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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	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
2	Fast Computation and Applications of Genome Mappability. <i>PLoS ONE</i> , 2012, 7, e30377.	2.5	458
3	A reference gene catalogue of the pig gut microbiome. <i>Nature Microbiology</i> , 2016, 1, 16161.	13.3	416
4	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
5	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
6	Tuning of Natural Killer Cell Reactivity by NKp46 and Helios Calibrates T Cell Responses. <i>Science</i> , 2012, 335, 344-348.	12.6	190
7	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
8	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
9	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012, 13, 547.	2.8	118
10	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
11	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
12	Diversity across major and candidate genes in European local pig breeds. <i>PLoS ONE</i> , 2018, 13, e0207475.	2.5	69
13	Differences in Muscle Transcriptome among Pigs Phenotypically Extreme for Fatty Acid Composition. <i>PLoS ONE</i> , 2014, 9, e99720.	2.5	66
14	Association between the pig genome and its gut microbiota composition. <i>Scientific Reports</i> , 2019, 9, 8791.	3.3	64
15	Association with litter size of new polymorphisms on ESR1 and ESR2 genes in a Chinese-European pig line. <i>Genetics Selection Evolution</i> , 2007, 39, 195-206.	3.0	63
16	Early <i>Salmonella Typhimurium</i> infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa. <i>Scientific Reports</i> , 2018, 8, 7788.	3.3	61
17	Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 49-59.	2.0	51
18	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. <i>BMC Genomics</i> , 2013, 14, 363.	2.8	48

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19	Extensive Expression Differences along Porcine Small Intestine Evidenced by Transcriptome Sequencing. PLoS ONE, 2014, 9, e88515.	2.5	44
20	Effect of the porcine IGF2-intron3-G3072A substitution in an outbred Large White population and in an Iberian × Landrace cross. Journal of Animal Science, 2005, 83, 2723-2728.	0.5	42
21	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, 639-646.	1.7	40
22	Influence of the Intestinal Microbiota on Colonization Resistance to Salmonella and the Shedding Pattern of Naturally Exposed Pigs. MSystems, 2019, 4, .	3.8	40
23	A quantitative trait locus genome scan for porcine muscle fiber traits reveals overdominance and epistasis. Journal of Animal Science, 2008, 86, 3290-3299.	0.5	39
24	The peripheral blood transcriptome reflects variations in immunity traits in swine: towards the identification of biomarkers. BMC Genomics, 2013, 14, 894.	2.8	37
25	Towards the quantitative characterisation of piglets' robustness to weaning: a modelling approach. Animal, 2019, 13, 2536-2546.	3.3	37
26	A Co-Association Network Analysis of the Genetic Determination of Pig Conformation, Growth and Fatness. PLoS ONE, 2014, 9, e114862.	2.5	36
27	Characterization of the porcine acyl-CoA synthetase long-chain 4 gene and its association with growth and meat quality traits. Animal Genetics, 2006, 37, 219-224.	1.7	35
28	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.	3.0	35
29	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. GigaScience, 2020, 9, .	6.4	35
30	On growth, fatness, and form: A further look at porcine Chromosome 4 in an Iberian × Landrace cross. Mammalian Genome, 2005, 16, 374-382.	2.2	33
31	Characterization of the porcine FABP5 gene and its association with the FAT1 QTL in an Iberian by Landrace cross. Animal Genetics, 2006, 37, 589-591.	1.7	33
32	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
33	Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs. Scientific Reports, 2017, 7, 46539.	3.3	30
34	A non-synonymous mutation in a conserved site of the MTP gene is strongly associated with protein activity and fatty acid profile in pigs. Animal Genetics, 2009, 40, 813-820.	1.7	28
35	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
36	Deciphering the genetic regulation of peripheral blood transcriptome in pigs through expression genome-wide association study and allele-specific expression analysis. BMC Genomics, 2017, 18, 967.	2.8	22

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37	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
38	Analysis of viromes and microbiomes from pig fecal samples reveals that phages and prophages rarely carry antibiotic resistance genes. <i>ISME Communications</i> , 2021, 1, .	4.2	20
39	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
40	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
41	Nucleotide variability and linkage disequilibrium patterns at the porcine <i>FABP5</i> gene. <i>Animal Genetics</i> , 2008, 39, 468-473.	1.7	14
42	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
43	Transport to the Slaughterhouse Affects the Salmonella Shedding and Modifies the Fecal Microbiota of Finishing Pigs. <i>Animals</i> , 2020, 10, 676.	2.3	13
44	Links between fecal microbiota and the response to vaccination against influenza A virus in pigs. <i>Npj Vaccines</i> , 2021, 6, 92.	6.0	13
45	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
46	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
47	Host genotype and amoxicillin administration affect the incidence of diarrhoea and faecal microbiota of weaned piglets during a natural multiresistant ETEC infection. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 60-72.	2.0	12
48	New susceptibility loci for cutaneous melanoma risk and progression revealed using a porcine model. <i>Oncotarget</i> , 2018, 9, 27682-27697.	1.8	11
49	Differences in caecal microbiota composition and Salmonella carriage between experimentally infected inbred lines of chickens. <i>Genetics Selection Evolution</i> , 2022, 54, 7.	3.0	11
50	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
51	Discovery of Predictors of <i>Mycoplasma hyopneumoniae</i> Vaccine Response Efficiency in Pigs: 16S rRNA Gene Fecal Microbiota Analysis. <i>Microorganisms</i> , 2020, 8, 1151.	3.6	10
52	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
53	<i>KIT</i> and melanoma predisposition in pigs: sequence variants and association analysis. <i>Animal Genetics</i> , 2014, 45, 445-448.	1.7	8
54	Influence of genetics and the pre-vaccination blood transcriptome on the variability of antibody levels after vaccination against <i>Mycoplasma hyopneumoniae</i> in pigs. <i>Genetics Selection Evolution</i> , 2021, 53, 24.	3.0	8

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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	RACK1 cooperates with NRAS Q61K to promote melanoma in vivo. <i>Cellular Signalling</i> , 2017, 36, 255-266.	3.6	7
57	Broilers divergently selected for digestibility differ for their digestive microbial ecosystems. <i>PLoS ONE</i> , 2020, 15, e0232418.	2.5	7
58	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
59	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
60	Influence of genetic background and dietary oleic acid on gut microbiota composition in Duroc and Iberian pigs. <i>PLoS ONE</i> , 2021, 16, e0251804.	2.5	4
61	Assignment of the mitochondrial glycerol-3-phosphate acyltransferase (GPAT) gene to porcine chromosome 14. <i>Animal Genetics</i> , 2003, 34, 387-387.	1.7	2
62	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
63	Applicability of an Unmedicated Feeding Program Aimed to Reduce the Use of Antimicrobials in Nursery Piglets: Impact on Performance and Fecal Microbiota. <i>Animals</i> , 2020, 10, 242.	2.3	2
64	Transcription from a gene desert in a melanoma porcine model. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1239-1252.	2.1	1
65	Assignment of RAD51C to porcine chromosome 12 and identification of intronic variability. <i>Animal Genetics</i> , 2005, 36, 461-462.	1.7	0
66	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
67	Special issue on livestock metagenomics. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 3-3.	2.0	0
68	Integrative analysis of blood and gut microbiota data suggests a non-alcoholic fatty liver disease (NAFLD)-related disorder in French SLAdd minipigs. <i>Scientific Reports</i> , 2020, 10, 234.	3.3	0
69	Iberian pigs: more than excellent ham!. <i>Peer Community in Animal Science</i> , 0, , 100004.	0.0	0
70	Understanding the development of the gut microbiome in pigs: an overview. <i>Burleigh Dodds Series in Agricultural Science</i> , 2022, , 179-202.	0.2	0