

# Anna Castell Farr

## List of Publications by Citations

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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 | 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> , <b>1992</b> , 130, 837-846                  | 4.8  | 136       |
| 65 | 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> , <b>1992</b> , 282 ( Pt 3), 765-72 | 3.8  | 130       |
| 64 | Real-time quantitative PCR-based system for determining transgene copy number in transgenic animals. <i>BioTechniques</i> , <b>2004</b> , 37, 610-3  | 2.5  | 108       |
| 63 | Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , <b>2012</b> , 13, 547   | 4.5  | 89        |
| 62 | Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. <i>BMC Genomics</i> , <b>2010</b> , 11, 593   | 4.5  | 86        |
| 61 | Regulation of GLUT5 gene expression in rat intestinal mucosa: regional distribution, circadian rhythm, perinatal development and effect of diabetes. <i>Biochemical Journal</i> , <b>1995</b> , 309 ( Pt 1), 271-7                       | 3.8  | 72        |
| 60 | Neuron-derived orphan receptor-1 (NOR-1) modulates vascular smooth muscle cell proliferation. <i>Circulation Research</i> , <b>2003</b> , 92, 96-103   | 15.7 | 70        |
| 59 | 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> , <b>2013</b> , 14, 843                                   | 4.5  | 58        |
| 58 | Genome-wide association study for intramuscular fatty acid composition in an Iberian Landrace cross. <i>Journal of Animal Science</i> , <b>2012</b> , 90, 2883-93  | 0.7  | 54        |
| 57 | Expression analysis of candidate genes for fatty acid composition in adipose tissue and identification of regulatory regions. <i>Scientific Reports</i> , <b>2018</b> , 8, 2045  | 4.9  | 41        |
| 56 | Determination of reference microRNAs for relative quantification in porcine tissues. <i>PLoS ONE</i> , <b>2012</b> , 7, e44413   | 3.7  | 41        |
| 55 | Expression-based GWAS identifies variants, gene interactions and key regulators affecting intramuscular fatty acid content and composition in porcine meat. <i>Scientific Reports</i> , <b>2016</b> , 6, 31803                           | 4.9  | 38        |
| 54 | Transcriptome architecture across tissues in the pig. <i>BMC Genomics</i> , <b>2008</b> , 9, 173   | 4.5  | 35        |
| 53 | Association between the pig genome and its gut microbiota composition. <i>Scientific Reports</i> , <b>2019</b> , 9, 8794.9   | 4.9  | 31        |
| 52 | From SNP co-association to RNA co-expression: novel insights into gene networks for intramuscular fatty acid composition in porcine. <i>BMC Genomics</i> , <b>2014</b> , 15, 232   | 4.5  | 31        |
| 51 | A RNA-Seq Analysis to Describe the Boar Sperm Transcriptome and Its Seasonal Changes. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 299   | 4.5  | 30        |
| 50 | 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> , <b>2017</b> , 12, e0177014   | 3.7  | 24        |

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| 49 | Genome-wide linkage analysis of QTL for growth and body composition employing the PorcineSNP60 BeadChip. <i>BMC Genetics</i> , <b>2012</b> , 13, 41  | 2.6 | 24 |
| 48 | miRNA expression profile analysis in kidney of different porcine breeds. <i>PLoS ONE</i> , <b>2013</b> , 8, e55402   | 3.7 | 23 |
| 47 | Differential expression of mRNA isoforms in the skeletal muscle of pigs with distinct growth and fatness profiles. <i>BMC Genomics</i> , <b>2018</b> , 19, 145   | 4.5 | 22 |
| 46 | A high throughput genotyping approach reveals distinctive autosomal genetic signatures for European and Near Eastern wild boar. <i>PLoS ONE</i> , <b>2013</b> , 8, e55891  | 3.7 | 22 |
| 45 | A technical assessment of the porcine ejaculated spermatozoa for a sperm-specific RNA-seq analysis. <i>Systems Biology in Reproductive Medicine</i> , <b>2018</b> , 64, 291-303  | 2.9 | 20 |
| 44 | 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> , <b>2016</b> , 47, 717-726                               | 2.5 | 19 |
| 43 | Evidence for posttranscriptional regulation of GLUT4 expression in muscle and adipose tissue from streptozotocin-induced diabetic and benfluorex-treated rats. <i>Biochemical Pharmacology</i> , <b>1996</b> , 52, 1665-73 | 6   | 19 |
| 42 | Differential sensitivity of insulin- and adaptive-regulation-induced system A activation to microtubular function in skeletal muscle. <i>Biochemical Journal</i> , <b>1992</b> , 281 ( Pt 2), 407-11                       | 3.8 | 19 |
| 41 | Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs. <i>Scientific Reports</i> , <b>2017</b> , 7, 46539                            | 4.9 | 18 |
| 40 | A genome-wide association analysis for porcine serum lipid traits reveals the existence of age-specific genetic determinants. <i>BMC Genomics</i> , <b>2014</b> , 15, 758  | 4.5 | 18 |
| 39 | The role of viral and host microRNAs in the Aujeszky disease virus during the infection process. <i>PLoS ONE</i> , <b>2014</b> , 9, e86965   | 3.7 | 17 |
| 38 | Identification of circular RNAs in porcine sperm and evaluation of their relation to sperm motility. <i>Scientific Reports</i> , <b>2020</b> , 10, 7985  | 4.9 | 16 |
| 37 | Analysis of the porcine APOA2 gene expression in liver, polymorphism identification and association with fatty acid composition traits. <i>Animal Genetics</i> , <b>2016</b> , 47, 552-9                                   | 2.5 | 15 |
| 36 | Endometrial gene expression profile of pregnant sows with extreme phenotypes for reproductive efficiency. <i>Scientific Reports</i> , <b>2015</b> , 5, 14416   | 4.9 | 14 |
| 35 | Evaluation of the porcine ACSL4 gene as a candidate gene for meat quality traits in pigs. <i>Animal Genetics</i> , <b>2012</b> , 43, 714-20  | 2.5 | 13 |
| 34 | New insight into the SSC8 genetic determination of fatty acid composition in pigs. <i>Genetics Selection Evolution</i> , <b>2014</b> , 46, 28  | 4.9 | 13 |
| 33 | Characterization of the dystrophin-syntrophin interaction using the two-hybrid system in yeast. <i>FEBS Letters</i> , <b>1996</b> , 383, 124-8   | 3.8 | 13 |
| 32 | 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> , <b>2019</b> , 20, 170                     | 4.5 | 12 |

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| 31 | Identification of strong candidate genes for backfat and intramuscular fatty acid composition in three crosses based on the Iberian pig. <i>Scientific Reports</i> , <b>2020</b> , 10, 13962                              | 4.9 | 11 |
| 30 | Worldwide genetic relationships of pigs as inferred from X chromosome SNPs. <i>Animal Genetics</i> , <b>2013</b> , 44, 130-8  | 2.5 | 9  |
| 29 | A quantitative real-time PCR method using an X-linked gene for sex typing in pigs. <i>Molecular Biotechnology</i> , <b>2013</b> , 54, 493-6   | 3   | 7  |
| 28 | Analysis of porcine IGF2 gene expression in adipose tissue and its effect on fatty acid composition. <i>PLoS ONE</i> , <b>2019</b> , 14, e0220708   | 3.7 | 6  |
| 27 | 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> , <b>2014</b> , 97, 7293-7            | 4   | 6  |
| 26 | Analysis of porcine MUC4 gene as a candidate gene for prolificacy QTL on SSC13 in an Iberian × Meishan F2 population. <i>BMC Genetics</i> , <b>2011</b> , 12, 93  | 2.6 | 6  |
| 25 | Analyzing the genomic and transcriptomic architecture of milk traits in Murciano-Granadina goats. <i>Journal of Animal Science and Biotechnology</i> , <b>2020</b> , 11, 35   | 6   | 5  |
| 24 | 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> , <b>2013</b> , 152, 143-146                | 1.7 | 5  |
| 23 | 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> , <b>2020</b> , 52, 72                                       | 4.9 | 4  |
| 22 | Association of genetic variants and expression levels of porcine FABP4 and FABP5 genes. <i>Animal Genetics</i> , <b>2017</b> , 48, 660-668  | 2.5 | 4  |
| 21 | Identification of protein-damaging mutations in 10 swine taste receptors and 191 appetite-reward genes. <i>BMC Genomics</i> , <b>2016</b> , 17, 685   | 4.5 | 4  |
| 20 | Analysing the Expression of Eight Clock Genes in Five Tissues From Fasting and Fed Sows. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 475  | 4.5 | 4  |
| 19 | About the existence of common determinants of gene expression in the porcine liver and skeletal muscle. <i>BMC Genomics</i> , <b>2019</b> , 20, 518   | 4.5 | 3  |
| 18 | Identification of eQTLs associated with lipid metabolism in Longissimus dorsi muscle of pigs with different genetic backgrounds. <i>Scientific Reports</i> , <b>2020</b> , 10, 9845                                       | 4.9 | 3  |
| 17 | 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> , <b>2011</b> , 128, 85-92                       | 2.1 | 3  |
| 16 | A genome-wide analysis of copy number variation in Murciano-Granadina goats. <i>Genetics Selection Evolution</i> , <b>2020</b> , 52, 44   | 4.9 | 3  |
| 15 | Indel detection from Whole Genome Sequencing data and association with lipid metabolism in pigs. <i>PLoS ONE</i> , <b>2019</b> , 14, e0218862   | 3.7 | 2  |
| 14 | 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> , <b>2016</b> , 94, 70-74 | 0.7 | 2  |

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|----|---|-----|---|
| 13 | 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> , <b>2021</b> , 8, 668158                                  | 3.1 | 2 |
| 12 | Associations between pig adiponectin (ADIPOQ) genotype and serum lipid levels are modulated by age-specific modifiers. <i>Journal of Animal Science</i> , <b>2014</b> , 92, 5367-73   | 0.7 | 1 |
| 11 | Identification of two paralogous caprine CD36 genes that display highly divergent mRNA expression profiles. <i>Comparative Immunology, Microbiology and Infectious Diseases</i> , <b>2013</b> , 36, 1-7                       | 2.6 | 1 |
| 10 | 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> , <b>2013</b> , 44, 296-304 | 2.5 | 1 |
| 9  | Identification of circular RNAs in porcine sperm and their relation to sperm motility   |     | 1 |
| 8  | A genome-wide association analysis for body, udder, and leg conformation traits recorded in Murciano-Granadina goats. <i>Journal of Dairy Science</i> , <b>2020</b> , 103, 11605-11617  | 4   | 1 |
| 7  | Whole genome sequencing identifies allelic ratio distortion in sperm involving genes related to spermatogenesis in a swine model. <i>DNA Research</i> , <b>2020</b> , 27,   | 4.5 | 1 |
| 6  | Variability in porcine microRNA genes and its association with mRNA expression and lipid phenotypes. <i>Genetics Selection Evolution</i> , <b>2021</b> , 53, 43   | 4.9 | 1 |
| 5  | Detecting the footprint of selection on the genomes of Murciano-Granadina goats. <i>Animal Genetics</i> , <b>2021</b> , 52, 683-693   | 2.5 | 1 |
| 4  | Assessing the levels of intraspecific admixture and interspecific hybridization in Iberian wild goats (). <i>Evolutionary Applications</i> , <b>2021</b> , 14, 2618-2634  | 4.8 | 1 |
| 3  | Estimating the copy number of the agouti signaling protein (ASIP) gene in goat breeds with different color patterns. <i>Livestock Science</i> , <b>2021</b> , 246, 104440   | 1.7 | 0 |
| 2  | 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> , <b>2016</b> , 190, 27-30                                      | 1.7 |   |
| 1  | 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> , <b>2021</b> , 16, e0245858  | 3.7 |   |