
4	Multi-Tissue Omics Analyses Reveal Molecular Regulatory Networks for Puberty in Composite Beef Cattle. <i>PLoS ONE</i> , 2014, 9, e102551.	2.5	125
5	Muscle transcriptomic profiles in pigs with divergent phenotypes for fatness traits. <i>BMC Genomics</i> , 2010, 11, 372.	2.8	103
6	GALLO: An R package for genomic annotation and integration of multiple data sources in livestock for positional candidate loci. <i>GigaScience</i> , 2020, 9, .	6.4	86
7	Comparative Analysis of Muscle Transcriptome between Pig Genotypes Identifies Genes and Regulatory Mechanisms Associated to Growth, Fatness and Metabolism. <i>PLoS ONE</i> , 2015, 10, e0145162.	2.5	83
8	RNA sequencing to study gene expression and single nucleotide polymorphism variation associated with citrate content in cow milk. <i>Journal of Dairy Science</i> , 2013, 96, 2637-2648.	3.4	68
9	Porcine intramuscular fat content and composition are regulated by quantitative trait loci with muscle-specific effects1. <i>Journal of Animal Science</i> , 2011, 89, 2963-2971.	0.5	56
10	Developmental Stage, Muscle and Genetic Type Modify Muscle Transcriptome in Pigs: Effects on Gene Expression and Regulatory Factors Involved in Growth and Metabolism. <i>PLoS ONE</i> , 2016, 11, e0167858.	2.5	56
11	RNA-Sequencing: A tool to explore new frontiers in animal genetics. <i>Livestock Science</i> , 2014, 166, 206-216.	1.6	53
12	RNA-seq based detection of differentially expressed genes in the skeletal muscle of Duroc pigs with distinct lipid profiles. <i>Scientific Reports</i> , 2017, 7, 40005.	3.3	46
13	Differential expression of mRNA isoforms in the skeletal muscle of pigs with distinct growth and fatness profiles. <i>BMC Genomics</i> , 2018, 19, 145.	2.8	43
14	Acetyl-CoA carboxylase and stearoyl-CoA desaturase protein expression in subcutaneous adipose tissue is reduced in pigs selected for decreased backfat thickness at constant intramuscular fat content1. <i>Journal of Animal Science</i> , 2009, 87, 3905-3914.	0.5	40
15	Peptidomic analysis of healthy and subclinically mastitic bovine milk. <i>International Dairy Journal</i> , 2015, 46, 46-52.	3.0	40
16	Genetic Influences on Cattle Grazing Distribution: Association of Genetic Markers with Terrain Use in Cattle. <i>Rangeland Ecology and Management</i> , 2015, 68, 142-149.	2.3	38
17	Segregation of Regulatory Polymorphisms with Effects on the Gluteus Medius Transcriptome in a Purebred Pig Population. <i>PLoS ONE</i> , 2012, 7, e35583.	2.5	38
18	Single Nucleotide Polymorphism (SNP) Variation of Wolves (<i>Canis lupus</i>) in Southeast Alaska and Comparison with Wolves, Dogs, and Coyotes in North America. <i>Journal of Heredity</i> , 2015, 106, 26-36.	2.4	35

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19	Wilson Disease: Epigenetic effects of choline supplementation on phenotype and clinical course in a mouse model. <i>Epigenetics</i> , 2016, 11, 804-818.	2.7	35
20	Joint QTL mapping and gene expression analysis identify positional candidate genes influencing pork quality traits. <i>Scientific Reports</i> , 2017, 7, 39830.	3.3	35
21	SNP detection using RNA-sequences of candidate genes associated with puberty in cattle. <i>Genetics and Molecular Research</i> , 2017, 16, .	0.2	35
22	STAT6, PBX2, and PBRM1 Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. <i>Frontiers in Genetics</i> , 2018, 9, 87.	2.3	34
23	Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. <i>PLoS ONE</i> , 2018, 13, e0205295.	2.5	33
24	Genetic mechanisms regulating the host response during mastitis. <i>Journal of Dairy Science</i> , 2019, 102, 9043-9059.	3.4	32
25	Genome-wide association study to identify genomic regions and positional candidate genes associated with male fertility in beef cattle. <i>Scientific Reports</i> , 2020, 10, 20102.	3.3	32
26	Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. <i>Canadian Journal of Animal Science</i> , 2020, 100, 587-604.	1.5	31
27	Invited review: Determination of large-scale individual dry matter intake phenotypes in dairy cattle. <i>Journal of Dairy Science</i> , 2019, 102, 7655-7663.	3.4	30
28	Genome-wide association analysis for $\hat{1}^2$ -hydroxybutyrate concentration in Milk in Holstein dairy cattle. <i>BMC Genetics</i> , 2019, 20, 58.	2.7	29
29	Functional and association studies on the pig HMGR gene, a cholesterol-synthesis limiting enzyme. <i>Animal</i> , 2010, 4, 224-233.	3.3	27
30	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers ¹ . <i>Journal of Animal Science</i> , 2016, 94, 3693-3702.	0.5	27
31	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers ¹ . <i>Journal of Animal Science</i> , 2017, 95, 599-615.	0.5	27
32	Comparing the mRNA expression profile and the genetic determinism of intramuscular fat traits in the porcine gluteus medius and longissimus dorsi muscles. <i>BMC Genomics</i> , 2019, 20, 170.	2.8	27
33	The dynamic behavior of feed efficiency in primiparous dairy cattle. <i>Journal of Dairy Science</i> , 2020, 103, 1528-1540.	3.4	23
34	Short communication: Characterizing ovine serum stress biomarkers during endotoxemia. <i>Journal of Dairy Science</i> , 2020, 103, 5501-5508.	3.4	21
35	Molecular Phylogeny and SNP Variation of Polar Bears (<i>Ursus maritimus</i>), Brown Bears (<i>U. arctos</i>), and Black Bears (<i>U. americanus</i>) Derived from Genome Sequences. <i>Journal of Heredity</i> , 2014, 105, 312-323.	2.4	20
36	Pre- and post-puberty expression of genes and proteins in the uterus of <i>Bos indicus</i> heifers: the luteal phase effect post-puberty. <i>Animal Genetics</i> , 2018, 49, 539-549.	1.7	20

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37	Implementation of Bayesian methods to identify SNP and haplotype regions with transmission ratio distortion across the whole genome: TRDscan v.1.0. <i>Journal of Dairy Science</i> , 2019, 102, 3175-3188.	3.4	19
38	Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. <i>Journal of Dairy Science</i> , 2021, 104, 1928-1950.	3.4	19
39	Heat stress and immune response phenotype affect DNA methylation in blood mononuclear cells from Holstein dairy cows. <i>Scientific Reports</i> , 2021, 11, 11371.	3.3	18
40	Genetic mechanisms underlying spermatic and testicular traits within and among cattle breeds: systematic review and prioritization of GWAS results1. <i>Journal of Animal Science</i> , 2018, 96, 4978-4999.	0.5	17
41	Identification of novel mRNA isoforms associated with meat tenderness using RNA sequencing data in beef cattle. <i>Meat Science</i> , 2021, 173, 108378.	5.5	17
42	Wolf Subspecies: Reply to Weckworth et al. and Fredrickson et al.: Table 1.. <i>Journal of Heredity</i> , 2015, 106, 417-419.	2.4	16
43	Parallel responses of human epidermal keratinocytes to inorganic SbIII and AsIII. <i>Environmental Chemistry</i> , 2016, 13, 963.	1.5	16
44	High confidence copy number variants identified in Holstein dairy cattle from whole genome sequence and genotype array data. <i>Scientific Reports</i> , 2020, 10, 8044.	3.3	16
45	Genome-wide association study between copy number variants and hoof health traits in Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2021, 104, 8050-8061.	3.4	15
46	About the existence of common determinants of gene expression in the porcine liver and skeletal muscle. <i>BMC Genomics</i> , 2019, 20, 518.	2.8	14
47	Development and comparison of RNA-sequencing pipelines for more accurate SNP identification: practical example of functional SNP detection associated with feed efficiency in Nellore beef cattle. <i>BMC Genomics</i> , 2020, 21, 703.	2.8	14
48	Weighted Gene Correlation Network Meta-Analysis Reveals Functional Candidate Genes Associated with High- and Sub-Fertile Reproductive Performance in Beef Cattle. <i>Genes</i> , 2020, 11, 543.	2.4	14
49	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers. <i>Journal of Animal Science</i> , 2017, 95, 599.	0.5	14
50	Neuropeptidome of the Hypothalamus and Pituitary Gland of Indicine \tilde{A} – Taurine Heifers: Evidence of Differential Neuropeptide Processing in the Pituitary Gland before and after Puberty. <i>Journal of Proteome Research</i> , 2018, 17, 1852-1865.	3.7	13
51	Transcriptomic Profiles of Monocyte-Derived Macrophages in Response to <i>Escherichia coli</i> is Associated with the Host Genetics. <i>Scientific Reports</i> , 2020, 10, 271.	3.3	13
52	A genetic evaluation of growth, ultrasound, and carcass traits at alternative slaughter endpoints in crossbred heavy lambs1. <i>Journal of Animal Science</i> , 2019, 97, 521-535.	0.5	12
53	Discovering lethal alleles across the turkey genome using a transmission ratio distortion approach. <i>Animal Genetics</i> , 2020, 51, 876-889.	1.7	12
54	Discriminating between allele- and genotype-specific transmission ratio distortion. <i>Animal Genetics</i> , 2020, 51, 847-854.	1.7	12

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55	Identification of Ovine Serum miRNAs Following Bacterial Lipopolysaccharide Challenge. International Journal of Molecular Sciences, 2020, 21, 7920.	4.1	12
56	Differential gene expression in dairy cows under negative energy balance and ketosis: A systematic review and meta-analysis. Journal of Dairy Science, 2021, 104, 602-615.	3.4	12
57	Comprehensive RNA-Seq Profiling Reveals Temporal and Tissue-Specific Changes in Gene Expression in Sprague-Dawley Rats as Response to Heat Stress Challenges. Frontiers in Genetics, 2021, 12, 651979.	2.3	11
58	Allelic frequencies of PRKAG3 in several pig breeds and its technological consequences on a Duroc-Landrace-WHITE cross. Journal of Animal Breeding and Genetics, 2013, 130, 382-393.	2.0	10
59	Genome-wide association studies of beef cow terrain-use traits using Bayesian multiple-SNP regression. Livestock Science, 2020, 232, 103900.	1.6	10
60	Use of gene expression profile to identify potentially relevant transcripts to myofibrillar fragmentation index trait. Functional and Integrative Genomics, 2020, 20, 609-619.	3.5	10
61	Characterization of novel lncRNA muscle expression profiles associated with meat quality in beef cattle. Evolutionary Applications, 2022, 15, 706-718.	3.1	10
62	Nucleotide Sequence and Association Analysis of Pig Apolipoprotein-B and LDL-Receptor Genes. Animal Biotechnology, 2009, 20, 110-123.	1.5	9
63	Expression patterns and genetic variation of the ovine skeletal muscle transcriptome of sheep from five Spanish meat breeds. Scientific Reports, 2018, 8, 10486.	3.3	8
64	Non-Coding RNA Sequencing of Equine Endometrium During Maternal Recognition of Pregnancy. Genes, 2019, 10, 821.	2.4	8
65	The potential for mitigation of methane emissions in ruminants through the application of metagenomics, metabolomics, and other -OMICS technologies. Journal of Animal Science, 2021, 99, .	0.5	8
66	Genetic and genomic analyses of embryo production in dairy cattle. Reproduction, Fertility and Development, 2020, 32, 50.	0.4	7
67	Technical note: Efficient protocol for isolation of total ribonucleic acid from lyophilized fat and muscle pig samples1. Journal of Animal Science, 2010, 88, 442-445.	0.5	6
68	Body composition and gene expression QTL mapping in mice reveals imprinting and interaction effects. BMC Genetics, 2013, 14, 103.	2.7	6
69	Gene expression profiles of bovine genital ridges during sex determination and early differentiation of the gonads. Biology of Reproduction, 2020, 102, 38-52.	2.7	6
70	Screening for epistatic selection signatures: A simulation study. Scientific Reports, 2019, 9, 1026.	3.3	6
71	Bovine and murine tissue expression of insulin like growth factor-I. Gene, 2014, 535, 101-105.	2.2	5
72	Comparison between methods for measuring fecal egg count and estimating genetic parameters for gastrointestinal parasite resistance traits in sheep. Journal of Animal Science, 2021, 99, .	0.5	5

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73	Genome-wide association study for meat tenderness in beef cattle identifies patterns of the genetic contribution in different post-mortem stages. <i>Meat Science</i> , 2022, 186, 108733.	5.5	5
74	Early postmortem gene expression and its relationship to composition and quality traits in pig Longissimus dorsi muscle1. <i>Journal of Animal Science</i> , 2012, 90, 3325-3336.	0.5	4
75	Deducing signaling pathways from parallel actions of arsenite and antimonite in human epidermal keratinocytes. <i>Scientific Reports</i> , 2020, 10, 2890.	3.3	4
76	Genome-wide association study using haplotype libraries and repeated-measures model to identify candidate genomic regions for stillbirth in Holstein cattle. <i>Journal of Dairy Science</i> , 2022, 105, 1314-1326.	3.4	4
77	Identification of novel alternative splicing associated with mastitis disease in Holstein dairy cows using large gap read mapping. <i>BMC Genomics</i> , 2022, 23, 222.	2.8	4
78	Omega-3 fatty acids partially revert the metabolic gene expression profile induced by long-term calorie restriction. <i>Experimental Gerontology</i> , 2016, 77, 29-37.	2.8	3
79	Associations between feed efficiency and aspects of lactation curves in primiparous Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2021, 104, 9304-9315.	3.4	3
80	Prediction of Genetic Resistance for Scrapie in Ugenotyped Sheep Using a Linear Animal Model. <i>Genes</i> , 2021, 12, 1432.	2.4	3
81	Looking Ahead: Applying new Genomic Technologies to Accelerate Genetic Improvement in Beef Cattle. <i>Ceiba</i> , 2016, 54, 41-49.	0.2	3
82	Dynamic changes in Holstein heifer circulatory stress biomarkers in response to lipopolysaccharide immune challenge. <i>Veterinary Immunology and Immunopathology</i> , 2022, 248, 110426.	1.2	3
83	2016 TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: New perspectives and insight on intramuscular adipose tissue1. <i>Journal of Animal Science</i> , 2017, 95, 2241-2243.	0.5	2
84	Gene expression profile of the taimen <i>Hucho taimen</i> in response to acute temperature changes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021, 38, 100824.	1.0	2
85	The value of incorporating carcass trait phenotypes in terminal sire selection indexes to improve carcass weight and quality of heavy lambs. <i>Journal of Animal Breeding and Genetics</i> , 2021, 138, 91-107.	2.0	1
86	Linfomatosis menÃngea tardÃa en linfoma del manto controlada con quimioterapia. <i>NeurologÃa</i> , 2018, 33, 201-202.	0.7	0
87	Small genetic variation affecting mRNA isoforms associated with marbling and meat color in beef cattle. <i>Functional and Integrative Genomics</i> , 2022, , 1.	3.5	0