

Josep M Folch

List of Publications by Year in descending order

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99
papers

3,185
citations

126901

33
h-index

182417

51
g-index

99
all docs

99
docs citations

99
times ranked

3073
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterisation of PCV-2 isolates from Spain, Germany and France. <i>Virus Research</i> , 2000, 66, 65-77.	2.2	164
2	Characterization of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions. <i>Scientific Reports</i> , 2018, 8, 12727.	3.3	141
3	Fine mapping of porcine chromosome 6 QTL and LEPR effects on body composition in multiple generations of an Iberian by Landrace intercross. <i>Genetical Research</i> , 2005, 85, 57-67.	0.9	127
4	Real-time quantitative PCR-based system for determining transgene copy number in transgenic animals. <i>BioTechniques</i> , 2004, 37, 610-613.	1.8	120
5	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012, 13, 547.	2.8	118
6	Integrating Y-Chromosome, Mitochondrial, and Autosomal Data to Analyze the Origin of Pig Breeds. <i>Molecular Biology and Evolution</i> , 2009, 26, 2061-2072.	8.9	103
7	Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. <i>BMC Genomics</i> , 2010, 11, 593.	2.8	102
8	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.	2.8	98
9	Detection of QTL affecting fatty acid composition in the pig. <i>Mammalian Genome</i> , 2003, 14, 650-656.	2.2	74
10	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.	3.3	71
11	QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects. <i>Genetical Research</i> , 2002, 80, 145-154.	0.9	68
12	Differences in Muscle Transcriptome among Pigs Phenotypically Extreme for Fatty Acid Composition. <i>PLoS ONE</i> , 2014, 9, e99720.	2.5	66
13	Association between the pig genome and its gut microbiota composition. <i>Scientific Reports</i> , 2019, 9, 8791.	3.3	64
14	Genome-wide association study for intramuscular fatty acid composition in an Iberian \times Landrace cross1. <i>Journal of Animal Science</i> , 2012, 90, 2883-2893.	0.5	63
15	Phylogenetic analysis of Sicilian goats reveals a new mtDNA lineage. <i>Animal Genetics</i> , 2006, 37, 376-378.	1.7	62
16	Expression analysis of candidate genes for fatty acid composition in adipose tissue and identification of regulatory regions. <i>Scientific Reports</i> , 2018, 8, 2045.	3.3	62
17	Identification of genes regulating growth and fatness traits in pig through hypothalamic transcriptome analysis. <i>Physiological Genomics</i> , 2014, 46, 195-206.	2.3	56
18	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.	2.5	52

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19	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.	2.5	47
20	Genome-wide analysis of porcine backfat and intramuscular fat fatty acid composition using high-density genotyping and expression data. <i>BMC Genomics</i> , 2013, 14, 845.	2.8	46
21	Transcriptome architecture across tissues in the pig. <i>BMC Genomics</i> , 2008, 9, 173.	2.8	45
22	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.	2.8	44
23	Selection in the Making: A Worldwide Survey of Haplotypic Diversity Around a Causative Mutation in Porcine <i>IGF2</i> . <i>Genetics</i> , 2008, 178, 1639-1652.	2.9	42
24	Hypothalamic expression of porcine leptin receptor (LEPR), neuropeptide Y (NPY), and cocaine- and amphetamine-regulated transcript (CART) genes is influenced by LEPR genotype. <i>Mammalian Genome</i> , 2010, 21, 583-591.	2.2	42
25	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.	2.5	42
26	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.	3.3	42
27	QTL detection on porcine chromosome 12 for fatty acid composition and association analyses of the <i>fatty acid synthase</i> , <i>gastric inhibitory polypeptide</i> and <i>acetyl-coenzyme A carboxylase alpha</i> genes. <i>Animal Genetics</i> , 2007, 38, 639-646.	1.7	40
28	A quantitative trait locus genome scan for porcine muscle fiber traits reveals overdominance and epistasis1. <i>Journal of Animal Science</i> , 2008, 86, 3290-3299.	0.5	39
29	Genetic polymorphism of the caprine kappa casein gene. <i>Journal of Dairy Research</i> , 2001, 68, 209-216.	1.4	36
30	A Co-Association Network Analysis of the Genetic Determination of Pig Conformation, Growth and Fatness. <i>PLoS ONE</i> , 2014, 9, e114862.	2.5	36
31	Characterization of the porcine acyl-CoA synthetase long-chain 4 gene and its association with growth and meat quality traits. <i>Animal Genetics</i> , 2006, 37, 219-224.	1.7	35
32	Unexpected High Polymorphism at the FABP4 Gene Unveils a Complex History for Pig Populations. <i>Genetics</i> , 2006, 174, 2119-2127.	2.9	35
33	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.	3.0	35
34	Nucleotide sequence of the goat β -casein cDNA. <i>Journal of Animal Science</i> , 1993, 71, 2833-2833.	0.5	33
35	Complete Sequence of the Caprine β -Lactoglobulin Gene. <i>Journal of Dairy Science</i> , 1994, 77, 3493-3497.	3.4	33
36	On growth, fatness, and form: A further look at porcine Chromosome 4 in an Iberian Landrace cross. <i>Mammalian Genome</i> , 2005, 16, 374-382.	2.2	33

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37	Characterization of the porcine FABP5 gene and its association with the FAT1 QTL in an Iberian by Landrace cross. <i>Animal Genetics</i> , 2006, 37, 589-591.	1.7	33
38	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.	3.3	30
39	A non-synonymous mutation in a conserved site of the <i>MTTP</i> gene is strongly associated with protein activity and fatty acid profile in pigs. <i>Animal Genetics</i> , 2009, 40, 813-820.	1.7	28
40	Genome-wide linkage analysis of QTL for growth and body composition employing the PorcineSNP60 BeadChip. <i>BMC Genetics</i> , 2012, 13, 41.	2.7	28
41	Differential expression of bovine β -lactoglobulin A and B promoter variants in transiently transfected HC11 cells. <i>Journal of Dairy Research</i> , 1999, 66, 537-544.	1.4	27
42	Characterization of genetic polymorphism in the goat β -lactoglobulin gene. <i>Journal of Dairy Research</i> , 2000, 67, 217-224.	1.4	27
43	Recombination rates across porcine autosomes inferred from high-density linkage maps. <i>Animal Genetics</i> , 2012, 43, 620-623.	1.7	27
44	Disruption of the mouse phospholipase C- β 1 gene in a β -lactoglobulin transgenic line affects viability, growth, and fertility in mice. <i>Gene</i> , 2004, 341, 279-289.	2.2	26
45	Adipocyte fatty-acid binding protein is closely associated to the porcine FAT1 locus on chromosome 41. <i>Journal of Animal Science</i> , 2006, 84, 2907-2913.	0.5	26
46	Identification of Single-Nucleotide Polymorphism in the Progesterone Receptor Gene and Its Association With Reproductive Traits in Rabbits. <i>Genetics</i> , 2008, 180, 1699-1705.	2.9	26
47	Phytogenic actives supplemented in hyperprolific sows: effects on maternal transfer of phytogenic compounds, colostrum and milk features, performance and antioxidant status of sows and their offspring, and piglet intestinal gene expression. <i>Journal of Animal Science</i> , 2020, 98, .	0.5	26
48	Exploring Alternative Models for Sex-Linked Quantitative Trait Loci in Outbred Populations: Application to an Iberian \times Landrace Pig Intercross. <i>Genetics</i> , 2002, 161, 1625-1632.	2.9	23
49	Joint effects of porcine <i>leptin</i> and <i>leptin receptor</i> polymorphisms on productivity and quality traits. <i>Animal Genetics</i> , 2012, 43, 805-809.	1.7	22
50	Using RNA-seq SNP data to reveal potential causal mutations related to pig production traits and RNA editing. <i>Animal Genetics</i> , 2017, 48, 151-165.	1.7	22
51	Characterization of a caprine β -lactoglobulin pseudogene, identification and chromosomal localization by in situ hybridization in goat, sheep and cow. <i>Gene</i> , 1996, 177, 87-91.	2.2	21
52	Polymorphisms in the goat β -lactoglobulin gene. <i>Journal of Dairy Research</i> , 2005, 72, 379-384.	1.4	21
53	Analysis of the porcine <i>APOA2</i> gene expression in liver, polymorphism identification and association with fatty acid composition traits. <i>Animal Genetics</i> , 2016, 47, 552-559.	1.7	20
54	Transcriptional analysis of intramuscular fatty acid composition in the longissimus thoracis muscle of Iberian \times Landrace backcrossed pigs. <i>Animal Genetics</i> , 2013, 44, 648-660.	1.7	19

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55	Candidate gene analysis for reproductive traits in two lines of rabbits divergently selected for uterine capacity1. <i>Journal of Animal Science</i> , 2010, 88, 828-836.	0.5	18
56	Evaluation of the porcine <i>ACSL4</i> gene as a candidate gene for meat quality traits in pigs. <i>Animal Genetics</i> , 2012, 43, 714-720.	1.7	18
57	Using genome wide association studies to identify common QTL regions in three different genetic backgrounds based on Iberian pig breed. <i>PLoS ONE</i> , 2018, 13, e0190184.	2.5	18
58	Structural Features of the 5â€™ Flanking Region of the Caprine Î²-Casein Gene. <i>Journal of Dairy Science</i> , 1995, 78, 973-977.	3.4	17
59	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. <i>Heredity</i> , 2011, 107, 256-264.	2.6	16
60	New insight into the SSC8 genetic determination of fatty acid composition in pigs. <i>Genetics Selection Evolution</i> , 2014, 46, 28.	3.0	16
61	Identification of eQTLs associated with lipid metabolism in Longissimus dorsi muscle of pigs with different genetic backgrounds. <i>Scientific Reports</i> , 2020, 10, 9845.	3.3	16
62	Transcriptional Characterization of Porcine Leptin and Leptin Receptor Genes. <i>PLoS ONE</i> , 2013, 8, e66398.	2.5	16
63	A growth hormone-based phylogenetic analysis of euteleostean fishes including a representative species of the Atheriniformes Order, <i>Odontesthes argentinensis</i> . <i>Genetics and Molecular Biology</i> , 2003, 26, 295-300.	1.3	15
64	Evolutionary study of a potential selection target region in the pig. <i>Heredity</i> , 2011, 106, 330-338.	2.6	15
65	Nucleotide variability and linkage disequilibrium patterns at the porcine <i>FABP5</i> gene. <i>Animal Genetics</i> , 2008, 39, 468-473.	1.7	14
66	Cloning and sequencing of the cDNA encoding goat Î²-lactoglobulin. <i>Journal of Animal Science</i> , 1993, 71, 2832.	0.5	12
67	Rabbit oviductal glycoprotein 1 gene: Genomic organization polymorphism analysis and mRNA expression. <i>Molecular Reproduction and Development</i> , 2007, 74, 687-693.	2.0	12
68	Expression of progesterone receptor related to the polymorphism in the PGR gene in the rabbit reproductive tract1. <i>Journal of Animal Science</i> , 2010, 88, 421-427.	0.5	12
69	Survey of SSC12 Regions Affecting Fatty Acid Composition of Intramuscular Fat Using High-Density SNP Data. <i>Frontiers in Genetics</i> , 2011, 2, 101.	2.3	12
70	Analysis of porcine IGF2 gene expression in adipose tissue and its effect on fatty acid composition. <i>PLoS ONE</i> , 2019, 14, e0220708.	2.5	12
71	Disentangling Two QTL on Porcine Chromosome 12 for Backfat Fatty Acid Composition. <i>Animal Biotechnology</i> , 2013, 24, 168-186.	1.5	11
72	Isolation, sequencing and relative quantitation by fluorescent-ratio PCR of feline Î²-lactoglobulin I, II, and III cDNAs. <i>Mammalian Genome</i> , 1999, 10, 560-564.	2.2	10

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73	Exclusion of the acyl CoA:diacylglycerol acyltransferase 1 gene (DGAT1) as a candidate for a fatty acid composition QTL on porcine chromosome 4. <i>Journal of Animal Breeding and Genetics</i> , 2005, 122, 161-164.	2.0	10
74	Analysis of the oviductal glycoprotein 1 polymorphisms and their effects on components of litter size in rabbits. <i>Animal Genetics</i> , 2009, 40, 756-758.	1.7	10
75	Evaluation of FABP2 as candidate gene for a fatty acid composition QTL in porcine chromosome 8. <i>Journal of Animal Breeding and Genetics</i> , 2009, 126, 52-58.	2.0	10
76	Investigation of the oviductal glycoprotein 1 (OVGP1) gene associated with embryo survival and development in the rabbit. <i>Journal of Animal Science</i> , 2010, 88, 1597-1602.	0.5	10
77	A Quantitative Real-Time PCR Method Using an X-Linked Gene for Sex Typing in Pigs. <i>Molecular Biotechnology</i> , 2013, 54, 493-496.	2.4	10
78	Transversal gene expression panel to evaluate intestinal health in broiler chickens in different challenging conditions. <i>Scientific Reports</i> , 2021, 11, 6315.	3.3	10
79	Chromatin Structures of Goat and Sheep β -Lactoglobulin Gene Differ. <i>Biochemical and Biophysical Research Communications</i> , 1998, 252, 649-653.	2.1	9
80	Building phenotype networks to improve QTL detection: a comparative analysis of fatty acid and fat traits in pigs. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 329-343.	2.0	9
81	Nucleotide variability of the porcine SERPINA6 gene and the origin of a putative causal mutation associated with meat quality. <i>Animal Genetics</i> , 2011, 42, 235-241.	1.7	9
82	Expression of caprine beta-lactoglobulin in the milk of transgenic mice. <i>Transgenic Research</i> , 1997, 6, 69-74.	2.4	8
83	TIMP-1 as candidate gene for embryo survival in two divergent lines selected for uterine capacity in rabbits. <i>Molecular Reproduction and Development</i> , 2006, 73, 678-684.	2.0	8
84	Characterization and Physical Mapping of the Porcine CDS1 and CDS2 Genes. <i>Animal Biotechnology</i> , 2007, 18, 23-35.	1.5	8
85	Association of genetic variants and expression levels of porcine FABP4 and FABP5 genes. <i>Animal Genetics</i> , 2017, 48, 660-668.	1.7	6
86	Porcine Digestible Peptides (PDP) in Weanling Diets Regulates the Expression of Genes Involved in Gut Barrier Function, Immune Response and Nutrient Transport in Nursery Pigs. <i>Animals</i> , 2020, 10, 2368.	2.3	6
87	Mapping of the goat stearoyl coenzyme A desaturase gene to chromosome 26. <i>Animal Genetics</i> , 2003, 34, 474-475.	1.7	5
88	Assignment of the microsomal triglyceride transfer protein large subunit (MTP) gene to porcine chromosome 8. <i>Animal Genetics</i> , 2005, 36, 354-355.	1.7	5
89	Polymorphism and chromosomal localization of the porcine signal transducer and activator of transcription 5B gene (STAT5B). <i>Journal of Animal Breeding and Genetics</i> , 2006, 123, 284-287.	2.0	5
90	Deciphering the regulation of porcine genes influencing growth, fatness and yield-related traits through genetical genomics. <i>Mammalian Genome</i> , 2017, 28, 130-142.	2.2	4

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91	Assignment of the acyl-CoA synthetase long-chain family member 4 (ACSL4) gene to porcine chromosome X. <i>Animal Genetics</i> , 2005, 36, 76-76.	1.7	3
92	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.	2.5	3
93	Assignment of the beta-lactoglobulin (BLG) gene to porcine chromosome 1. <i>Animal Genetics</i> , 2005, 36, 356-358.	1.7	2
94	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.	1.7	2
95	Indel detection from Whole Genome Sequencing data and association with lipid metabolism in pigs. <i>PLoS ONE</i> , 2019, 14, e0218862.	2.5	2
96	Assignment of the phospholipase C β 1 (PLCB1) gene to porcine chromosome 17. <i>Animal Genetics</i> , 2005, 36, 516-517.	1.7	1
97	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-342J.	1.1	1
98	Assignment of the oviductal glycoprotein 1 gene (OVGP1) to porcine chromosome 4q22-q23 by radiation hybrid panel mapping. <i>Cytogenetic and Genome Research</i> , 2006, 114, 93C-93C.	1.1	1
99	Expression of Recombinant Human Follicle-Stimulating Hormone in the Mammary Gland of Transgenic Mice. <i>Molecular Biotechnology</i> , 2006, 34, 37-44.	2.4	0