Shuhong Zhao

List of Publications by Year in Descending Order

120 papers	2,640 citations	19 h-index	49 g-index
126 ext. papers	3,778 ext. citations	5.9 avg, IF	4.67 L-index

#	Paper	IF	Citations
120	Epigenomics analysis of miRNA cis-regulatory elements in pig muscle and fat tissues.. *Genomics*, **2022**, 110276	4.3	1
119	Integrative analysis of transcriptomic and metabolomic profiles reveal the complex molecular regulatory network of meat quality in Enshi black pigs. *Meat Science*, **2022**, 183, 108642	6.4	5
118	Gene expression and chromatin conformation differs between worker bees performing different tasks.. *Genomics*, **2022**, 110362	4.3	
117	Genome-wide CRISPR/Cas9 screen identifies host factors important for porcine reproductive and respiratory syndrome virus replication.. *Virus Research*, **2022**, 314, 198738	6.4	0
116	Identification of the CKM Gene as a Potential Muscle-Specific Safe Harbor Locus in Pig Genome. *Genes*, **2022**, 13, 921	4.2	0
115	An Inexpensive CRISPR-Based Point-of-Care Test for the Identification of Meat Species and Meat Products. *Genes*, **2022**, 13, 912	4.2	2
114	Genome-scale CRISPR screen identifies TMEM41B as a multi-function host factor required for coronavirus replication. *PLoS Pathogens*, **2021**, 17, e1010113	7.6	6
113	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated tool for Genome-Wide Association Study. *Genomics, Proteomics and Bioinformatics*, **2021**,	6.5	78
112	A compendium and comparative epigenomics analysis of cis-regulatory elements in the pig genome. *Nature Communications*, **2021**, 12, 2217	17.4	13
111	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. *BMC Genomics*, **2021**, 22, 294	4.5	2
110	The assembly of caprine Y chromosome sequence reveals a unique paternal phylogenetic pattern and improves our understanding of the origin of domestic goat. *Ecology and Evolution*, **2021**, 11, 7779-7795	2.8	0
109	The advancements, challenges, and future implications of the CRISPR/Cas9 system in swine research. *Journal of Genetics and Genomics*, **2021**, 48, 347-360	4	2
108	Identification of new semen trait-related candidate genes in Duroc boars through genome-wide association and weighted gene co-expression network analyses. *Journal of Animal Science*, **2021**, 99,	0.7	2
107	Rv3722c Promotes Survival in Macrophages by Interacting With TRAF3. *Frontiers in Cellular and Infection Microbiology*, **2021**, 11, 627798	5.9	1
106	Integrating LCM-Based Spatio-Temporal Transcriptomics Uncovers Conceptus and Endometrial Luminal Epithelium Communication that Coordinates the Conceptus Attachment in Pigs. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	3
105	Glycomics reveal that ST6GAL1-mediated sialylation regulates uterine lumen closure during implantation.. *Cell Proliferation*, **2021**, e13169	7.9	1
104	Rapid Visual CRISPR Assay: A Naked-Eye Colorimetric Detection Method for Nucleic Acids Based on CRISPR/Cas12a and a Convolutional Neural Network.. *ACS Synthetic Biology*, **2021**,	5.7	4

103	Three functional mutation sites affect the immune response of pigs through altering the expression pattern and IgV domain of the CD4 protein. *BMC Molecular and Cell Biology*, **2020**, 21, 91	2.7	
102	Whole genome variants across 57 pig breeds enable comprehensive identification of genetic signatures that underlie breed features. *Journal of Animal Science and Biotechnology*, **2020**, 11, 115	6	1
101	Porcine Deltacoronavirus Accessory Protein NS7a Antagonizes IFN-β Production by Competing With TRAF3 and IRF3 for Binding to IKKβ *Frontiers in Cellular and Infection Microbiology*, **2020**, 10, 257	5.9	11
100	Identification of functional mutations at FOXP3 binding site within BIC gene that alter the expression of miR-155 in pigs. *Gene*, **2020**, 744, 144631	3.8	1
99	Ammonia Exposure Induced Cilia Dysfunction of Nasal Mucosa in the Piglets. *BioMed Research International*, **2020**, 2020, 1705387	3	1
98	KAML: improving genomic prediction accuracy of complex traits using machine learning determined parameters. *Genome Biology*, **2020**, 21, 146	18.3	26
97	Genome-Wide Patterns of Homozygosity and Relevant Characterizations on the Population Structure in Piétrain Pigs. *Genes*, **2020**, 11,	4.2	4
96	Whole-Genome Methylation Analysis Reveals Epigenetic Variation in Cloned and Donor Pigs. *Frontiers in Genetics*, **2020**, 11, 23	4.5	2
95	Genome-Wide Association Study and Fine Mapping Reveals Candidate Genes for Birth Weight of Yorkshire and Landrace Pigs. *Frontiers in Genetics*, **2020**, 11, 183	4.5	3
94	Chromatin accessibility is associated with the changed expression of miRNAs that target members of the Hippo pathway during myoblast differentiation. *Cell Death and Disease*, **2020**, 11, 148	9.8	4
93	miR-208b modulating skeletal muscle development and energy homoeostasis through targeting distinct targets. *RNA Biology*, **2020**, 17, 743-754	4.8	11
92	Dynamics of cardiomyocyte and muscle stem cell proliferation in pig. *Experimental Cell Research*, **2020**, 388, 111854	4.2	3
91	Genome editing with the CRISPR-Cas system: an art, ethics and global regulatory perspective. *Plant Biotechnology Journal*, **2020**, 18, 1651-1669	11.6	50
90	Association of α/β-Hydrolase D16B with Bovine Conception Rate and Sperm Plasma Membrane Lipid Composition. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	2
89	Melatonin protects against defects induced by malathion during porcine oocyte maturation. *Journal of Cellular Physiology*, **2020**, 235, 2836-2846	7	9
88	Association of single nucleotide polymorphism in NLRC3, NLRC5, HIP1, and LRP8 genes with fecal egg counts in goats naturally infected with Haemonchus contortus. *Tropical Animal Health and Production*, **2020**, 52, 1583-1598	1.7	1
87	Characterization of immune pleiotropy of ESR1 gene in pigs. *Immunogenetics*, **2020**, 72, 413-422	3.2	
86	Genome-wide analysis of expression QTL (eQTL) and allele-specific expression (ASE) in pig muscle identifies candidate genes for meat quality traits. *Genetics Selection Evolution*, **2020**, 52, 59	4.9	8

85	CRISPR screening of porcine sgRNA library identifies host factors associated with Japanese encephalitis virus replication. *Nature Communications*, **2020**, 11, 5178	17.4	13
84	Identification of ACTB Gene as a Potential Safe Harbor Locus in Pig Genome. *Molecular Biotechnology*, **2020**, 62, 589-597	3	2
83	Enhancing the antibacterial activities of sow milk via site-specific knock-in of a lactoferrin gene in pigs using CRISPR/Cas9 technology. *Cell and Bioscience*, **2020**, 10, 133	9.8	5
82	LncRNAs are regulated by chromatin states and affect the skeletal muscle cell differentiation. *Cell Proliferation*, **2020**, 53, e12879	7.9	4
81	Application of CRISPR-Cas12a Enhanced Fluorescence Assay Coupled with Nucleic Acid Amplification for the Sensitive Detection of African Swine Fever Virus. *ACS Synthetic Biology*, **2020**, 9, 2339-2350	5.7	18
80	Identification of reliable reference genes for expression studies in maternal reproductive tissues and foetal tissues of pregnant cows. *Reproduction in Domestic Animals*, **2020**, 55, 1554-1564	1.6	4
79	lncMGPF is a novel positive regulator of muscle growth and regeneration. *Journal of Cachexia, Sarcopenia and Muscle*, **2020**, 11, 1723-1746	10.3	13
78	A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. *Communications Biology*, **2020**, 3, 502	6.7	10
77	Identification of Glyceraldehyde-3-Phosphate Dehydrogenase Gene as an Alternative Safe Harbor Locus in Pig Genome. *Genes*, **2019**, 10,	4.2	4
76	Novel Polymorphisms in Gene Associated with Egg-Laying Rate in Chinese Jing Hong Chicken using Genome-Wide SNP Scan. *Genes*, **2019**, 10,	4.2	3
75	The dynamics of FTO binding and demethylation from the mA motifs. *RNA Biology*, **2019**, 16, 1179-1189	4.8	19
74	Genome-Wide Association Study Reveals Candidate Genes for Growth Relevant Traits in Pigs. *Frontiers in Genetics*, **2019**, 10, 302	4.5	19
73	Identification and Conservation Analysis of -Regulatory Elements in Pig Liver. *Genes*, **2019**, 10,	4.2	3
72	Identifying Selection Signatures for Backfat Thickness in Yorkshire Pigs Highlights New Regions Affecting Fat Metabolism. *Genes*, **2019**, 10,	4.2	6
71	Quantification of allelic differential expression using a simple Fluorescence primer PCR-RFLP-based method. *Scientific Reports*, **2019**, 9, 6334	4.9	
70	H3K27me3 Depletion during Differentiation Promotes Myogenic Transcription in Porcine Satellite Cells. *Genes*, **2019**, 10,	4.2	7
69	Single nucleotide polymorphisms in candidate genes are significantly associated with resistance to infection in goats. *Journal of Animal Science and Biotechnology*, **2019**, 10, 30	6	7
68	The DNA Methylation Status of Wnt and Tgf Signals Is a Key Factor on Functional Regulation of Skeletal Muscle Satellite Cell Development. *Frontiers in Genetics*, **2019**, 10, 220	4.5	6

67	Genome-Wide Identification of Histone Modifications Involved in Placental Development in Pigs. *Frontiers in Genetics*, **2019**, 10, 277	4.5	5
66	Tris(1,3-dichloro-2-propyl) phosphate disturbs mouse embryonic development by inducing apoptosis and abnormal DNA methylation. *Environmental and Molecular Mutagenesis*, **2019**, 60, 807-815	3.2	5
65	Duplex Quantitative Polymerase Chain Reaction of ISG15 and RSAD2 Increases Accuracy of Early Pregnancy Diagnosis in Dairy Cows. *Annals of Animal Science*, **2019**, 19, 383-401	2	1
64	Identification of mRNAs Related to Tibial Cartilage Development of Yorkshire Piglets. *BioMed Research International*, **2019**, 2019, 2365416	3	1
63	Evaluation of the effects of sequence length and microsatellite instability on single-guide RNA activity and specificity. *International Journal of Biological Sciences*, **2019**, 15, 2641-2653	11.2	5
62	Excess of retrogene traffic in pig X chromosome. *Genetica*, **2019**, 147, 23-32	1.5	0
61	sRNAPrimerDB: comprehensive primer design and search web service for small non-coding RNAs. *Bioinformatics*, **2019**, 35, 1566-1572	7.2	11
60	DNA methylation changes and evolution of RNA-based duplication in Sus scrofa: based on a two-step strategy. *Epigenomics*, **2018**, 10, 199-218	4.4	5
59	Integrated analysis of methylome, transcriptome and miRNAome of three pig breeds. *Epigenomics*, **2018**, 10, 597-612	4.4	9
58	Transcriptome Analysis of Adipose Tissue Indicates That the cAMP Signaling Pathway Affects the Feed Efficiency of Pigs. *Genes*, **2018**, 9,	4.2	18
57	Detecting the Population Structure and Scanning for Signatures of Selection in Horses () From Whole-Genome Sequencing Data. *Evolutionary Bioinformatics*, **2018**, 14, 1176934318775106	1.9	11
56	Selective constraints in cold-region wild boars may defuse the effects of small effective population size on molecular evolution of mitogenomes. *Ecology and Evolution*, **2018**, 8, 8102-8114	2.8	10
55	Population size may shape the accumulation of functional mutations following domestication. *BMC Evolutionary Biology*, **2018**, 18, 4	3	6
54	De novo assembly of mitochondrial genomes provides insights into genetic diversity and molecular evolution in wild boars and domestic pigs. *Genetica*, **2018**, 146, 277-285	1.5	4
53	Synergistic effects of TGF, WNT9a, and FGFR4 signals attenuate satellite cell differentiation during skeletal muscle development. *Aging Cell*, **2018**, 17, e12788	9.9	11
52	Proteomic Analyses of Cysteine Redox in High-Fat-Fed and Fasted Mouse Livers: Implications for Liver Metabolic Homeostasis. *Journal of Proteome Research*, **2018**, 17, 129-140	5.6	19
51	Cidec differentially regulates lipid deposition and secretion through two tissue-specific isoforms. *Gene*, **2018**, 641, 265-271	3.8	6
50	Neuronal Signal Transduction-Involved Genes in Pig Hypothalamus Affect Feed Efficiency as Revealed by Transcriptome Analysis. *BioMed Research International*, **2018**, 2018, 5862571	3	11

49	Transcriptional Profiling of Leucocyte Count Variation from Porcine Peripheral Blood Reveals Differential Gene Expression. *BioMed Research International*, **2018**, 2018, 1496536	3	2
48	Genomic Analysis To Identify Signatures of Artificial Selection and Loci Associated with Important Economic Traits in Duroc Pigs. *G3: Genes, Genomes, Genetics*, **2018**, 8, 3617-3625	3.2	12
47	Prostate Luminal Progenitor Cells in Development and Cancer. *Trends in Cancer*, **2018**, 4, 769-783	12.5	30
46	Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens. *Scientific Reports*, **2018**, 8, 13185	4.9	8
45	Transcriptome Analysis of Potential miRNA Involved in Adipogenic Differentiation of C2C12 Myoblasts. *Lipids*, **2018**, 53, 375-386	1.6	14
44	A survey of transcriptome complexity in Sus scrofa using single-molecule long-read sequencing. *DNA Research*, **2018**, 25, 421-437	4.5	34
43	Identification of bta-miR-15a~16a cluster expression, localization and regulated target in Holsteins. *Molecular and Cellular Probes*, **2018**, 40, 8-12	3.3	2
42	Proteomic analysis indicates that mitochondrial energy metabolism in skeletal muscle tissue is negatively correlated with feed efficiency in pigs. *Scientific Reports*, **2017**, 7, 45291	4.9	28
41	MicroRNA-29a mediates the impairment of intestinal epithelial integrity induced by intrauterine growth restriction in pig. *American Journal of Physiology - Renal Physiology*, **2017**, 312, G434-G442	5.1	15
40	Genetic diversity and population structure among eight Chinese indigenous goat breeds in the Yellow River valley. *Small Ruminant Research*, **2017**, 148, 87-92	1.7	2
39	Fibroblast Growth Factor 21 (FGF21) Promotes Formation of Aerobic Myofibers via the FGF21-SIRT1-AMPK-PGC1Pathway. *Journal of Cellular Physiology*, **2017**, 232, 1893-1906	7	26
38	Candidate Gene Identification of Feed Efficiency and Coat Color Traits in a C57BL/6J Kunming F2 Mice Population Using Genome-Wide Association Study. *BioMed Research International*, **2017**, 2017, 7132941	3	2
37	E-cadherin and ZEB2 modulate trophoblast cell differentiation during placental development in pigs. *Reproduction*, **2017**, 154, 765-775	3.8	20
36	Characterization of porcine simple sequence repeat variation on a population scale with genome resequencing data. *Scientific Reports*, **2017**, 7, 2376	4.9	7
35	Comprehensive variation discovery and recovery of missing sequence in the pig genome using multiple de novo assemblies. *Genome Research*, **2017**, 27, 865-874	9.7	54
34	CRISPR-offinder: a CRISPR guide RNA design and off-target searching tool for user-defined protospacer adjacent motif. *International Journal of Biological Sciences*, **2017**, 13, 1470-1478	11.2	26
33	Exploring the Genetic Resistance to Gastrointestinal Nematodes Infection in Goat Using RNA-Sequencing. *International Journal of Molecular Sciences*, **2017**, 18,	6.3	14
32	Fibroblast Growth Factor 21 Promotes C2C12 Cells Myogenic Differentiation by Enhancing Cell Cycle Exit. *BioMed Research International*, **2017**, 2017, 1648715	3	3

31	Cis-Natural Antisense Transcripts Are Mainly Co-expressed with Their Sense Transcripts and Primarily Related to Energy Metabolic Pathways during Muscle Development. *International Journal of Biological Sciences*, **2016**, 12, 1010-21	11.2	5
30	Natural Functional SNPs in miR-155 Alter Its Expression Level, Blood Cell Counts, and Immune Responses. *Frontiers in Immunology*, **2016**, 7, 295	8.4	10
29	Difference in expression patterns of placental cholesterol transporters, ABCA1 and SR-BI, in Meishan and Yorkshire pigs with different placental efficiency. *Scientific Reports*, **2016**, 6, 20503	4.9	10
28	Transcriptome Analysis Reveals that Vitamin A Metabolism in the Liver Affects Feed Efficiency in Pigs. *G3: Genes, Genomes, Genetics*, **2016**, 6, 3615-3624	3.2	21
27	The complete mitochondrial genome of Mong Cai pig () in Vietnam. *Mitochondrial DNA Part B: Resources*, **2016**, 1, 226-227	0.5	4
26	miR-124 attenuates Japanese encephalitis virus replication by targeting DNM2. *Virology Journal*, **2016**, 13, 105	6.1	13
25	Identification of LncRNAs/mRNAs related to endometrium function regulated by Homeobox A10 in Ishikawa cells. *Cell Biology International*, **2015**, 39, 842-51	4.5	4
24	Transcriptome analysis of mRNA and miRNA in skeletal muscle indicates an important network for differential Residual Feed Intake in pigs. *Scientific Reports*, **2015**, 5, 11953	4.9	69
23	RNA sequencing identifies upregulated kyphoscoliosis peptidase and phosphatidic acid signaling pathways in muscle hypertrophy generated by transgenic expression of myostatin propeptide. *International Journal of Molecular Sciences*, **2015**, 16, 7976-94	6.3	14
22	Expression profiling reveals genes involved in the regulation of wool follicle bulb regression and regeneration in sheep. *International Journal of Molecular Sciences*, **2015**, 16, 9152-66	6.3	13
21	The Expression Pattern of MicroRNAs and the Associated Pathways Involved in the Development of Porcine Placental Folds That Contribute to the Expansion of the Exchange Surface Area. *Biology of Reproduction*, **2015**, 93, 62	3.9	19
20	Quantification of mature microRNAs using pincer probes and real-time PCR amplification. *PLoS ONE*, **2015**, 10, e0120160	3.7	8
19	Fibroblast Growth Factor 21 Suppresses Adipogenesis in Pig Intramuscular Fat Cells. *International Journal of Molecular Sciences*, **2015**, 17,	6.3	17
18	An update of the goat genome assembly using dense radiation hybrid maps allows detailed analysis of evolutionary rearrangements in Bovidae. *BMC Genomics*, **2014**, 15, 625	4.5	16
17	Pseudorabies viral replication is inhibited by a novel target of miR-21. *Virology*, **2014**, 456-457, 319-28	3.6	26
16	Whole blood transcriptome comparison of pigs with extreme production of in vivo dsRNA-induced serum IFN-a. *Developmental and Comparative Immunology*, **2014**, 44, 35-43	3.2	13
15	miRNA transcriptome of hypertrophic skeletal muscle with overexpressed myostatin propeptide. *BioMed Research International*, **2014**, 2014, 328935	3	10
14	The inflammation-related gene S100A12 is positively regulated by C/EBP and AP-1 in pigs. *International Journal of Molecular Sciences*, **2014**, 15, 13802-16	6.3	4

13	Interactome mapping reveals important pathways in skeletal muscle development of pigs. *International Journal of Molecular Sciences*, **2014**, 15, 21788-802	6.3	3
12	Identification of differentially expressed miRNAs between white and black hair follicles by RNA-sequencing in the goat (Capra hircus). *International Journal of Molecular Sciences*, **2014**, 15, 9531-45	6.3	25
11	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (Capra hircus). *Nature Biotechnology*, **2013**, 31, 135-41	44.5	355
10	MicroRNA-124 reduces caveolar density by targeting caveolin-1 in porcine kidney epithelial PK15 cells. *Molecular and Cellular Biochemistry*, **2013**, 384, 213-9	4.2	16
9	Japanese encephalitis virus infects porcine kidney epithelial PK15 cells via clathrin- and cholesterol-dependent endocytosis. *Virology Journal*, **2013**, 10, 258	6.1	32
8	In vivo study of hepatitis B vaccine effects on inflammation and metabolism gene expression. *Molecular Biology Reports*, **2012**, 39, 3225-33	2.8	3
7	Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, **2012**, 491, 393-8	50.4	928
6	Immunogenomics for identification of disease resistance genes in pigs: a review focusing on Gram-negative bacilli. *Journal of Animal Science and Biotechnology*, **2012**, 3, 34	6	14
5	Porcine S100A8 and S100A9: molecular characterizations and crucial functions in response to Haemophilus parasuis infection. *Developmental and Comparative Immunology*, **2011**, 35, 490-500	3.2	12
4	Molecular characterization of the porcine GBP1 and GBP2 genes. *Molecular Immunology*, **2008**, 45, 2797-807	4.3	27
3	Effect of breed, sex and birth parity on growth, carcass and meat quality in pigs. *Frontiers of Agriculture in China*, **2008**, 2, 331-337		10
2	LongSAGE analysis of skeletal muscle at three prenatal stages in Tongcheng and Landrace pigs. *Genome Biology*, **2007**, 8, R115	18.3	93
1	Molecular characterization and expression analysis of the porcine caveolin-3 gene. *Biochemical and Biophysical Research Communications*, **2006**, 346, 7-13	3.4	7