Josep M Folch

List of Publications by Citations

99 papers	2,403 citations	30 h-index	44 g-index
99 ext. papers	2,851 ext. citations	2.9 avg, IF	4.43 L-index

#	Paper	IF	Citations
99	Characterisation of PCV-2 isolates from Spain, Germany and France. *Virus Research*, **2000**, 66, 65-77	6.4	146
98	Fine mapping of porcine chromosome 6 QTL and LEPR effects on body composition in multiple generations of an Iberian by Landrace intercross. *Genetical Research*, **2005**, 85, 57-67	1.1	110
97	Real-time quantitative PCR-based system for determining transgene copy number in transgenic animals. *BioTechniques*, **2004**, 37, 610-3	2.5	108
96	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. *BMC Genomics*, **2012**, 13, 547	4.5	89
95	Integrating Y-chromosome, mitochondrial, and autosomal data to analyze the origin of pig breeds. *Molecular Biology and Evolution*, **2009**, 26, 2061-72	8.3	89
94	Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. *BMC Genomics*, **2010**, 11, 593	4.5	86
93	Characterization of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions. *Scientific Reports*, **2018**, 8, 12727	4.9	75
92	Detection of QTL affecting fatty acid composition in the pig. *Mammalian Genome*, **2003**, 14, 650-6	3.2	68
91	QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects. *Genetical Research*, **2002**, 80, 145-54	1.1	64
90	Analysis of porcine adipose tissue transcriptome reveals differences in de novo fatty acid synthesis in pigs with divergent muscle fatty acid composition. *BMC Genomics*, **2013**, 14, 843	4.5	58
89	Genome-wide association study for intramuscular fatty acid composition in an Iberian Landrace cross. *Journal of Animal Science*, **2012**, 90, 2883-93	0.7	54
88	Phylogenetic analysis of Sicilian goats reveals a new mtDNA lineage. *Animal Genetics*, **2006**, 37, 376-8	2.5	53
87	Differences in muscle transcriptome among pigs phenotypically extreme for fatty acid composition. *PLoS ONE*, **2014**, 9, e99720	3.7	44
86	Expression analysis of candidate genes for fatty acid composition in adipose tissue and identification of regulatory regions. *Scientific Reports*, **2018**, 8, 2045	4.9	41
85	Selection in the making: a worldwide survey of haplotypic diversity around a causative mutation in porcine IGF2. *Genetics*, **2008**, 178, 1639-52	4	39
84	Genome-wide analysis of porcine backfat and intramuscular fat fatty acid composition using high-density genotyping and expression data. *BMC Genomics*, **2013**, 14, 845	4.5	38
83	Expression-based GWAS identifies variants, gene interactions and key regulators affecting intramuscular fatty acid content and composition in porcine meat. *Scientific Reports*, **2016**, 6, 31803	4.9	38

82	Polymorphism in the ELOVL6 gene is associated with a major QTL effect on fatty acid composition in pigs. *PLoS ONE*, **2013**, 8, e53687	3.7	36
81	Transcriptome architecture across tissues in the pig. *BMC Genomics*, **2008**, 9, 173	4.5	35
80	QTL detection on porcine chromosome 12 for fatty-acid composition and association analyses of the fatty acid synthase, gastric inhibitory polypeptide and acetyl-coenzyme A carboxylase alpha genes. *Animal Genetics*, **2007**, 38, 639-46	2.5	34
79	Hypothalamic expression of porcine leptin receptor (LEPR), neuropeptide Y (NPY), and cocaine- and amphetamine-regulated transcript (CART) genes is influenced by LEPR genotype. *Mammalian Genome*, **2010**, 21, 583-91	3.2	33
78	Unexpected high polymorphism at the FABP4 gene unveils a complex history for pig populations. *Genetics*, **2006**, 174, 2119-27	4	33
77	Genetic polymorphism of the caprine kappa casein gene. *Journal of Dairy Research*, **2001**, 68, 209-16	1.6	32
76	Association between the pig genome and its gut microbiota composition. *Scientific Reports*, **2019**, 9, 8794	4.9	31
75	From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. *BMC Genomics*, **2014**, 15, 232	4.5	31
74	DAG expression: high-throughput gene expression analysis of real-time PCR data using standard curves for relative quantification. *PLoS ONE*, **2013**, 8, e80385	3.7	31
73	A quantitative trait locus genome scan for porcine muscle fiber traits reveals overdominance and epistasis. *Journal of Animal Science*, **2008**, 86, 3290-9	0.7	31
72	On growth, fatness, and form: a further look at porcine chromosome 4 in an Iberian x Landrace cross. *Mammalian Genome*, **2005**, 16, 374-82	3.2	31
71	Characterization of the porcine acyl-CoA synthetase long-chain 4 gene and its association with growth and meat quality traits. *Animal Genetics*, **2006**, 37, 219-24	2.5	30
70	Characterization of the porcine FABP5 gene and its association with the FAT1 QTL in an Iberian by Landrace cross. *Animal Genetics*, **2006**, 37, 589-91	2.5	30
69	Nucleotide sequence of the goat kappa-casein cDNA. *Journal of Animal Science*, **1993**, 71, 2833	0.7	28
68	Complete sequence of the caprine beta-lactoglobulin gene. *Journal of Dairy Science*, **1994**, 77, 3493-7	4	25
67	Epigenetic regulation of the ELOVL6 gene is associated with a major QTL effect on fatty acid composition in pigs. *Genetics Selection Evolution*, **2015**, 47, 20	4.9	24
66	A global analysis of CNVs in swine using whole genome sequence data and association analysis with fatty acid composition and growth traits. *PLoS ONE*, **2017**, 12, e0177014	3.7	24
65	Genome-wide linkage analysis of QTL for growth and body composition employing the PorcineSNP60 BeadChip. *BMC Genetics*, **2012**, 13, 41	2.6	24

64	A non-synonymous mutation in a conserved site of the MTTP gene is strongly associated with protein activity and fatty acid profile in pigs. *Animal Genetics*, **2009**, 40, 813-20	2.5	24
63	Adipocyte fatty-acid binding protein is closely associated to the porcine FAT1 locus on chromosome 4. *Journal of Animal Science*, **2006**, 84, 2907-13	0.7	23
62	A co-association network analysis of the genetic determination of pig conformation, growth and fatness. *PLoS ONE*, **2014**, 9, e114862	3.7	23
61	Differential expression of bovine beta-lactoglobulin A and B promoter variants in transiently transfected HC11 cells. *Journal of Dairy Research*, **1999**, 66, 537-44	1.6	22
60	Characterization of a caprine beta-lactoglobulin pseudogene, identification and chromosomal localization by in situ hybridization in goat, sheep and cow. *Gene*, **1996**, 177, 87-91	3.8	21
59	Disruption of the mouse phospholipase C-beta1 gene in a beta-lactoglobulin transgenic line affects viability, growth, and fertility in mice. *Gene*, **2004**, 341, 279-89	3.8	20
58	Recombination rates across porcine autosomes inferred from high-density linkage maps. *Animal Genetics*, **2012**, 43, 620-3	2.5	19
57	Using RNA-Seq SNP data to reveal potential causal mutations related to pig production traits and RNA editing. *Animal Genetics*, **2017**, 48, 151-165	2.5	19
56	Identification of genes regulating growth and fatness traits in pig through hypothalamic transcriptome analysis. *Physiological Genomics*, **2014**, 46, 195-206	3.6	19
55	Identification of single-nucleotide polymorphism in the progesterone receptor gene and its association with reproductive traits in rabbits. *Genetics*, **2008**, 180, 1699-705	4	19
54	Characterization of genetic polymorphism in the goat beta-lactoglobulin gene. *Journal of Dairy Research*, **2000**, 67, 217-24	1.6	19
53	Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs. *Scientific Reports*, **2017**, 7, 46539	4.9	18
52	Polymorphisms in the goat beta-lactoglobulin gene. *Journal of Dairy Research*, **2005**, 72, 379-84	1.6	16
51	Exploring alternative models for sex-linked quantitative trait loci in outbred populations: application to an iberian x landrace pig intercross. *Genetics*, **2002**, 161, 1625-32	4	16
50	Transcriptional analysis of intramuscular fatty acid composition in the longissimus thoracis muscle of Iberian□Landrace back-crossed pigs. *Animal Genetics*, **2013**, 44, 648-60	2.5	15
49	Evolutionary study of a potential selection target region in the pig. *Heredity*, **2011**, 106, 330-8	3.6	15
48	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. *Heredity*, **2011**, 107, 256-64	3.6	15
47	Structural features of the 5Tflanking region of the caprine kappa-casein gene. *Journal of Dairy Science*, **1995**, 78, 973-7	4	15

46	Analysis of the porcine APOA2 gene expression in liver, polymorphism identification and association with fatty acid composition traits. *Animal Genetics*, **2016**, 47, 552-9	2.5	15
45	Joint effects of porcine leptin and leptin receptor polymorphisms on productivity and quality traits. *Animal Genetics*, **2012**, 43, 805-9	2.5	14
44	Evaluation of the porcine ACSL4 gene as a candidate gene for meat quality traits in pigs. *Animal Genetics*, **2012**, 43, 714-20	2.5	13
43	New insight into the SSC8 genetic determination of fatty acid composition in pigs. *Genetics Selection Evolution*, **2014**, 46, 28	4.9	13
42	Candidate gene analysis for reproductive traits in two lines of rabbits divergently selected for uterine capacity. *Journal of Animal Science*, **2010**, 88, 828-36	0.7	13
41	Nucleotide variability and linkage disequilibrium patterns at the porcine FABP5 gene. *Animal Genetics*, **2008**, 39, 468-73	2.5	12
40	Cloning and sequencing of the cDNA encoding goat beta-lactoglobulin. *Journal of Animal Science*, **1993**, 71, 2832	0.7	12
39	Survey of SSC12 Regions Affecting Fatty Acid Composition of Intramuscular Fat Using High-Density SNP Data. *Frontiers in Genetics*, **2011**, 2, 101	4.5	11
38	A growth hormone-based phylogenetic analysis of euteleostean fishes including a representative species of the Atheriniformes Order, Odontesthes argentinensis. *Genetics and Molecular Biology*, **2003**, 26, 295-300	2	11
37	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. *Journal of Animal Science*, **2020**, 98,	0.7	11
36	Identification of strong candidate genes for backfat and intramuscular fatty acid composition in three crosses based on the Iberian pig. *Scientific Reports*, **2020**, 10, 13962	4.9	11
35	Expression of progesterone receptor related to the polymorphism in the PGR gene in the rabbit reproductive tract. *Journal of Animal Science*, **2010**, 88, 421-7	0.7	10
34	Rabbit oviductal glycoprotein 1 gene: genomic organization polymorphism analysis and mRNA expression. *Molecular Reproduction and Development*, **2007**, 74, 687-93	2.6	10
33	Building phenotype networks to improve QTL detection: a comparative analysis of fatty acid and fat traits in pigs. *Journal of Animal Breeding and Genetics*, **2011**, 128, 329-43	2.9	9
32	Nucleotide variability of the porcine SERPINA6 gene and the origin of a putative causal mutation associated with meat quality. *Animal Genetics*, **2011**, 42, 235-41	2.5	9
31	Chromatin structures of goat and sheep beta-lactoglobulin gene differ. *Biochemical and Biophysical Research Communications*, **1998**, 252, 649-53	3.4	9
30	Using genome wide association studies to identify common QTL regions in three different genetic backgrounds based on Iberian pig breed. *PLoS ONE*, **2018**, 13, e0190184	3.7	8
29	Disentangling two QTL on porcine chromosome 12 for backfat fatty acid composition. *Animal Biotechnology*, **2013**, 24, 168-86	1.4	8

28	Analysis of the oviductal glycoprotein 1 polymorphisms and their effects on components of litter size in rabbits. *Animal Genetics*, **2009**, 40, 756-8	2.5	8
27	Evaluation of FABP2 as candidate gene for a fatty acid composition QTL in porcine chromosome 8. *Journal of Animal Breeding and Genetics*, **2009**, 126, 52-8	2.9	8
26	Expression of caprine beta-lactoglobulin in the milk of transgenic mice. *Transgenic Research*, **1997**, 6, 69-74	3.3	8
25	Exclusion of the acyl CoA:diacylglycerol acyltransferase 1 gene (DGAT1) as a candidate for a fatty acid composition QTL on porcine chromosome 4. *Journal of Animal Breeding and Genetics*, **2005**, 122, 161-4	2.9	8
24	Isolation, sequencing and relative quantitation by fluorescent-ratio PCR of feline beta-lactoglobulin I, II, and III cDNAs. *Mammalian Genome*, **1999**, 10, 560-4	3.2	8
23	Transcriptional Characterization of Porcine Leptin and Leptin Receptor Genes. *PLoS ONE*, **2013**, 8, e66398	3.7	8
22	A quantitative real-time PCR method using an X-linked gene for sex typing in pigs. *Molecular Biotechnology*, **2013**, 54, 493-6	3	7
21	Investigation of the oviductal glycoprotein 1 (OVGP1) gene associated with embryo survival and development in the rabbit. *Journal of Animal Science*, **2010**, 88, 1597-602	0.7	7
20	Characterization and physical mapping of the porcine CDS1 and CDS2 genes. *Animal Biotechnology*, **2007**, 18, 23-35	1.4	7
19	TIMP-1 as candidate gene for embryo survival in two divergent lines selected for uterine capacity in rabbits. *Molecular Reproduction and Development*, **2006**, 73, 678-84	2.6	7
18	Analysis of porcine IGF2 gene expression in adipose tissue and its effect on fatty acid composition. *PLoS ONE*, **2019**, 14, e0220708	3.7	6
17	Transversal gene expression panel to evaluate intestinal health in broiler chickens in different challenging conditions. *Scientific Reports*, **2021**, 11, 6315	4.9	6
16	Assignment of the microsomal triglyceride transfer protein large subunit (MTP) gene to porcine chromosome 8. *Animal Genetics*, **2005**, 36, 354-5	2.5	5
15	Deciphering the regulation of porcine genes influencing growth, fatness and yield-related traits through genetical genomics. *Mammalian Genome*, **2017**, 28, 130-142	3.2	4
14	Association of genetic variants and expression levels of porcine FABP4 and FABP5 genes. *Animal Genetics*, **2017**, 48, 660-668	2.5	4
13	Mapping of the goat stearoyl coenzyme A desaturase gene to chromosome 26. *Animal Genetics*, **2003**, 34, 474-5	2.5	4
12	Identification of eQTLs associated with lipid metabolism in Longissimus dorsi muscle of pigs with different genetic backgrounds. *Scientific Reports*, **2020**, 10, 9845	4.9	3
11	Polymorphism and chromosomal localization of the porcine signal transducer and activator of transcription 5B gene (STAT5B). *Journal of Animal Breeding and Genetics*, **2006**, 123, 284-7	2.9	3

10	Assignment of the acyl-CoA synthetase long-chain family member 4 (ACSL4) gene to porcine chromosome X. *Animal Genetics*, **2005**, 36, 76	2.5	3
9	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. *Animals*, **2020**, 10,	3.1	2
8	Indel detection from Whole Genome Sequencing data and association with lipid metabolism in pigs. *PLoS ONE*, **2019**, 14, e0218862	3.7	2
7	Identification of differentially expressed genes in the oviduct of two rabbit lines divergently selected for uterine capacity using suppression subtractive hybridization. *Animal Genetics*, **2013**, 44, 296-304	2.5	1
6	Assignment of Signal Transducer and Activator of Transcription 5A (STAT5A) gene to porcine chromosome 12p13-->p11 by radiation hybrid panel mapping. *Cytogenetic and Genome Research*, **2006**, 112, 342J	1.9	1
5	Assignment of the oviductal glycoprotein 1 gene (OVGP1) to porcine chromosome 4q22-->q23 by radiation hybrid panel mapping. *Cytogenetic and Genome Research*, **2006**, 114, 93C	1.9	1
4	Assignment of the beta-lactoglobulin (BLG) gene to porcine chromosome 1. *Animal Genetics*, **2005**, 36, 356-8	2.5	1
3	Assignment of the phospholipase Cbeta1 (PLCB1) gene to porcine chromosome 17. *Animal Genetics* , **2005**, 36, 516-7	2.5	1
2	Expression of recombinant human follicle-stimulating hormone in the mammary gland of transgenic mice. *Molecular Biotechnology*, **2006**, 34, 37-44	3	
1	Expression analysis of porcine miR-33a/b in liver, adipose tissue and muscle and its potential role in fatty acid metabolism. *PLoS ONE*, **2021**, 16, e0245858	3.7	