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List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

4,695
citations

159585

30
h-index

110387

64
g-index

73
all docs

73
docs citations

73
times ranked

8331
citing authors

#	ARTICLE	IF	CITATIONS
1	Understanding the development of the gut microbiome in pigs: an overview. Burleigh Dodds Series in Agricultural Science, 2022, , 179-202.	0.2	0
2	Differences in caecal microbiota composition and Salmonella carriage between experimentally infected inbred lines of chickens. Genetics Selection Evolution, 2022, 54, 7.	3.0	11
3	Influence of genetics and the pre-vaccination blood transcriptome on the variability of antibody levels after vaccination against Mycoplasma hyopneumoniae in pigs. Genetics Selection Evolution, 2021, 53, 24.	3.0	8
4	Influence of genetic background and dietary oleic acid on gut microbiota composition in Duroc and Iberian pigs. PLoS ONE, 2021, 16, e0251804.	2.5	4
5	Links between fecal microbiota and the response to vaccination against influenza A virus in pigs. Npj Vaccines, 2021, 6, 92.	6.0	13
6	Analysis of viromes and microbiomes from pig fecal samples reveals that phages and prophages rarely carry antibiotic resistance genes. ISME Communications, 2021, 1, .	4.2	20
7	Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. Journal of Animal Breeding and Genetics, 2020, 137, 49-59.	2.0	51
8	Host genotype and amoxicillin administration affect the incidence of diarrhoea and faecal microbiota of weaned piglets during a natural multiresistant ETEC infection. Journal of Animal Breeding and Genetics, 2020, 137, 60-72.	2.0	12
9	Special issue on livestock metagenomics. Journal of Animal Breeding and Genetics, 2020, 137, 3-3.	2.0	0
10	Discovery of Predictors of Mycoplasma hyopneumoniae Vaccine Response Efficiency in Pigs: 16S rRNA Gene Fecal Microbiota Analysis. Microorganisms, 2020, 8, 1151.	3.6	10
11	Broilers divergently selected for digestibility differ for their digestive microbial ecosystems. PLoS ONE, 2020, 15, e0232418.	2.5	7
12	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. GigaScience, 2020, 9, .	6.4	35
13	Transcription from a gene desert in a melanoma porcine model. Molecular Genetics and Genomics, 2020, 295, 1239-1252.	2.1	1
14	Applicability of an Unmedicated Feeding Program Aimed to Reduce the Use of Antimicrobials in Nursery Piglets: Impact on Performance and Fecal Microbiota. Animals, 2020, 10, 242.	2.3	2
15	Late weaning is associated with increased microbial diversity and Faecalibacterium prausnitzii abundance in the fecal microbiota of piglets. Animal Microbiome, 2020, 2, 2.	3.8	31
16	Integrative analysis of blood and gut microbiota data suggests a non-alcoholic fatty liver disease (NAFLD)-related disorder in French SLAdd minipigs. Scientific Reports, 2020, 10, 234.	3.3	0
17	Transport to the Slaughterhouse Affects the Salmonella Shedding and Modifies the Fecal Microbiota of Finishing Pigs. Animals, 2020, 10, 676.	2.3	13
18	Growth Performance and Adaptability of European Sea Bass (Dicentrarchus labrax) Gut Microbiota to Alternative Diets Free of Fish Products. Microorganisms, 2020, 8, 1346.	3.6	24

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19	Association between the pig genome and its gut microbiota composition. <i>Scientific Reports</i> , 2019, 9, 8791.	3.3	64
20	Genomic diversity, linkage disequilibrium and selection signatures in European local pig breeds assessed with a high density SNP chip. <i>Scientific Reports</i> , 2019, 9, 13546.	3.3	78
21	Towards the quantitative characterisation of piglets' robustness to weaning: a modelling approach. <i>Animal</i> , 2019, 13, 2536-2546.	3.3	37
22	Influence of the Intestinal Microbiota on Colonization Resistance to <i>Salmonella</i> and the Shedding Pattern of Naturally Exposed Pigs. <i>MSystems</i> , 2019, 4, .	3.8	40
23	Benefits from the joint analysis of host genomes and metagenomes: Select the holobiont. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 75-76.	2.0	12
24	Characterization of whole blood transcriptome and early-life fecal microbiota in high and low responder pigs before, and after vaccination for <i>Mycoplasma hyopneumoniae</i> . <i>Vaccine</i> , 2019, 37, 1743-1755.	3.8	16
25	Inferring the evolution of the major histocompatibility complex of wild pigs and peccaries using hybridisation DNA capture-based sequencing. <i>Immunogenetics</i> , 2018, 70, 401-417.	2.4	6
26	Diversity across major and candidate genes in European local pig breeds. <i>PLoS ONE</i> , 2018, 13, e0207475.	2.5	69
27	Early <i>Salmonella</i> Typhimurium infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa. <i>Scientific Reports</i> , 2018, 8, 7788.	3.3	61
28	Immune differences between porcine ileal and jejunal Peyer's patches revealed by global transcriptome sequencing of gut-associated lymphoid tissues. <i>Scientific Reports</i> , 2018, 8, 9077.	3.3	12
29	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
30	New susceptibility loci for cutaneous melanoma risk and progression revealed using a porcine model. <i>Oncotarget</i> , 2018, 9, 27682-27697.	1.8	11
31	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
32	RACK1 cooperates with NRAS Q61K to promote melanoma in vivo. <i>Cellular Signalling</i> , 2017, 36, 255-266.	3.6	7
33	Transcriptome of melanoma cells from two mouse models, Tyr:NRas Q61K and Tyr:Rack1-HA, Tyr:NRas Q61K. <i>Data in Brief</i> , 2017, 14, 32-34.	1.0	0
34	Deciphering the genetic regulation of peripheral blood transcriptome in pigs through expression genome-wide association study and allele-specific expression analysis. <i>BMC Genomics</i> , 2017, 18, 967.	2.8	22
35	Phylogenetic network analysis applied to pig gut microbiota identifies an ecosystem structure linked with growth traits. <i>ISME Journal</i> , 2016, 10, 2973-2977.	9.8	308
36	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	13.3	416

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37	P1016 The pig's other genome: A reference gene catalog of the gut microbiome as a new resource for deep studies of the interplay between the host and its microbiome. <i>Journal of Animal Science</i> , 2016, 94, 22-22.	0.5	13
38	Chronic <i>Trichuris muris</i> Infection Decreases Diversity of the Intestinal Microbiota and Concomitantly Increases the Abundance of Lactobacilli. <i>PLoS ONE</i> , 2015, 10, e0125495.	2.5	190
39	Comparison of whole-genome (13X) and capture (87X) resequencing methods for SNP and genotype callings. <i>Animal Genetics</i> , 2015, 46, 82-86.	1.7	2
40	Genome-wide immunity studies in the rabbit: transcriptome variations in peripheral blood mononuclear cells after in vitro stimulation by LPS or PMA-Ionomycin. <i>BMC Genomics</i> , 2015, 16, 26.	2.8	21
41	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
42	Early-life establishment of the swine gut microbiome and impact on host phenotypes. <i>Environmental Microbiology Reports</i> , 2015, 7, 554-569.	2.4	320
43	Extensive Expression Differences along Porcine Small Intestine Evidenced by Transcriptome Sequencing. <i>PLoS ONE</i> , 2014, 9, e88515.	2.5	44
44	<i>KIT</i> and melanoma predisposition in pigs: sequence variants and association analysis. <i>Animal Genetics</i> , 2014, 45, 445-448.	1.7	8
45	Differences in Muscle Transcriptome among Pigs Phenotypically Extreme for Fatty Acid Composition. <i>PLoS ONE</i> , 2014, 9, e99720.	2.5	66
46	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
47	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. <i>BMC Genomics</i> , 2013, 14, 363.	2.8	48
48	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	6.5	1,064
49	The peripheral blood transcriptome reflects variations in immunity traits in swine: towards the identification of biomarkers. <i>BMC Genomics</i> , 2013, 14, 894.	2.8	37
50	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
51	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012, 13, 547.	2.8	118
52	Tuning of Natural Killer Cell Reactivity by NKp46 and Helios Calibrates T Cell Responses. <i>Science</i> , 2012, 335, 344-348.	12.6	190
53	Fast Computation and Applications of Genome Mappability. <i>PLoS ONE</i> , 2012, 7, e30377.	2.5	458
54	Prediction of Altered 3' UTR miRNA-Binding Sites from RNA-Seq Data: The Swine Leukocyte Antigen Complex (SLA) as a Model Region. <i>PLoS ONE</i> , 2012, 7, e48607.	2.5	15

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55	Genetic and functional evaluation of MITF as a candidate gene for cutaneous melanoma predisposition in pigs. <i>Mammalian Genome</i> , 2011, 22, 602-612.	2.2	7
56	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
57	Evaluation of <i>FABP2</i> 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
58	Nucleotide variability and linkage disequilibrium patterns at the porcine <i>FABP5</i> gene. <i>Animal Genetics</i> , 2008, 39, 468-473.	1.7	14
59	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
60	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
61	Association with litter size of new polymorphisms on <i>ESR1</i> and <i>ESR2</i> genes in a Chinese-European pig line. <i>Genetics Selection Evolution</i> , 2007, 39, 195-206.	3.0	63
62	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
63	Characterization of the porcine <i>FABP5</i> gene and its association with the <i>FAT1</i> QTL in an Iberian by Landrace cross. <i>Animal Genetics</i> , 2006, 37, 589-591.	1.7	33
64	<i>TIMP-1</i> 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
65	Assignment of the microsomal triglyceride transfer protein large subunit (<i>MTP</i>) gene to porcine chromosome 8. <i>Animal Genetics</i> , 2005, 36, 354-355.	1.7	5
66	Assignment of <i>RAD51C</i> to porcine chromosome 12 and identification of intronic variability. <i>Animal Genetics</i> , 2005, 36, 461-462.	1.7	0
67	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
68	Effect of the porcine <i>IGF2</i> -intron3-G3072A substitution in an outbred Large White population and in an Iberian – Landrace cross1. <i>Journal of Animal Science</i> , 2005, 83, 2723-2728.	0.5	42
69	Assignment of the mitochondrial glycerol-3-phosphate acyltransferase (<i>GPAT</i>) gene to porcine chromosome 14. <i>Animal Genetics</i> , 2003, 34, 387-387.	1.7	2
70	Iberian pigs: more than excellent ham!. <i>Peer Community in Animal Science</i> , 0, , 100004.	0.0	0