

Nares Trakooljul

List of Publications by Year in descending order

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65
papers

1,188
citations

448610

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511568

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times ranked

1749
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.2	6
2	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.	1.1	3
3	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.	1.8	5
4	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.	1.8	8
5	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.	1.1	12
6	rePROBE: Workflow for Revised Probe Assignment and Updated Probe-set Annotation in Microarrays. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 1043-1049.	3.0	4
7	Genetic regulation and heritability of miRNA and mRNA expression link to phosphorus utilization and gut microbiome. <i>Open Biology</i> , 2021, 11, 200182.	1.5	4
8	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.	1.8	4
9	mRNA Profiles of Porcine Parathyroid Glands Following Variable Phosphorus Supplies throughout Fetal and Postnatal Life. <i>Biomedicines</i> , 2021, 9, 454.	1.4	8
10	Transcriptional responses in jejunum of two layer chicken strains following variations in dietary calcium and phosphorus levels. <i>BMC Genomics</i> , 2021, 22, 485.	1.2	11
11	Wnt signaling related transcripts and their relationship to energy metabolism in C2C12 myoblasts under temperature stress. <i>PeerJ</i> , 2021, 9, e11625.	0.9	8
12	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.	1.6	5
13	Genetic background and production periods shape the microRNA profiles of the gut in laying hens. <i>Genomics</i> , 2021, 113, 1790-1801.	1.3	6
14	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.	1.1	5
15	Pig genome functional annotation enhances the biological interpretation of complex traits and human disease. <i>Nature Communications</i> , 2021, 12, 5848.	5.8	70
16	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.	3.9	2
17	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.	1.8	3
18	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.	1.8	3

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19	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.	1.8	7
20	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.	1.2	7
21	A natural Ala610Val substitution causing glucocorticoid receptor hypersensitivity aggravates consequences of endotoxemia. <i>Brain, Behavior, and Immunity</i> , 2020, 90, 174-183.	2.0	6
22	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.	1.2	16
23	Ileal Transcriptome Profiles of Japanese Quail Divergent in Phosphorus Utilization. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2762.	1.8	8
24	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.	1.8	14
25	Deep sequencing of small non-coding RNA highlights brain-specific expression patterns and RNA cleavage. <i>RNA Biology</i> , 2019, 16, 1764-1774.	1.5	6
26	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.	1.2	17
27	Transcriptome Responses to Dexamethasone Depending on Dose and Glucocorticoid Receptor Sensitivity in the Liver. <i>Frontiers in Genetics</i> , 2019, 10, 559.	1.1	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.	1.1	14
29	Breed, Diet, and Interaction Effects on Adipose Tissue Transcriptome in Iberian and Duroc Pigs Fed Different Energy Sources. <i>Genes</i> , 2019, 10, 589.	1.0	27
30	Transcriptome profiles of hypothalamus and adrenal gland linked to haplotype related to coping behavior in pigs. <i>Scientific Reports</i> , 2019, 9, 13038.	1.6	7
31	Haplotypes of coping behavior associated QTL regions reveal distinct transcript profiles in amygdala and hippocampus. <i>Behavioural Brain Research</i> , 2019, 372, 112038.	1.2	5
32	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.	1.2	29
33	Genetic Regulation of Liver Metabolites and Transcripts Linking to Biochemical-Clinical Parameters. <i>Frontiers in Genetics</i> , 2019, 10, 348.	1.1	8
34	Kinetics of Physiological and Behavioural Responses in Endotoxemic Pigs with or without Dexamethasone Treatment. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1393.	1.8	2
35	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.	1.1	43
36	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.	1.5	7

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37	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.	1.0	21
38	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.	1.2	56
39	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.	1.2	25
40	Transcriptional shifts account for divergent resource allocation in feed efficient broiler chickens. <i>Scientific Reports</i> , 2018, 8, 12903.	1.6	12
41	miRNAs regulate acute transcriptional changes in broiler embryos in response to modification of incubation temperature. <i>Scientific Reports</i> , 2018, 8, 11371.	1.6	13
42	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.	1.2	19
43	Genetic architecture and regulatory impact on hepatic microRNA expression linked to immune and metabolic traits. <i>Open Biology</i> , 2017, 7, 170101.	1.5	14
44	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.	1.6	16
45	Sex-Specific Muscular Maturation Responses Following Prenatal Exposure to Methylation-Related Micronutrients in Pigs. <i>Nutrients</i> , 2017, 9, 74.	1.7	8
46	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.	1.1	8
47	Genetically regulated hepatic transcripts and pathways orchestrate haematological, biochemical and body composition traits. <i>Scientific Reports</i> , 2016, 6, 39614.	1.6	13
48	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.	1.2	23
49	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.	1.2	7
50	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.	1.0	6
51	Single- and Bayesian Multi-Marker Genome-Wide Association for Haematological Parameters in Pigs. <i>PLoS ONE</i> , 2016, 11, e0159212.	1.1	22
52	Integrated Genome-wide association and hypothalamus eQTL studies indicate a link between the circadian rhythm-related gene <i>PER1</i> and coping behavior. <i>Scientific Reports</i> , 2015, 5, 16264.	1.6	29
53	Muscle Transcriptional Profile Based on Muscle Fiber, Mitochondrial Respiratory Activity, and Metabolic Enzymes. <i>International Journal of Biological Sciences</i> , 2015, 11, 1348-1362.	2.6	27
54	Identification of Common Regulators of Genes in Co-Expression Networks Affecting Muscle and Meat Properties. <i>PLoS ONE</i> , 2015, 10, e0123678.	1.1	39

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55	MicroRNAs Regulate Cellular ATP Levels by Targeting Mitochondrial Energy Metabolism Genes during C2C12 Myoblast Differentiation. PLoS ONE, 2015, 10, e0127850.	1.1	44
56	Pre- and post-natal muscle microRNA expression profiles of two pig breeds differing in muscularity. Gene, 2015, 561, 190-198.	1.0	33
57	Discovery of Candidate Genes for Muscle Traits Based on GWAS Supported by eQTL-analysis. International Journal of Biological Sciences, 2014, 10, 327-337.	2.6	41
58	Characterization of miR-10a mediated gene regulation in avian splenocytes. Gene, 2012, 500, 107-114.	1.0	5
59	Integrated analysis of microRNA expression and mRNA transcriptome in lungs of avian influenza virus infected broilers. BMC Genomics, 2012, 13, 278.	1.2	99
60	Transcriptional and pathway analysis in the hypothalamus of newly hatched chicks during fasting and delayed feeding. BMC Genomics, 2010, 11, 162.	1.2	57
61	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 ¹ . Journal of Animal Science, 2010, 88, 275-283.	0.2	20
62	Discovery of chicken microRNAs associated with lipogenesis and cell proliferation. Physiological Genomics, 2010, 41, 185-193.	1.0	37
63	Age and Dietary Iron Affect Expression of Genes Involved in Iron Acquisition and Homeostasis in Young Pigs. Journal of Nutrition, 2010, 140, 271-277.	1.3	14
64	Iron Transporters Are Differentially Regulated by Dietary Iron, and Modifications Are Associated with Changes in Manganese Metabolism in Young Pigs. Journal of Nutrition, 2009, 139, 1474-1479.	1.3	64
65	Polymorphisms of the porcine androgen receptor gene affecting its amino acid sequence and expression level. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2004, 1678, 94-101.	2.4	8