

Nares Trakooljul

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

1,188
citations

394421

19
h-index

454955

30
g-index

67
all docs

67
docs citations

67
times ranked

1630
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated analysis of microRNA expression and mRNA transcriptome in lungs of avian influenza virus infected broilers. <i>BMC Genomics</i> , 2012, 13, 278.	2.8	99
2	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. <i>Nature Communications</i> , 2021, 12, 5848.	12.8	70
3	Iron Transporters Are Differentially Regulated by Dietary Iron, and Modifications Are Associated with Changes in Manganese Metabolism in Young Pigs. <i>Journal of Nutrition</i> , 2009, 139, 1474-1479.	2.9	64
4	Transcriptional and pathway analysis in the hypothalamus of newly hatched chicks during fasting and delayed feeding. <i>BMC Genomics</i> , 2010, 11, 162.	2.8	57
5	RNA-seq of muscle from pigs divergent in feed efficiency and product quality identifies differences in immune response, growth, and macronutrient and connective tissue metabolism. <i>BMC Genomics</i> , 2018, 19, 791.	2.8	56
6	MicroRNAs Regulate Cellular ATP Levels by Targeting Mitochondrial Energy Metabolism Genes during C2C12 Myoblast Differentiation. <i>PLoS ONE</i> , 2015, 10, e0127850.	2.5	44
7	RNA-Seq of Liver From Pigs Divergent in Feed Efficiency Highlights Shifts in Macronutrient Metabolism, Hepatic Growth and Immune Response. <i>Frontiers in Genetics</i> , 2019, 10, 117.	2.3	43
8	Discovery of Candidate Genes for Muscle Traits Based on GWAS Supported by eQTL-analysis. <i>International Journal of Biological Sciences</i> , 2014, 10, 327-337.	6.4	41
9	Identification of Common Regulators of Genes in Co-Expression Networks Affecting Muscle and Meat Properties. <i>PLoS ONE</i> , 2015, 10, e0123678.	2.5	39
10	Discovery of chicken microRNAs associated with lipogenesis and cell proliferation. <i>Physiological Genomics</i> , 2010, 41, 185-193.	2.3	37
11	Pre- and post-natal muscle microRNA expression profiles of two pig breeds differing in muscularity. <i>Gene</i> , 2015, 561, 190-198.	2.2	33
12	Integrated Genome-wide association and hypothalamus eQTL studies indicate a link between the circadian rhythm-related gene PER1 and coping behavior. <i>Scientific Reports</i> , 2015, 5, 16264.	3.3	29
13	Epigenome-wide skeletal muscle DNA methylation profiles at the background of distinct metabolic types and ryanodine receptor variation in pigs. <i>BMC Genomics</i> , 2019, 20, 492.	2.8	29
14	Muscle Transcriptional Profile Based on Muscle Fiber, Mitochondrial Respiratory Activity, and Metabolic Enzymes. <i>International Journal of Biological Sciences</i> , 2015, 11, 1348-1362.	6.4	27
15	Breed, Diet, and Interaction Effects on Adipose Tissue Transcriptome in Iberian and Duroc Pigs Fed Different Energy Sources. <i>Genes</i> , 2019, 10, 589.	2.4	27
16	Transcriptional profiling of liver during the critical embryo-to-hatchling transition period in the chicken (<i>Gallus gallus</i>). <i>BMC Genomics</i> , 2018, 19, 695.	2.8	25
17	MicroRNA-mRNA regulatory networking fine-tunes the porcine muscle fiber type, muscular mitochondrial respiratory and metabolic enzyme activities. <i>BMC Genomics</i> , 2016, 17, 531.	2.8	23
18	Single- and Bayesian Multi-Marker Genome-Wide Association for Haematological Parameters in Pigs. <i>PLoS ONE</i> , 2016, 11, e0159212.	2.5	22

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19	Transcriptome analysis of adipose tissue from pigs divergent in feed efficiency reveals alteration in gene networks related to adipose growth, lipid metabolism, extracellular matrix, and immune response. <i>Molecular Genetics and Genomics</i> , 2019, 294, 395-408.	2.1	21
20	Proteins involved in iron metabolism in beef cattle are affected by copper deficiency in combination with high dietary manganese, but not by copper deficiency alone. <i>Journal of Animal Science</i> , 2010, 88, 275-283.	0.5	20
21	Transcriptional profiling of liver in riboflavin-deficient chicken embryos explains impaired lipid utilization, energy depletion, massive hemorrhaging, and delayed feathering. <i>BMC Genomics</i> , 2018, 19, 177.	2.8	19
22	DNA methylation analysis of porcine mammary epithelial cells reveals differentially methylated loci associated with immune response against <i>Escherichia coli</i> challenge. <i>BMC Genomics</i> , 2019, 20, 623.	2.8	17
23	Mitochondrial-nuclear crosstalk, haplotype and copy number variation distinct in muscle fiber type, mitochondrial respiratory and metabolic enzyme activities. <i>Scientific Reports</i> , 2017, 7, 14024.	3.3	16
24	Transcriptome analyses of liver in newly-hatched chicks during the metabolic perturbation of fasting and re-feeding reveals THRSPA as the key lipogenic transcription factor. <i>BMC Genomics</i> , 2020, 21, 109.	2.8	16
25	Age and Dietary Iron Affect Expression of Genes Involved in Iron Acquisition and Homeostasis in Young Pigs. <i>Journal of Nutrition</i> , 2010, 140, 271-277.	2.9	14
26	Genetic architecture and regulatory impact on hepatic microRNA expression linked to immune and metabolic traits. <i>Open Biology</i> , 2017, 7, 170101.	3.6	14
27	Transcriptome Responses to Dexamethasone Depending on Dose and Glucocorticoid Receptor Sensitivity in the Liver. <i>Frontiers in Genetics</i> , 2019, 10, 559.	2.3	14
28	Cross-talk between energy metabolism and epigenetics during temperature stress response in C2C12 myoblasts. <i>International Journal of Hyperthermia</i> , 2019, 36, 775-783.	2.5	14
29	Identification of the Key Molecular Drivers of Phosphorus Utilization Based on Host miRNA-mRNA and Gut Microbiome Interactions. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2818.	4.1	14
30	Genetically regulated hepatic transcripts and pathways orchestrate haematological, biochemical and body composition traits. <i>Scientific Reports</i> , 2016, 6, 39614.	3.3	13
31	miRNAs regulate acute transcriptional changes in broiler embryos in response to modification of incubation temperature. <i>Scientific Reports</i> , 2018, 8, 11371.	3.3	13
32	Transcriptional shifts account for divergent resource allocation in feed efficient broiler chickens. <i>Scientific Reports</i> , 2018, 8, 12903.	3.3	12
33	Effects of glyphosate residues and different concentrate feed proportions in dairy cow rations on hepatic gene expression, liver histology and biochemical blood parameters. <i>PLoS ONE</i> , 2021, 16, e0246679.	2.5	12
34	Transcriptional responses in jejunum of two layer chicken strains following variations in dietary calcium and phosphorus levels. <i>BMC Genomics</i> , 2021, 22, 485.	2.8	11
35	Polymorphisms of the porcine androgen receptor gene affecting its amino acid sequence and expression level. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1678, 94-101.	2.4	8
36	Transient Shifts of Incubation Temperature Reveal Immediate and Long-Term Transcriptional Response in Chicken Breast Muscle Underpinning Resilience and Phenotypic Plasticity. <i>PLoS ONE</i> , 2016, 11, e0162485.	2.5	8

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37	Sex-Specific Muscular Maturation Responses Following Prenatal Exposure to Methylation-Related Micronutrients in Pigs. <i>Nutrients</i> , 2017, 9, 74.	4.1	8
38	Genetic Regulation of Liver Metabolites and Transcripts Linking to Biochemical-Clinical Parameters. <i>Frontiers in Genetics</i> , 2019, 10, 348.	2.3	8
39	Ileal Transcriptome Profiles of Japanese Quail Divergent in Phosphorus Utilization. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2762.	4.1	8
40	Transcriptome analysis of porcine PBMCs reveals lipopolysaccharide-induced immunomodulatory responses and crosstalk of immune and glucocorticoid receptor signaling. <i>Virulence</i> , 2021, 12, 1808-1824.	4.4	8
41	mRNA Profiles of Porcine Parathyroid Glands Following Variable Phosphorus Supplies throughout Fetal and Postnatal Life. <i>Biomedicines</i> , 2021, 9, 454.	3.2	8
42	Wnt signaling related transcripts and their relationship to energy metabolism in C2C12 myoblasts under temperature stress. <i>PeerJ</i> , 2021, 9, e11625.	2.0	8
43	Immediate and long-term transcriptional response of hind muscle tissue to transient variation of incubation temperature in broilers. <i>BMC Genomics</i> , 2016, 17, 323.	2.8	7
44	Transcriptome profiles of hypothalamus and adrenal gland linked to haplotype related to coping behavior in pigs. <i>Scientific Reports</i> , 2019, 9, 13038.	3.3	7
45	Alterations in cellular and viral microRNA and cellular gene expression in Marek's disease virus-transformed T-cell lines treated with sodium butyrate. <i>Poultry Science</i> , 2019, 98, 642-652.	3.4	7
46	Does Maternal Stress Affect the Early Embryonic Microenvironment? Impact of Long-Term Cortisol Stimulation on the Oviduct Epithelium. <i>International Journal of Molecular Sciences</i> , 2020, 21, 443.	4.1	7
47	Reduced phosphorus intake throughout gestation and lactation of sows is mitigated by transcriptional adaptations in kidney and intestine. <i>BMC Genomics</i> , 2020, 21, 626.	2.8	7
48	Molecular changes in mitochondrial respiratory activity and metabolic enzyme activity in muscle of four pig breeds with distinct metabolic types. <i>Journal of Bioenergetics and Biomembranes</i> , 2016, 48, 55-65.	2.3	6
49	Deep sequencing of small non-coding RNA highlights brain-specific expression patterns and RNA cleavage. <i>RNA Biology</i> , 2019, 16, 1764-1774.	3.1	6
50	A natural Ala610Val substitution causing glucocorticoid receptor hypersensitivity aggravates consequences of endotoxemia. <i>Brain, Behavior, and Immunity</i> , 2020, 90, 174-183.	4.1	6
51	Brain Transcriptome Responses to Dexamethasone Depending on Dose and Sex Reveal Factors Contributing to Sex-Specific Vulnerability to Stress-Induced Disorders. <i>Neuroendocrinology</i> , 2022, 112, 235-251.	2.5	6
52	Genetic background and production periods shape the microRNA profiles of the gut in laying hens. <i>Genomics</i> , 2021, 113, 1790-1801.	2.9	6
53	Characterization of miR-10a mediated gene regulation in avian splenocytes. <i>Gene</i> , 2012, 500, 107-114.	2.2	5
54	Haplotypes of coping behavior associated QTL regions reveal distinct transcript profiles in amygdala and hippocampus. <i>Behavioural Brain Research</i> , 2019, 372, 112038.	2.2	5

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55	Dietary phosphorus and calcium in feed affects miRNA profiles and their mRNA targets in jejunum of two strains of laying hens. <i>Scientific Reports</i> , 2021, 11, 13534.	3.3	5
56	Multi-Transcript Level Profiling Revealed Distinct mRNA, miRNA, and tRNA-Derived Fragment Bio-Signatures for Coping Behavior Linked Haplotypes in HPA Axis and Limbic System. <i>Frontiers in Genetics</i> , 2021, 12, 635794.	2.3	5
57	Genetic regulation and variation of expression of miRNA and mRNA transcripts in fetal muscle tissue in the context of sex, dam and variable fetal weight. <i>Biology of Sex Differences</i> , 2022, 13, 24.	4.1	5
58	rePROBE: Workflow for Revised Probe Assignment and Updated Probe-set Annotation in Microarrays. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 1043-1049.	6.9	4
59	Genetic regulation and heritability of miRNA and mRNA expression link to phosphorus utilization and gut microbiome. <i>Open Biology</i> , 2021, 11, 200182.	3.6	4
60	Control of Protein and Energy Metabolism in the Pituitary Gland in Response to Three-Week Running Training in Adult Male Mice. <i>Cells</i> , 2021, 10, 736.	4.1	4
61	Ablation of Red Stable Transfected Claudin Expressing Canine Prostate Adenocarcinoma and Transitional Cell Carcinoma Cell Lines by C-CPE Gold-Nanoparticle-Mediated Laser Intervention. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12289.	4.1	3
62	Central Suppression of the GH/IGF Axis and Abrogation of Exercise-Related mTORC1/2 Activation in the Muscle of Phenotype-Selected Male Marathon Mice (DUhTP). <i>Cells</i> , 2021, 10, 3418.	4.1	3
63	Multi-Omics Reveals Different Strategies in the Immune and Metabolic Systems of High-Yielding Strains of Laying Hens. <i>Frontiers in Genetics</i> , 2022, 13, 858232.	2.3	3
64	Kinetics of Physiological and Behavioural Responses in Endotoxemic Pigs with or without Dexamethasone Treatment. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1393.	4.1	2
65	Insights into molecular pathways and fatty acid membrane composition during the temperature stress response in the murine C2C12 cell model. <i>Science of the Total Environment</i> , 2021, 807, 151019.	8.0	2