

Angela Canovas

List of Publications by Year in Descending Order

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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	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	6.4	1
82	Characterization of novel muscle expression profiles associated with meat quality in beef cattle.. <i>Evolutionary Applications</i> , 2022 , 15, 706-718	4.8	2
81	Small genetic variation affecting mRNA isoforms associated with marbling and meat color in beef cattle.. <i>Functional and Integrative Genomics</i> , 2022 , 1	3.8	
80	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	4.5	1
79	Dynamic changes in Holstein heifer circulatory stress biomarkers in response to lipopolysaccharide immune challenge.. <i>Veterinary Immunology and Immunopathology</i> , 2022 , 248, 110426	2	0
78	Comprehensive RNA-Seq Profiling Reveals Temporal and Tissue-Specific Changes in Gene Expression in Sprague-Dawley Rats as Response to Heat Stress Challenges. <i>Frontiers in Genetics</i> , 2021 , 12, 651979	4.5	3
77	Heat stress and immune response phenotype affect DNA methylation in blood mononuclear cells from Holstein dairy cows. <i>Scientific Reports</i> , 2021 , 11, 11371	4.9	5
76	Gene expression profile of the taimen Hucho taimen in response to acute temperature changes. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2021 , 38, 100824	2	0
75	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	4	2
74	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	2.9	1
73	Identification of novel mRNA isoforms associated with meat tenderness using RNA sequencing data in beef cattle. <i>Meat Science</i> , 2021 , 173, 108378	6.4	5
72	Differential gene expression in dairy cows under negative energy balance and ketosis: A systematic review and meta-analysis. <i>Journal of Dairy Science</i> , 2021 , 104, 602-615	4	3
71	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	4	6
70	Associations between feed efficiency and aspects of lactation curves in primiparous Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2021 , 104, 9304-9315	4	2
69	The potential for mitigation of methane emissions in ruminants through the application of metagenomics, metabolomics, and other -OMICS technologies. <i>Journal of Animal Science</i> , 2021 , 99,	0.7	1
68	Gene expression profiles of bovine genital ridges during sex determination and early differentiation of the gonads. <i>Biology of Reproduction</i> , 2020 , 102, 38-52	3.9	4
67	Identification of Ovine Serum miRNAs Following Bacterial Lipopolysaccharide Challenge. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	5

66	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	4.9	6
65	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	0.9	7
64	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,	4.2	3
63	Deducing signaling pathways from parallel actions of arsenite and antimonite in human epidermal keratinocytes. <i>Scientific Reports</i> , 2020 , 10, 2890	4.9	1
62	Transcriptomic Profiles of Monocyte-Derived Macrophages in Response to Escherichia coli is Associated with the Host Genetics. <i>Scientific Reports</i> , 2020 , 10, 271	4.9	9
61	Short communication: Characterizing ovine serum stress biomarkers during endotoxemia. <i>Journal of Dairy Science</i> , 2020 , 103, 5501-5508	4	7
60	GALLO: An R package for genomic annotation and integration of multiple data sources in livestock for positional candidate loci. <i>GigaScience</i> , 2020 , 9,	7.6	15
59	Genome-wide association studies of beef cow terrain-use traits using Bayesian multiple-SNP regression. <i>Livestock Science</i> , 2020 , 232, 103900	1.7	7
58	The dynamic behavior of feed efficiency in primiparous dairy cattle. <i>Journal of Dairy Science</i> , 2020 , 103, 1528-1540	4	12
57	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	4.5	6
56	Discovering lethal alleles across the turkey genome using a transmission ratio distortion approach. <i>Animal Genetics</i> , 2020 , 51, 876-889	2.5	3
55	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	4.9	8
54	Discriminating between allele- and genotype-specific transmission ratio distortion. <i>Animal Genetics</i> , 2020 , 51, 847-854	2.5	2
53	Use of gene expression profile to identify potentially relevant transcripts to myofibrillar fragmentation index trait. <i>Functional and Integrative Genomics</i> , 2020 , 20, 609-619	3.8	7
52	Non-Coding RNA Sequencing of Equine Endometrium During Maternal Recognition of Pregnancy. <i>Genes</i> , 2019 , 10,	4.2	3
51	Screening for epistatic selection signatures: A simulation study. <i>Scientific Reports</i> , 2019 , 9, 1026	4.9	3
50	About the existence of common determinants of gene expression in the porcine liver and skeletal muscle. <i>BMC Genomics</i> , 2019 , 20, 518	4.5	3
49	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	4.5	12

48	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	4	7
47	Invited review: Determination of large-scale individual dry matter intake phenotypes in dairy cattle. <i>Journal of Dairy Science</i> , 2019 , 102, 7655-7663	4	18
46	Genome-wide association analysis for β -hydroxybutyrate concentration in Milk in Holstein dairy cattle. <i>BMC Genetics</i> , 2019 , 20, 58	2.6	16
45	Genetic mechanisms regulating the host response during mastitis. <i>Journal of Dairy Science</i> , 2019 , 102, 9043-9059	4	13
44	Genetic and genomic analyses of embryo production in dairy cattle. <i>Reproduction, Fertility and Development</i> , 2019 , 32, 50-55	1.8	1
43	A genetic evaluation of growth, ultrasound, and carcass traits at alternative slaughter endpoints in crossbred heavy lambs. <i>Journal of Animal Science</i> , 2019 , 97, 521-535	0.7	4
42	Neuropeptidome of the Hypothalamus and Pituitary Gland of Indicine 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	5.6	8
41	Late-onset meningeal lymphomatosis in mantle cell lymphoma controlled with chemotherapy. <i>Neurologia</i> , 2018 , 33, 201-202	1.4	
40	, , and Emerge as Predicted Regulators of 452 Differentially Expressed Genes Associated With Puberty in Brahman Heifers. <i>Frontiers in Genetics</i> , 2018 , 9, 87	4.5	16
39	Expression patterns and genetic variation of the ovine skeletal muscle transcriptome of sheep from five Spanish meat breeds. <i>Scientific Reports</i> , 2018 , 8, 10486	4.9	4
38	Differential expression of mRNA isoforms in the skeletal muscle of pigs with distinct growth and fatness profiles. <i>BMC Genomics</i> , 2018 , 19, 145	4.5	22
37	Genetic mechanisms underlying spermatic and testicular traits within and among cattle breeds: systematic review and prioritization of GWAS results. <i>Journal of Animal Science</i> , 2018 , 96, 4978-4999	0.7	10
36	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	3.7	22
35	Pre- and post-puberty expression of genes and proteins in the uterus of Bos indicus heifers: the luteal phase effect post-puberty. <i>Animal Genetics</i> , 2018 , 49, 539-549	2.5	8
34	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	4.9	32
33	Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. <i>BMC Genomics</i> , 2017 , 18, 229	4.5	70
32	Joint QTL mapping and gene expression analysis identify positional candidate genes influencing pork quality traits. <i>Scientific Reports</i> , 2017 , 7, 39830	4.9	25
31	SNP detection using RNA-sequences of candidate genes associated with puberty in cattle. <i>Genetics and Molecular Research</i> , 2017 , 16,	1.2	26

30	2016 TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM: New perspectives and insight on intramuscular adipose tissue. <i>Journal of Animal Science</i> , 2017 , 95, 2241-2243	0.7	2
29	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, 599-615	0.7	16
28	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	0.7	10
27	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	4.5	3
26	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	2.7	32
25	Transcriptome analyses identify five transcription factors differentially expressed in the hypothalamus of post- versus prepubertal Brahman heifers. <i>Journal of Animal Science</i> , 2016 , 94, 3693-3702	0.7	16
24	Parallel responses of human epidermal keratinocytes to inorganic SbIII and AsIII. <i>Environmental Chemistry</i> , 2016 , 13, 963-970	3.2	9
23	Wilson Disease: Epigenetic effects of choline supplementation on phenotype and clinical course in a mouse model. <i>Epigenetics</i> , 2016 , 11, 804-818	5.7	23
22	Wolf Subspecies: Reply to Weckworth et al. and Fredrickson et al. <i>Journal of Heredity</i> , 2015 , 106, 417-9	2.4	9
21	Peptidomic analysis of healthy and subclinically mastitic bovine milk. <i>International Dairy Journal</i> , 2015 , 46, 46-52	3.5	27
20	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	27
19	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	3.7	52
18	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	2.2	30
17	Comparison of five different RNA sources to examine the lactating bovine mammary gland transcriptome using RNA-Sequencing. <i>Scientific Reports</i> , 2014 , 4, 5297	4.9	92
16	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, 312-23	2.4	14
15	RNA-Sequencing: A tool to explore new frontiers in animal genetics. <i>Livestock Science</i> , 2014 , 166, 206-216	1.7	43
14	Bovine and murine tissue expression of insulin like growth factor-I. <i>Gene</i> , 2014 , 535, 101-5	3.8	5
13	Multi-tissue omics analyses reveal molecular regulatory networks for puberty in composite beef cattle. <i>PLoS ONE</i> , 2014 , 9, e102551	3.7	71

12	Allelic frequencies of PRKAG3 in several pig breeds and its technological consequences on a Duroc x Landrace-Large White cross. <i>Journal of Animal Breeding and Genetics</i> , 2013 , 130, 382-93	2.9	8
11	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	4	39
10	Body composition and gene expression QTL mapping in mice reveals imprinting and interaction effects. <i>BMC Genetics</i> , 2013 , 14, 103	2.6	5
9	Early postmortem gene expression and its relationship to composition and quality traits in pig Longissimus dorsi muscle. <i>Journal of Animal Science</i> , 2012 , 90, 3325-36	0.7	4
8	Segregation of regulatory polymorphisms with effects on the gluteus medius transcriptome in a purebred pig population. <i>PLoS ONE</i> , 2012 , 7, e35583	3.7	19
7	Porcine intramuscular fat content and composition are regulated by quantitative trait loci with muscle-specific effects. <i>Journal of Animal Science</i> , 2011 , 89, 2963-71	0.7	44
6	Technical note: Efficient protocol for isolation of total ribonucleic acid from lyophilized fat and muscle pig samples. <i>Journal of Animal Science</i> , 2010 , 88, 442-5	0.7	6
5	Functional and association studies on the pig HMGCR gene, a cholesterol-synthesis limiting enzyme. <i>Animal</i> , 2010 , 4, 224-33	3.1	19
4	SNP discovery in the bovine milk transcriptome using RNA-Seq technology. <i>Mammalian Genome</i> , 2010 , 21, 592-8	3.2	120
3	Muscle transcriptomic profiles in pigs with divergent phenotypes for fatness traits. <i>BMC Genomics</i> , 2010 , 11, 372	4.5	78
2	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. <i>Journal of Animal Science</i> , 2009 , 87, 3905-14	0.7	34
1	Nucleotide sequence and association analysis of pig apolipoprotein-B and LDL-receptor genes. <i>Animal Biotechnology</i> , 2009 , 20, 110-23	1.4	9