

Maria Ballester Devis

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.

71
papers

1,999
citations

24
h-index

43
g-index

73
ext. papers

3,077
ext. citations

4.1
avg, IF

4.39
L-index

#	Paper	IF	Citations
71	A Co-Association Network Analysis Reveals Putative Regulators for Health-Related Traits in Pigs.. <i>Frontiers in Immunology</i> , 2021 , 12, 784978	8.4	1
70	Leveraging host-genetics and gut microbiota to determine immunocompetence in pigs. <i>Animal Microbiome</i> , 2021 , 3, 74	4.1	0
69	Type I and III IFNs produced by the nasal epithelia and dimmed inflammation are features of alpacas resolving MERS-CoV infection. <i>PLoS Pathogens</i> , 2021 , 17, e1009229	7.6	2
68	Comparative Transcriptome Profile between Iberian Pig Varieties Provides New Insights into Their Distinct Fat Deposition and Fatty Acids Content. <i>Animals</i> , 2021 , 11,	3.1	4
67	A gene co-association network regulating gut microbial communities in a Duroc pig population. <i>Microbiome</i> , 2021 , 9, 52	16.6	6
66	Expression analysis of porcine miR-33a/b in liver, adipose tissue and muscle and its potential role in fatty acid metabolism. <i>PLoS ONE</i> , 2021 , 16, e0245858	3.7	
65	Guidelines for the use and interpretation of assays for monitoring autophagy (4th edition). <i>Autophagy</i> , 2021 , 17, 1-382	10.2	440
64	Gut eukaryotic communities in pigs: diversity, composition and host genetics contribution. <i>Animal Microbiome</i> , 2020 , 2, 18	4.1	9
63	Identification of eQTLs associated with lipid metabolism in Longissimus dorsi muscle of pigs with different genetic backgrounds. <i>Scientific Reports</i> , 2020 , 10, 9845	4.9	3
62	Dietary intake of bioactive ingredients impacts liver and adipose tissue transcriptomes in a porcine model of prepubertal early obesity. <i>Scientific Reports</i> , 2020 , 10, 5375	4.9	1
61	Genetic parameters and associated genomic regions for global immunocompetence and other health-related traits in pigs. <i>Scientific Reports</i> , 2020 , 10, 18462	4.9	5
60	Identification of strong candidate genes for backfat and intramuscular fatty acid composition in three crosses based on the Iberian pig. <i>Scientific Reports</i> , 2020 , 10, 13962	4.9	11
59	Integrating genome-wide co-association and gene expression to identify putative regulators and predictors of feed efficiency in pigs. <i>Genetics Selection Evolution</i> , 2019 , 51, 48	4.9	14
58	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
57	Machine learning applied to transcriptomic data to identify genes associated with feed efficiency in pigs. <i>Genetics Selection Evolution</i> , 2019 , 51, 10	4.9	12
56	Analysis of porcine IGF2 gene expression in adipose tissue and its effect on fatty acid composition. <i>PLoS ONE</i> , 2019 , 14, e0220708	3.7	6
55	Indel detection from Whole Genome Sequencing data and association with lipid metabolism in pigs. <i>PLoS ONE</i> , 2019 , 14, e0218862	3.7	2

54	Association between the pig genome and its gut microbiota composition. <i>Scientific Reports</i> , 2019 , 9, 8791-9	4.9	31
53	Expression analysis of candidate genes for fatty acid composition in adipose tissue and identification of regulatory regions. <i>Scientific Reports</i> , 2018 , 8, 2045	4.9	41
52	Integrative approach using liver and duodenum RNA-Seq data identifies candidate genes and pathways associated with feed efficiency in pigs. <i>Scientific Reports</i> , 2018 , 8, 558	4.9	28
51	Characterization of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions. <i>Scientific Reports</i> , 2018 , 8, 12727	4.9	75
50	Analysing the Expression of Eight Clock Genes in Five Tissues From Fasting and Fed Sows. <i>Frontiers in Genetics</i> , 2018 , 9, 475	4.5	4
49	Role of AMPK signalling pathway during compensatory growth in pigs. <i>BMC Genomics</i> , 2018 , 19, 682	4.5	7
48	Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs. <i>Scientific Reports</i> , 2017 , 7, 46539	4.9	18
47	A global analysis of CNVs in swine using whole genome sequence data and association analysis with fatty acid composition and growth traits. <i>PLoS ONE</i> , 2017 , 12, e0177014	3.7	24
46	Association of genetic variants and expression levels of porcine FABP4 and FABP5 genes. <i>Animal Genetics</i> , 2017 , 48, 660-668	2.5	4
45	The Effects of Weaning Methods on Gut Microbiota Composition and Horse Physiology. <i>Frontiers in Physiology</i> , 2017 , 8, 535	4.6	34
44	Multi-breed and multi-trait co-association analysis of meat tenderness and other meat quality traits in three French beef cattle breeds. <i>Genetics Selection Evolution</i> , 2016 , 48, 37	4.9	40
43	Analysis of the porcine APOA2 gene expression in liver, polymorphism identification and association with fatty acid composition traits. <i>Animal Genetics</i> , 2016 , 47, 552-9	2.5	15
42	Expression-based GWAS identifies variants, gene interactions and key regulators affecting intramuscular fatty acid content and composition in porcine meat. <i>Scientific Reports</i> , 2016 , 6, 31803	4.9	38
41	Genome data from a sixteenth century pig illuminate modern breed relationships. <i>Heredity</i> , 2015 , 114, 175-84	3.6	25
40	Epigenetic regulation of the ELOVL6 gene is associated with a major QTL effect on fatty acid composition in pigs. <i>Genetics Selection Evolution</i> , 2015 , 47, 20	4.9	24
39	In situ hybridization with labeled probes: assessment of african Swine Fever virus in formalin-fixed paraffin-embedded tissues. <i>Methods in Molecular Biology</i> , 2015 , 1247, 209-18	1.4	
38	Live attenuated African swine fever viruses as ideal tools to dissect the mechanisms involved in viral pathogenesis and immune protection. <i>Veterinary Research</i> , 2015 , 46, 135	3.8	46
37	The NS segment of H5N1 avian influenza viruses (AIV) enhances the virulence of an H7N1 AIV in chickens. <i>Veterinary Research</i> , 2014 , 45, 7	3.8	8

36	From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. <i>BMC Genomics</i> , 2014 , 15, 232	4.5	31
35	Expression library immunization can confer protection against lethal challenge with African swine fever virus. <i>Journal of Virology</i> , 2014 , 88, 13322-32	6.6	66
34	New insight into the SSC8 genetic determination of fatty acid composition in pigs. <i>Genetics Selection Evolution</i> , 2014 , 46, 28	4.9	13
33	Differences in muscle transcriptome among pigs phenotypically extreme for fatty acid composition. <i>PLoS ONE</i> , 2014 , 9, e99720	3.7	44
32	A co-association network analysis of the genetic determination of pig conformation, growth and fatness. <i>PLoS ONE</i> , 2014 , 9, e114862	3.7	23
31	A quantitative real-time PCR method using an X-linked gene for sex typing in pigs. <i>Molecular Biotechnology</i> , 2013 , 54, 493-6	3	7
30	Standardization of pathological investigations in the framework of experimental ASFV infections. <i>Virus Research</i> , 2013 , 173, 180-90	6.4	59
29	Analysis of porcine adipose tissue transcriptome reveals differences in de novo fatty acid synthesis in pigs with divergent muscle fatty acid composition. <i>BMC Genomics</i> , 2013 , 14, 843	4.5	58
28	Swine, human or avian influenza viruses differentially activates porcine dendritic cells cytokine profile. <i>Veterinary Immunology and Immunopathology</i> , 2013 , 154, 25-35	2	15
27	Identification of differentially expressed genes in the oviduct of two rabbit lines divergently selected for uterine capacity using suppression subtractive hybridization. <i>Animal Genetics</i> , 2013 , 44, 296-304	2.5	1
26	Polymorphism in the ELOVL6 gene is associated with a major QTL effect on fatty acid composition in pigs. <i>PLoS ONE</i> , 2013 , 8, e53687	3.7	36
25	DAG expression: high-throughput gene expression analysis of real-time PCR data using standard curves for relative quantification. <i>PLoS ONE</i> , 2013 , 8, e80385	3.7	31
24	Evaluation of the porcine ACSL4 gene as a candidate gene for meat quality traits in pigs. <i>Animal Genetics</i> , 2012 , 43, 714-20	2.5	13
23	VtaA8 and VtaA9 from <i>Haemophilus parasuis</i> delay phagocytosis by alveolar macrophages. <i>Veterinary Research</i> , 2012 , 43, 57	3.8	33
22	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012 , 13, 547	4.5	89
21	DNA vaccination partially protects against African swine fever virus lethal challenge in the absence of antibodies. <i>PLoS ONE</i> , 2012 , 7, e40942	3.7	80
20	Conserved synthetic peptides from the hemagglutinin of influenza viruses induce broad humoral and T-cell responses in a pig model. <i>PLoS ONE</i> , 2012 , 7, e40524	3.7	23
19	Expression profile and subcellular localization of Torque teno sus virus proteins. <i>Journal of General Virology</i> , 2011 , 92, 2446-2457	4.9	17

18	Disruption of nuclear organization during the initial phase of African swine fever virus infection. <i>Journal of Virology</i> , 2011 , 85, 8263-9	6.6	27
17	Increased numbers of myeloid and lymphoid IL-10 producing cells in spleen of pigs with naturally occurring postweaning multisystemic wasting syndrome. <i>Veterinary Immunology and Immunopathology</i> , 2010 , 136, 305-10	2	10
16	Epigenetic modifications in 3D: nuclear organization of the differentiating mammary epithelial cell. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2010 , 15, 73-83	2.4	13
15	Intranuclear detection of African swine fever virus DNA in several cell types from formalin-fixed and paraffin-embedded tissues using a new in situ hybridisation protocol. <i>Journal of Virological Methods</i> , 2010 , 168, 38-43	2.6	23
14	Differences in phagocytosis susceptibility in <i>Haemophilus parasuis</i> strains. <i>Veterinary Research</i> , 2009 , 40, 24	3.8	54
13	Epigenetic modifications and chromatin loop organization explain the different expression profiles of the <i>Tbrg4</i> , <i>WAP</i> and <i>Ramp3</i> genes. <i>Experimental Cell Research</i> , 2008 , 314, 975-87	4.2	13
12	The nuclear localization of <i>WAP</i> and <i>CSN</i> genes is modified by lactogenic hormones in HC11 cells. <i>Journal of Cellular Biochemistry</i> , 2008 , 105, 262-70	4.7	18
11	Individual identification and genetic traceability in the pig using the SNPlex(TM) genotyping system. <i>Animal Genetics</i> , 2007 , 38, 663-5	2.5	7
10	Assignment of Signal Transducer and Activator of Transcription 5A (STAT5A) gene to porcine chromosome 12p13-->p11 by radiation hybrid panel mapping. <i>Cytogenetic and Genome Research</i> , 2006 , 112, 342J	1.9	1
9	Polymorphism and chromosomal localization of the porcine signal transducer and activator of transcription 5B gene (<i>STAT5B</i>). <i>Journal of Animal Breeding and Genetics</i> , 2006 , 123, 284-7	2.9	3
8	Phylogenetic analysis of Sicilian goats reveals a new mtDNA lineage. <i>Animal Genetics</i> , 2006 , 37, 376-8	2.5	53
7	Expression of recombinant human follicle-stimulating hormone in the mammary gland of transgenic mice. <i>Molecular Biotechnology</i> , 2006 , 34, 37-44	3	
6	Assignment of the beta-lactoglobulin (BLG) gene to porcine chromosome 1. <i>Animal Genetics</i> , 2005 , 36, 356-8	2.5	1
5	Assignment of the phospholipase Cbeta1 (PLCB1) gene to porcine chromosome 17. <i>Animal Genetics</i> , 2005 , 36, 516-7	2.5	1
4	Polymorphisms in the goat beta-lactoglobulin gene. <i>Journal of Dairy Research</i> , 2005 , 72, 379-84	1.6	16
3	Real-time quantitative PCR-based system for determining transgene copy number in transgenic animals. <i>BioTechniques</i> , 2004 , 37, 610-3	2.5	108
2	Disruption of the mouse phospholipase C-beta1 gene in a beta-lactoglobulin transgenic line affects viability, growth, and fertility in mice. <i>Gene</i> , 2004 , 341, 279-89	3.8	20
1	Gut eukaryotic communities in pigs: diversity, composition and host genetics contribution		2

