Angela Canovas

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

83 papers	1,326 citations	20 h-index	33 g-index
89 ext. papers	1,954 ext. citations	3.2 avg, IF	4.46 L-index

#	Paper	IF	Citations
83	SNP discovery in the bovine milk transcriptome using RNA-Seq technology. *Mammalian Genome*, **2010**, 21, 592-8	3.2	120
82	Comparison of five different RNA sources to examine the lactating bovine mammary gland transcriptome using RNA-Sequencing. *Scientific Reports*, **2014**, 4, 5297	4.9	92
81	Muscle transcriptomic profiles in pigs with divergent phenotypes for fatness traits. *BMC Genomics*, **2010**, 11, 372	4.5	78
80	Multi-tissue omics analyses reveal molecular regulatory networks for puberty in composite beef cattle. *PLoS ONE*, **2014**, 9, e102551	3.7	71
79	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. *BMC Genomics*, **2017**, 18, 229	4.5	70
78	Comparative Analysis of Muscle Transcriptome between Pig Genotypes Identifies Genes and Regulatory Mechanisms Associated to Growth, Fatness and Metabolism. *PLoS ONE*, **2015**, 10, e0145162	3.7	52
77	Porcine intramuscular fat content and composition are regulated by quantitative trait loci with muscle-specific effects. *Journal of Animal Science*, **2011**, 89, 2963-71	0.7	44
76	RNA-Sequencing: A tool to explore new frontiers in animal genetics. *Livestock Science*, **2014**, 166, 206-216	1.7	43
75	RNA sequencing to study gene expression and single nucleotide polymorphism variation associated with citrate content in cow milk. *Journal of Dairy Science*, **2013**, 96, 2637-2648	4	39
74	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 content. *Journal of Animal Science*, **2009**, 87, 3905-14	0.7	34
73	RNA-seq based detection of differentially expressed genes in the skeletal muscle of Duroc pigs with distinct lipid profiles. *Scientific Reports*, **2017**, 7, 40005	4.9	32
72	Developmental Stage, Muscle and Genetic Type Modify Muscle Transcriptome in Pigs: Effects on Gene Expression and Regulatory Factors Involved in Growth and Metabolism. *PLoS ONE*, **2016**, 11, e0167858	3.7	32
71	Genetic Influences on Cattle Grazing Distribution: Association of Genetic Markers with Terrain Use in Cattle. *Rangeland Ecology and Management*, **2015**, 68, 142-149	2.2	30
70	Peptidomic analysis of healthy and subclinically mastitic bovine milk. *International Dairy Journal*, **2015**, 46, 46-52	3.5	27
69	Single nucleotide polymorphism (SNP) variation of wolves (Canis lupus) in Southeast Alaska and comparison with wolves, dogs, and coyotes in North America. *Journal of Heredity*, **2015**, 106, 26-36	2.4	27
68	SNP detection using RNA-sequences of candidate genes associated with puberty in cattle. *Genetics and Molecular Research*, **2017**, 16,	1.2	26
67	Joint QTL mapping and gene expression analysis identify positional candidate genes influencing pork quality traits. *Scientific Reports*, **2017**, 7, 39830	4.9	25

66	Wilson Disease: Epigenetic effects of choline supplementation on phenotype and clinical course in a mouse model. *Epigenetics*, **2016**, 11, 804-818	5.7	23
65	Differential expression of mRNA isoforms in the skeletal muscle of pigs with distinct growth and fatness profiles. *BMC Genomics*, **2018**, 19, 145	4.5	22
64	Combining multi-OMICs information to identify key-regulator genes for pleiotropic effect on fertility and production traits in beef cattle. *PLoS ONE*, **2018**, 13, e0205295	3.7	22
63	Functional and association studies on the pig HMGCR gene, a cholesterol-synthesis limiting enzyme. *Animal*, **2010**, 4, 224-33	3.1	19
62	Segregation of regulatory polymorphisms with effects on the gluteus medius transcriptome in a purebred pig population. *PLoS ONE*, **2012**, 7, e35583	3.7	19
61	Invited review: Determination of large-scale individual dry matter intake phenotypes in dairy cattle. *Journal of Dairy Science*, **2019**, 102, 7655-7663	4	18
60	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers. *Journal of Animal Science*, **2017**, 95, 599-615	0.7	16
59	, , and Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. *Frontiers in Genetics*, **2018**, 9, 87	4.5	16
58	Genome-wide association analysis for ∎hydroxybutyrate concentration in Milk in Holstein dairy cattle. *BMC Genetics*, **2019**, 20, 58	2.6	16
57	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers. *Journal of Animal Science*, **2016**, 94, 3693-3702	0.7	16
56	GALLO: An R package for genomic annotation and integration of multiple data sources in livestock for positional candidate loci. *GigaScience*, **2020**, 9,	7.6	15
55	Molecular phylogeny and SNP variation of polar bears (Ursus maritimus), brown bears (U. arctos), and black bears (U. americanus) derived from genome sequences. *Journal of Heredity*, **2014**, 105, 312-23	2.4	14
54	Genetic mechanisms regulating the host response during mastitis. *Journal of Dairy Science*, **2019**, 102, 9043-9059	4	13
53	Comparing the mRNA expression profile and the genetic determinism of intramuscular fat traits in the porcine gluteus medius and longissimus dorsi muscles. *BMC Genomics*, **2019**, 20, 170	4.5	12
52	The dynamic behavior of feed efficiency in primiparous dairy cattle. *Journal of Dairy Science*, **2020**, 103, 1528-1540	4	12
51	Global differential gene expression in the pituitary gland and the ovaries of pre- and postpubertal Brahman heifers. *Journal of Animal Science*, **2017**, 95, 599	0.7	10
50	Genetic mechanisms underlying spermatic and testicular traits within and among cattle breeds: systematic review and prioritization of GWAS results. *Journal of Animal Science*, **2018**, 96, 4978-4999	0.7	10
49	Wolf Subspecies: Reply to Weckworth et al. and Fredrickson et al. *Journal of Heredity*, **2015**, 106, 417-9	2.4	9

48	Transcriptomic Profiles of Monocyte-Derived Macrophages in Response to Escherichia coli is Associated with the Host Genetics. *Scientific Reports*, **2020**, 10, 271	4.9	9
47	Nucleotide sequence and association analysis of pig apolipoprotein-B and LDL-receptor genes. *Animal Biotechnology*, **2009**, 20, 110-23	1.4	9
46	Parallel responses of human epidermal keratinocytes to inorganic SbIII and AsIII. *Environmental Chemistry*, **2016**, 13, 963-970	3.2	9
45	Neuropeptidome of the Hypothalamus and Pituitary Gland of Indicine Taurine Heifers: Evidence of Differential Neuropeptide Processing in the Pituitary Gland before and after Puberty. *Journal of Proteome Research*, **2018**, 17, 1852-1865	5.6	8
44	Allelic frequencies of PRKAG3 in several pig breeds and its technological consequences on a Duroc Landrace-Large White cross. *Journal of Animal Breeding and Genetics*, **2013**, 130, 382-93	2.9	8
43	Genome-wide association study to identify genomic regions and positional candidate genes associated with male fertility in beef cattle. *Scientific Reports*, **2020**, 10, 20102	4.9	8
42	Pre- and post-puberty expression of genes and proteins in the uterus of Bos indicus heifers: the luteal phase effect post-puberty. *Animal Genetics*, **2018**, 49, 539-549	2.5	8
41	Implementation of Bayesian methods to identify SNP and haplotype regions with transmission ratio distortion across the whole genome: TRDscan v.1.0. *Journal of Dairy Science*, **2019**, 102, 3175-3188	4	7
40	Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. *Canadian Journal of Animal Science*, **2020**, 100, 587-604	0.9	7
39	Short communication: Characterizing ovine serum stress biomarkers during endotoxemia. *Journal of Dairy Science*, **2020**, 103, 5501-5508	4	7
38	Genome-wide association studies of beef cow terrain-use traits using Bayesian multiple-SNP regression. *Livestock Science*, **2020**, 232, 103900	1.7	7
37	Use of gene expression profile to identify potentially relevant transcripts to myofibrillar fragmentation index trait. *Functional and Integrative Genomics*, **2020**, 20, 609-619	3.8	7
36	High confidence copy number variants identified in Holstein dairy cattle from whole genome sequence and genotype array data. *Scientific Reports*, **2020**, 10, 8044	4.9	6
35	Technical note: Efficient protocol for isolation of total ribonucleic acid from lyophilized fat and muscle pig samples. *Journal of Animal Science*, **2010**, 88, 442-5	0.7	6
34	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. *BMC Genomics*, **2020**, 21, 703	4.5	6
33	Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. *Journal of Dairy Science*, **2021**, 104, 1928-1950	4	6
32	Identification of Ovine Serum miRNAs Following Bacterial Lipopolysaccharide Challenge. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	5
31	Bovine and murine tissue expression of insulin like growth factor-I. *Gene*, **2014**, 535, 101-5	3.8	5

30	Body composition and gene expression QTL mapping in mice reveals imprinting and interaction effects. *BMC Genetics*, **2013**, 14, 103	2.6	5
29	Heat stress and immune response phenotype affect DNA methylation in blood mononuclear cells from Holstein dairy cows. *Scientific Reports*, **2021**, 11, 11371	4.9	5
28	Identification of novel mRNA isoforms associated with meat tenderness using RNA sequencing data in beef cattle. *Meat Science*, **2021**, 173, 108378	6.4	5
27	Gene expression profiles of bovine genital ridges during sex determination and early differentiation of the gonads*Biology of Reproduction*, **2020**, 102, 38-52	3.9	4
26	Expression patterns and genetic variation of the ovine skeletal muscle transcriptome of sheep from five Spanish meat breeds. *Scientific Reports*, **2018**, 8, 10486	4.9	4
25	Early postmortem gene expression and its relationship to composition and quality traits in pig Longissimus dorsi muscle. *Journal of Animal Science*, **2012**, 90, 3325-36	0.7	4
24	A genetic evaluation of growth, ultrasound, and carcass traits at alternative slaughter endpoints in crossbred heavy lambs. *Journal of Animal Science*, **2019**, 97, 521-535	0.7	4
23	Non-Coding RNA Sequencing of Equine Endometrium During Maternal Recognition of Pregnancy. *Genes*, **2019**, 10,	4.2	3
22	Screening for epistatic selection signatures: A simulation study. *Scientific Reports*, **2019**, 9, 1026	4.9	3
21	About the existence of common determinants of gene expression in the porcine liver and skeletal muscle. *BMC Genomics*, **2019**, 20, 518	4.5	3
20	Weighted Gene Correlation Network Meta-Analysis Reveals Functional Candidate Genes Associated with High- and Sub-Fertile Reproductive Performance in Beef Cattle. *Genes*, **2020**, 11,	4.2	3
19	Omega-3 fatty acids partially revert the metabolic gene expression profile induced by long-term calorie restriction. *Experimental Gerontology*, **2016**, 77, 29-37	4.5	3
18	Discovering lethal alleles across the turkey genome using a transmission ratio distortion approach. *Animal Genetics*, **2020**, 51, 876-889	2.5	3
17	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	4.5	3
16	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	4	3
15	2016 TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: New perspectives and insight on intramuscular adipose tissue. *Journal of Animal Science*, **2017**, 95, 2241-2243	0.7	2
14	Discriminating between allele- and genotype-specific transmission ratio distortion. *Animal Genetics*, **2020**, 51, 847-854	2.5	2
13	Genome-wide association study between copy number variants and hoof health traits in Holstein dairy cattle. *Journal of Dairy Science*, **2021**, 104, 8050-8061	4	2

12	Associations between feed efficiency and aspects of lactation curves in primiparous Holstein dairy cattle. *Journal of Dairy Science*, **2021**, 104, 9304-9315	4	2
11	Characterization of novel muscle expression profiles associated with meat quality in beef cattle.. *Evolutionary Applications*, **2022**, 15, 706-718	4.8	2
10	Deducing signaling pathways from parallel actions of arsenite and antimonite in human epidermal keratinocytes. *Scientific Reports*, **2020**, 10, 2890	4.9	1
9	Genome-wide association study for meat tenderness in beef cattle identifies patterns of the genetic contribution in different post-mortem stages.. *Meat Science*, **2022**, 186, 108733	6.4	1
8	Genetic and genomic analyses of embryo production in dairy cattle. *Reproduction, Fertility and Development*, **2019**, 32, 50-55	1.8	1
7	The value of incorporating carcass trait phenotypes in terminal sire selection indexes to improve carcass weight and quality of heavy lambs. *Journal of Animal Breeding and Genetics*, **2021**, 138, 91-107	2.9	1
6	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,	0.7	1
5	Identification of novel alternative splicing associated with mastitis disease in Holstein dairy cows using large gap read mapping.. *BMC Genomics*, **2022**, 23, 222	4.5	1
4	Gene expression profile of the taimen Hucho taimen in response to acute temperature changes. *Comparative Biochemistry and Physiology Part D: Genomics and Proteomics*, **2021**, 38, 100824	2	0
3	Dynamic changes in Holstein heifer circulatory stress biomarkers in response to lipopolysaccharide immune challenge.. *Veterinary Immunology and Immunopathology*, **2022**, 248, 110426	2	0
2	Late-onset meningeal lymphomatosis in mantle cell lymphoma controlled with chemotherapy. *Neurologia*, **2018**, 33, 201-202	1.4	
1	Small genetic variation affecting mRNA isoforms associated with marbling and meat color in beef cattle.. *Functional and Integrative Genomics*, **2022**, 1	3.8	