Yuliaxis Ramayo Caldas

List of Publications by Year
in descending order

64 papers	2,821 citations	236612 25 h-index	189595 50 g-index
73 all docs	73 docs citations	73 times ranked	3553 citing authors

#	Article	IF	Citations
1	A reference gene catalogue of the pig gut microbiome. Nature Microbiology, 2016, 1, 16161.	5.9	416
2	Phylogenetic network analysis applied to pig gut microbiota identifies an ecosystem structure linked with growth traits. ISME Journal, 2016, 10, 2973-2977.	4.4	308
3	Chronic Trichuris muris Infection Decreases Diversity of the Intestinal Microbiota and Concomitantly Increases the Abundance of Lactobacilli. PLoS ONE, 2015, 10, e0125495.	1.1	190
4	Characterization of bacterial microbiota compositions along the intestinal tract in pigs and their interactions and functions. Scientific Reports, 2018, 8, 12727.	1.6	141
5	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. BMC Genomics, 2012, 13, 547.	1.2	118
6	Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. BMC Genomics, 2010, 11, 593.	1.2	102
7	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.	1.2	98
8	A marker-derived gene network reveals the regulatory role of PPARGC1A, HNF4G, and FOXP3 in intramuscular fat deposition of beef cattle1. Journal of Animal Science, 2014, 92, 2832-2845.	0.2	77
9	Integrative approach using liver and duodenum RNA-Seq data identifies candidate genes and pathways associated with feed efficiency in pigs. Scientific Reports, 2018, 8, 558.	1.6	68
10	A functional regulatory variant of MYH3 influences muscle fiber-type composition and intramuscular fat content in pigs. PLoS Genetics, 2019, 15, e1008279.	1.5	66
11	Differences in Muscle Transcriptome among Pigs Phenotypically Extreme for Fatty Acid Composition. PLoS ONE, 2014, 9, e99720.	1.1	66
12	Genome-wide association study for intramuscular fatty acid composition in an Iberian Ã— Landrace cross1. Journal of Animal Science, 2012, 90, 2883-2893.	0.2	63
13	Porcine colonization of the Americas: a 60k SNP story. Heredity, 2013, 110, 321-330.	1.2	58
14	Polymorphism in the ELOVL6 Gene Is Associated with a Major QTL Effect on Fatty Acid Composition in Pigs. PLoS ONE, 2013, 8, e53687.	1.1	52
15	Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. Journal of Animal Breeding and Genetics, 2020, 137, 49-59.	0.8	51
16	Multi-breed and multi-trait co-association analysis of meat tenderness and other meat quality traits in three French beef cattle breeds. Genetics Selection Evolution, 2016, 48, 37.	1.2	50
17	Sequence-based GWAS, network and pathway analyses reveal genes co-associated with milk cheese-making properties and milk composition in MontbÃ©liarde cows. Genetics Selection Evolution, 2019, 51, 34.	1.2	46
18	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.	1.2	44

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19	Understanding the response to endurance exercise using a systems biology approach: combining blood metabolomics, transcriptomics and miRNomics in horses. BMC Genomics, 2017, 18, 187.	1.2	42
20	Priming for welfare: gut microbiota is associated with equitation conditions and behavior in horse athletes. Scientific Reports, 2020, 10, 8311.	1.6	42
21	Integration of GWAS, pathway and network analyses reveals novel mechanistic insights into the synthesis of milk proteins in dairy cows. Scientific Reports, 2018, 8, 566.	1.6	39
22	A Co-Association Network Analysis of the Genetic Determination of Pig Conformation, Growth and Fatness. PLoS ONE, 2014, 9, e114862.	1.1	36
23	A catalog of microbial genes from the bovine rumen unveils a specialized and diverse biomass-degrading environment. GigaScience, 2020, 9, .	3.3	35
24	Integration of liver gene co-expression networks and eGWAs analyses highlighted candidate regulators implicated in lipid metabolism in pigs. Scientific Reports, 2017, 7, 46539.	1.6	30
25	Genome-wide linkage analysis of QTL for growth and body composition employing the PorcineSNP60 BeadChip. BMC Genetics, 2012, 13, 41.	2.7	28
26	Recombination rates across porcine autosomes inferred from high‐density linkage maps. Animal Genetics, 2012, 43, 620-623.	0.6	27
27	A system-based analysis of the genetic determinism of udder conformation and health phenotypes across three French dairy cattle breeds. PLoS ONE, 2018, 13, e0199931.	1.1	25
28	A systems biology framework integrating GWAS and RNA-seq to shed light on the molecular basis of sperm quality in swine. Genetics Selection Evolution, 2020, 52, 72.	1.2	25
29	Gut eukaryotic communities in pigs: diversity, composition and host genetics contribution. Animal Microbiome, 2020, 2, 18.	1.5	25
30	Integrating genome-wide co-association and gene expression to identify putative regulators and predictors of feed efficiency in pigs. Genetics Selection Evolution, 2019, 51, 48.	1.2	24
31	Diet, Immunity, and Microbiota Interactions: An Integrative Analysis of the Intestine Transcriptional Response and Microbiota Modulation in Gilthead Seabream (Sparus aurata) Fed an Essential Oils-Based Functional Diet. Frontiers in Immunology, 2021, 12, 625297.	2.2	24
32	Porcine Tissue-Specific Regulatory Networks Derived from Meta-Analysis of the Transcriptome. PLoS ONE, 2012, 7, e46159.	1.1	23
33	Genetic parameters and associated genomic regions for global immunocompetence and other health-related traits in pigs. Scientific Reports, 2020, 10, 18462.	1.6	23
34	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.	1.2	22
35	SNP co-association and network analyses identify E2F3, KDM5A and BACH2 as key regulators of the bovine milk fatty acid profile. Scientific Reports, 2017, 7, 17317.	1.6	21
36	A pilot RNA-seq study in 40 pietrain ejaculates to characterize the porcine sperm microbiome. Theriogenology, 2020, 157, 525-533.	0.9	19

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37	A gene co-association network regulating gut microbial communities in a Duroc pig population. Microbiome, 2021, 9, 52.	4.9	19
38	Evaluation of the porcine <scp><i>ACSL4</i></scp> gene as a candidate gene for meat quality traits in pigs. Animal Genetics, 2012, 43, 714-720.	0.6	18
39	Modulatory Effect of Protein and Carotene Dietary Levels on Pig gut Microbiota. Scientific Reports, 2019, 9, 14582.	1.6	18
40	Co-expression network analysis predicts a key role of microRNAs in the adaptation of the porcine skeletal muscle to nutrient supply. Journal of Animal Science and Biotechnology, 2020, 11, 10.	2.1	17
41	Opportunities and limits of combining microbiome and genome data for complex trait prediction. Genetics Selection Evolution, 2021, 53, 65.	1.2	17
42	Understanding host-microbiota interactions in the commercial piglet around weaning. Scientific Reports, 2021, 11, 23488.	1.6	17
43	New insight into the SSC8 genetic determination of fatty acid composition in pigs. Genetics Selection Evolution, 2014, 46, 28.	1.2	16
44	Breeding farm, level of feeding and presence of antibiotics in the feed influence rabbit cecal microbiota. Animal Microbiome, 2020, 2, 40.	1.5	15
45	Single-step genome-wide association study for social genetic effects and direct genetic effects on growth in Landrace pigs. Scientific Reports, 2020, 10, 14958.	1.6	15
46	About the existence of common determinants of gene expression in the porcine liver and skeletal muscle. BMC Genomics, 2019, 20, 518.	1.2	14
47	P1016 The pigâ€™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. Journal of Animal Science, 2016, 94, 22-22.	0.2	13
48	The value of gut microbiota to predict feed efficiency and growth of rabbits under different feeding regimes. Scientific Reports, 2021, 11, 19495.	1.6	13
49	Supplementation of xylo-oligosaccharides to suckling piglets promotes the growth of fiber-degrading gut bacterial populations during the lactation and nursery periods. Scientific Reports, 2022, 12, .	1.6	12
50	A Quantitative Real-Time PCR Method Using an X-Linked Gene for Sex Typing in Pigs. Molecular Biotechnology, 2013, 54, 493-496.	1.3	10
51	Early socialization and environmental enrichment of lactating piglets affects the caecal microbiota and metabolomic response after weaning. Scientific Reports, 2021, 11, 6113.	1.6	10
52	Mitochondrial DNA diversity in wild boar from the Primorsky Krai Region (East Russia). Animal Genetics, 2011, 42, 96-99.	0.6	9
53	Genetic diversity and selection signatures of the beef â€˜Charolais de Cubaâ€™ breed. Scientific Reports, 2018, 8, 11005.	1.6	9
54	Gene networks for three feed efficiency criteria reveal shared and specific biological processes. Genetics Selection Evolution, 2020, 52, 67.	1.2	9

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55	kernInt: A Kernel Framework for Integrating Supervised and Unsupervised Analyses in Spatio-Temporal Metagenomic Datasets. Frontiers in Microbiology, 2021, 12, 609048.	1.5	9
56	Leveraging host-genetics and gut microbiota to determine immunocompetence in pigs. Animal Microbiome, 2021, 3, 74.	1.5	9
57	Link-HD: a versatile framework to explore and integrate heterogeneous microbial communities. Bioinformatics, 2020, 36, 2298-2299.	1.8	8
58	Detection of selection signatures in Limousin cattle using whole‐genome resequencing. Animal Genetics, 2020, 51, 815-819.	0.6	6
59	Whole-genome sequencing reveals insights into the adaptation of French Charolais cattle to Cuban tropical conditions. Genetics Selection Evolution, 2021, 53, 3.	1.2	5
60	A Co-Association Network Analysis Reveals Putative Regulators for Health-Related Traits in Pigs. Frontiers in Immunology, 2021, 12, 784978.	2.2	3
61	Use of Bayes factors to evaluate the effects of host genetics, litter and cage on the rabbit cecal microbiota. Genetics Selection Evolution, 2022, 54, .	1.2	2
62	P5007 Systems biology approach provides novel insights into gene networks controlling tenderness and meat quality traits across French beef breeds. Journal of Animal Science, 2016, 94, 118-119.	0.2	0
63	The Identification of Runs of Homozygosity Gives a Focus on the Genetic Diversity and Adaptation of the "Charolais de Cuba" Cattle. Animals, 2020, 10, 2233.	1.0	0
64	Analyse génétique de la « fromageabilité » du lait de vache prédite par spectrométrie dans le moyen infrarouge en race Montbéliarde. INRA Productions Animales, 2019, 32, 379-398.	0.3	0