

Anna Castell Farr

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.

66

papers

1,490

citations

21

h-index

37

g-index

68

ext. papers

1,853

ext. citations

3.7

avg, IF

4.26

L-index

#	Paper	IF	Citations
66	Estimating the copy number of the agouti signaling protein (ASIP) gene in goat breeds with different color patterns. <i>Livestock Science</i> , 2021 , 246, 104440	1.7	0
65	Variability in porcine microRNA genes and its association with mRNA expression and lipid phenotypes. <i>Genetics Selection Evolution</i> , 2021 , 53, 43	4.9	1
64	Detecting the footprint of selection on the genomes of Murciano-Granadina goats. <i>Animal Genetics</i> , 2021 , 52, 683-693	2.5	1
63	Characterization of the Impact of Density Gradient Centrifugation on the Profile of the Pig Sperm Transcriptome by RNA-Seq. <i>Frontiers in Veterinary Science</i> , 2021 , 8, 668158	3.1	2
62	Assessing the levels of intraspecific admixture and interspecific hybridization in Iberian wild goats (). <i>Evolutionary Applications</i> , 2021 , 14, 2618-2634	4.8	1
61	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	
60	A systems biology framework integrating GWAS and RNA-seq to shed light on the molecular basis of sperm quality in swine. <i>Genetics Selection Evolution</i> , 2020 , 52, 72	4.9	4
59	Identification of circular RNAs in porcine sperm and evaluation of their relation to sperm motility. <i>Scientific Reports</i> , 2020 , 10, 7985	4.9	16
58	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
57	Analyzing the genomic and transcriptomic architecture of milk traits in Murciano-Granadina goats. <i>Journal of Animal Science and Biotechnology</i> , 2020 , 11, 35	6	5
56	A genome-wide association analysis for body, udder, and leg conformation traits recorded in Murciano-Granadina goats. <i>Journal of Dairy Science</i> , 2020 , 103, 11605-11617	4	1
55	A genome-wide analysis of copy number variation in Murciano-Granadina goats. <i>Genetics Selection Evolution</i> , 2020 , 52, 44	4.9	3
54	Whole genome sequencing identifies allelic ratio distortion in sperm involving genes related to spermatogenesis in a swine model. <i>DNA Research</i> , 2020 , 27,	4.5	1
53	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
52	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
51	A RNA-Seq Analysis to Describe the Boar Sperm Transcriptome and Its Seasonal Changes. <i>Frontiers in Genetics</i> , 2019 , 10, 299	4.5	30
50	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

49	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
48	Indel detection from Whole Genome Sequencing data and association with lipid metabolism in pigs. <i>PLoS ONE</i> , 2019 , 14, e0218862	3.7	2
47	Association between the pig genome and its gut microbiota composition. <i>Scientific Reports</i> , 2019 , 9, 8794.9		31
46	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
45	A technical assessment of the porcine ejaculated spermatozoa for a sperm-specific RNA-seq analysis. <i>Systems Biology in Reproductive Medicine</i> , 2018 , 64, 291-303	2.9	20
44	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
43	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
42	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
41	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
40	Association of genetic variants and expression levels of porcine FABP4 and FABP5 genes. <i>Animal Genetics</i> , 2017 , 48, 660-668	2.5	4
39	An association analysis between a missense polymorphism at the pig PCSK9 gene and serum lipid and meat quality traits in Duroc pigs. <i>Livestock Science</i> , 2016 , 190, 27-30	1.7	
38	Variations at regulatory regions of the milk protein genes are associated with milk traits and coagulation properties in the Sarda sheep. <i>Animal Genetics</i> , 2016 , 47, 717-726	2.5	19
37	Identification of protein-damaging mutations in 10 swine taste receptors and 191 appetite-reward genes. <i>BMC Genomics</i> , 2016 , 17, 685	4.5	4
36	Study of the ability of <i>Bacillus toyonensis</i> to interfere with the quorum-sensing systems of enterotoxigenic <i>Escherichia coli</i> K88 in the pig gut. <i>Journal of Animal Science</i> , 2016 , 94, 70-74	0.7	2
35	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
34	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
33	Endometrial gene expression profile of pregnant sows with extreme phenotypes for reproductive efficiency. <i>Scientific Reports</i> , 2015 , 5, 14416	4.9	14
32	Associations between pig adiponectin (ADIPOQ) genotype and serum lipid levels are modulated by age-specific modifiers. <i>Journal of Animal Science</i> , 2014 , 92, 5367-73	0.7	1

31	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
30	The role of viral and host microRNAs in the Aujeszky disease virus during the infection process. <i>PLoS ONE</i> , 2014 , 9, e86965	3.7	17
29	Technical note: Advantages and limitations of authenticating Palmera goat dairy products by pyrosequencing the melanocortin 1 receptor (MC1R) gene. <i>Journal of Dairy Science</i> , 2014 , 97, 7293-7	4	6
28	New insight into the SSC8 genetic determination of fatty acid composition in pigs. <i>Genetics Selection Evolution</i> , 2014 , 46, 28	4.9	13
27	A genome-wide association analysis for porcine serum lipid traits reveals the existence of age-specific genetic determinants. <i>BMC Genomics</i> , 2014 , 15, 758	4.5	18
26	Worldwide genetic relationships of pigs as inferred from X chromosome SNPs. <i>Animal Genetics</i> , 2013 , 44, 130-8	2.5	9
25	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
24	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
23	Identification of two paralogous caprine CD36 genes that display highly divergent mRNA expression profiles. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , 2013 , 36, 1-7	2.6	1
22	An association analysis between polymorphisms of the pig solute carrier family 27A (SLC27A), member 1 and 4 genes and serum and muscle lipid traits. <i>Livestock Science</i> , 2013 , 152, 143-146	1.7	5
21	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
20	miRNA expression profile analysis in kidney of different porcine breeds. <i>PLoS ONE</i> , 2013 , 8, e55402	3.7	23
19	A high throughput genotyping approach reveals distinctive autosomal genetic signatures for European and Near Eastern wild boar. <i>PLoS ONE</i> , 2013 , 8, e55891	3.7	22
18	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
17	Genome-wide linkage analysis of QTL for growth and body composition employing the PorcineSNP60 BeadChip. <i>BMC Genetics</i> , 2012 , 13, 41	2.6	24
16	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012 , 13, 547	4.5	89
15	Determination of reference microRNAs for relative quantification in porcine tissues. <i>PLoS ONE</i> , 2012 , 7, e44413	3.7	41
14	Genome-wide association study for intramuscular fatty acid composition in an Iberian Landrace cross. <i>Journal of Animal Science</i> , 2012 , 90, 2883-93	0.7	54

13	Sequencing and gene expression of the porcine ITIH SSC13 cluster and its effect on litter size in an Iberian [Meishan F2 population. <i>Animal Reproduction Science</i> , 2011 , 128, 85-92	2.1	3
12	Analysis of porcine MUC4 gene as a candidate gene for prolificacy QTL on SSC13 in an Iberian [Meishan F2 population. <i>BMC Genetics</i> , 2011 , 12, 93	2.6	6
11	Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. <i>BMC Genomics</i> , 2010 , 11, 593	4.5	86
10	Transcriptome architecture across tissues in the pig. <i>BMC Genomics</i> , 2008 , 9, 173	4.5	35
9	Real-time quantitative PCR-based system for determining transgene copy number in transgenic animals. <i>BioTechniques</i> , 2004 , 37, 610-3	2.5	108
8	Neuron-derived orphan receptor-1 (NOR-1) modulates vascular smooth muscle cell proliferation. <i>Circulation Research</i> , 2003 , 92, 96-103	15.7	70
7	Characterization of the dystrophin-syntrophin interaction using the two-hybrid system in yeast. <i>FEBS Letters</i> , 1996 , 383, 124-8	3.8	13
6	Evidence for posttranscriptional regulation of GLUT4 expression in muscle and adipose tissue from streptozotocin-induced diabetic and benfluorex-treated rats. <i>Biochemical Pharmacology</i> , 1996 , 52, 1665-73	6	19
5	Regulation of GLUT5 gene expression in rat intestinal mucosa: regional distribution, circadian rhythm, perinatal development and effect of diabetes. <i>Biochemical Journal</i> , 1995 , 309 (Pt 1), 271-7	3.8	72
4	Differential sensitivity of insulin- and adaptive-regulation-induced system A activation to microtubular function in skeletal muscle. <i>Biochemical Journal</i> , 1992 , 281 (Pt 2), 407-11	3.8	19
3	Effect of diabetes and fasting on GLUT-4 (muscle/fat) glucose-transporter expression in insulin-sensitive tissues. Heterogeneous response in heart, red and white muscle. <i>Biochemical Journal</i> , 1992 , 282 (Pt 3), 765-72	3.8	130
2	Developmental regulation of GLUT-1 (erythroid/Hep G2) and GLUT-4 (muscle/fat) glucose transporter expression in rat heart, skeletal muscle, and brown adipose tissue. <i>Endocrinology</i> , 1992 , 130, 837-846	4.8	136
1	Identification of circular RNAs in porcine sperm and their relation to sperm motility		1