

Shuhong Zhao

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012 , 491, 393-8	50.4	928
119	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra hircus</i>). <i>Nature Biotechnology</i> , 2013 , 31, 135-41	44.5	355
118	LongSAGE analysis of skeletal muscle at three prenatal stages in Tongcheng and Landrace pigs. <i>Genome Biology</i> , 2007 , 8, R115	18.3	93
117	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated tool for Genome-Wide Association Study. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	78
116	Transcriptome analysis of mRNA and miRNA in skeletal muscle indicates an important network for differential Residual Feed Intake in pigs. <i>Scientific Reports</i> , 2015 , 5, 11953	4.9	69
115	Comprehensive variation discovery and recovery of missing sequence in the pig genome using multiple de novo assemblies. <i>Genome Research</i> , 2017 , 27, 865-874	9.7	54
114	Genome editing with the CRISPR-Cas system: an art, ethics and global regulatory perspective. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1651-1669	11.6	50
113	A survey of transcriptome complexity in <i>Sus scrofa</i> using single-molecule long-read sequencing. <i>DNA Research</i> , 2018 , 25, 421-437	4.5	34
112	Japanese encephalitis virus infects porcine kidney epithelial PK15 cells via clathrin- and cholesterol-dependent endocytosis. <i>Virology Journal</i> , 2013 , 10, 258	6.1	32
111	Prostate Luminal Progenitor Cells in Development and Cancer. <i>Trends in Cancer</i> , 2018 , 4, 769-783	12.5	30
110	Proteomic analysis indicates that mitochondrial energy metabolism in skeletal muscle tissue is negatively correlated with feed efficiency in pigs. <i>Scientific Reports</i> , 2017 , 7, 45291	4.9	28
109	Molecular characterization of the porcine GBP1 and GBP2 genes. <i>Molecular Immunology</i> , 2008 , 45, 2797-807	4.9	27
108	Fibroblast Growth Factor 21 (FGF21) Promotes Formation of Aerobic Myofibers via the FGF21-SIRT1-AMPK-PGC1 β Pathway. <i>Journal of Cellular Physiology</i> , 2017 , 232, 1893-1906	7	26
107	KAML: improving genomic prediction accuracy of complex traits using machine learning determined parameters. <i>Genome Biology</i> , 2020 , 21, 146	18.3	26
106	Pseudorabies viral replication is inhibited by a novel target of miR-21. <i>Virology</i> , 2014 , 456-457, 319-28	3.6	26
105	CRISPR-offfinder: a CRISPR guide RNA design and off-target searching tool for user-defined protospacer adjacent motif. <i>International Journal of Biological Sciences</i> , 2017 , 13, 1470-1478	11.2	26
104	Identification of differentially expressed miRNAs between white and black hair follicles by RNA-sequencing in the goat (<i>Capra hircus</i>). <i>International Journal of Molecular Sciences</i> , 2014 , 15, 9531-45	6.3	25

103	Transcriptome Analysis Reveals that Vitamin A Metabolism in the Liver Affects Feed Efficiency in Pigs. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3615-3624	3.2	21
102	E-cadherin and ZEB2 modulate trophoblast cell differentiation during placental development in pigs. <i>Reproduction</i> , 2017 , 154, 765-775	3.8	20
101	The dynamics of FTO binding and demethylation from the mA motifs. <i>RNA Biology</i> , 2019 , 16, 1179-1189	4.8	19
100	Genome-Wide Association Study Reveals Candidate Genes for Growth Relevant Traits in Pigs. <i>Frontiers in Genetics</i> , 2019 , 10, 302	4.5	19
99	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. <i>Biology of Reproduction</i> , 2015 , 93, 62	3.9	19
98	Proteomic Analyses of Cysteine Redox in High-Fat-Fed and Fasted Mouse Livers: Implications for Liver Metabolic Homeostasis. <i>Journal of Proteome Research</i> , 2018 , 17, 129-140	5.6	19
97	Transcriptome Analysis of Adipose Tissue Indicates That the cAMP Signaling Pathway Affects the Feed Efficiency of Pigs. <i>Genes</i> , 2018 , 9,	4.2	18
96	Application of CRISPR-Cas12a Enhanced Fluorescence Assay Coupled with Nucleic Acid Amplification for the Sensitive Detection of African Swine Fever Virus. <i>ACS Synthetic Biology</i> , 2020 , 9, 2339-2350	5.7	18
95	Fibroblast Growth Factor 21 Suppresses Adipogenesis in Pig Intramuscular Fat Cells. <i>International Journal of Molecular Sciences</i> , 2015 , 17,	6.3	17
94	An update of the goat genome assembly using dense radiation hybrid maps allows detailed analysis of evolutionary rearrangements in Bovidae. <i>BMC Genomics</i> , 2014 , 15, 625	4.5	16
93	MicroRNA-124 reduces caveolar density by targeting caveolin-1 in porcine kidney epithelial PK15 cells. <i>Molecular and Cellular Biochemistry</i> , 2013 , 384, 213-9	4.2	16
92	MicroRNA-29a mediates the impairment of intestinal epithelial integrity induced by intrauterine growth restriction in pig. <i>American Journal of Physiology - Renal Physiology</i> , 2017 , 312, G434-G442	5.1	15
91	RNA sequencing identifies upregulated kyphoscoliosis peptidase and phosphatidic acid signaling pathways in muscle hypertrophy generated by transgenic expression of myostatin propeptide. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 7976-94	6.3	14
90	Exploring the Genetic Resistance to Gastrointestinal Nematodes Infection in Goat Using RNA-Sequencing. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	14
89	Immunogenomics for identification of disease resistance genes in pigs: a review focusing on Gram-negative bacilli. <i>Journal of Animal Science and Biotechnology</i> , 2012 , 3, 34	6	14
88	Transcriptome Analysis of Potential miRNA Involved in Adipogenic Differentiation of C2C12 Myoblasts. <i>Lipids</i> , 2018 , 53, 375-386	1.6	14
87	Expression profiling reveals genes involved in the regulation of wool follicle bulb regression and regeneration in sheep. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 9152-66	6.3	13
86	Whole blood transcriptome comparison of pigs with extreme production of in vivo dsRNA-induced serum IFN- α . <i>Developmental and Comparative Immunology</i> , 2014 , 44, 35-43	3.2	13

85	CRISPR screening of porcine sgRNA library identifies host factors associated with Japanese encephalitis virus replication. <i>Nature Communications</i> , 2020 , 11, 5178	17.4	13
84	lncMGPF is a novel positive regulator of muscle growth and regeneration. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2020 , 11, 1723-1746	10.3	13
83	A compendium and comparative epigenomics analysis of cis-regulatory elements in the pig genome. <i>Nature Communications</i> , 2021 , 12, 2217	17.4	13
82	miR-124 attenuates Japanese encephalitis virus replication by targeting DNM2. <i>Virology Journal</i> , 2016 , 13, 105	6.1	13
81	Porcine S100A8 and S100A9: molecular characterizations and crucial functions in response to <i>Haemophilus parasuis</i> infection. <i>Developmental and Comparative Immunology</i> , 2011 , 35, 490-500	3.2	12
80	Genomic Analysis To Identify Signatures of Artificial Selection and Loci Associated with Important Economic Traits in Duroc Pigs. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3617-3625	3.2	12
79	Porcine Deltacoronavirus Accessory Protein NS7a Antagonizes IFN- β Production by Competing With TRAF3 and IRF3 for Binding to IKK β <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 257	5.9	11
78	miR-208b modulating skeletal muscle development and energy homeostasis through targeting distinct targets. <i>RNA Biology</i> , 2020 , 17, 743-754	4.8	11
77	Detecting the Population Structure and Scanning for Signatures of Selection in Horses () From Whole-Genome Sequencing Data. <i>Evolutionary Bioinformatics</i> , 2018 , 14, 1176934318775106	1.9	11
76	Synergistic effects of TGF β , WNT9a, and FGFR4 signals attenuate satellite cell differentiation during skeletal muscle development. <i>Aging Cell</i> , 2018 , 17, e12788	9.9	11
75	sRNAPrimerDB: comprehensive primer design and search web service for small non-coding RNAs. <i>Bioinformatics</i> , 2019 , 35, 1566-1572	7.2	11
74	Neuronal Signal Transduction-Involved Genes in Pig Hypothalamus Affect Feed Efficiency as Revealed by Transcriptome Analysis. <i>BioMed Research International</i> , 2018 , 2018, 5862571	3	11
73	Selective constraints in cold-region wild boars may defuse the effects of small effective population size on molecular evolution of mitogenomes. <i>Ecology and Evolution</i> , 2018 , 8, 8102-8114	2.8	10
72	miRNA transcriptome of hypertrophic skeletal muscle with overexpressed myostatin propeptide. <i>BioMed Research International</i> , 2014 , 2014, 328935	3	10
71	Effect of breed, sex and birth parity on growth, carcass and meat quality in pigs. <i>Frontiers of Agriculture in China</i> , 2008 , 2, 331-337		10
70	A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. <i>Communications Biology</i> , 2020 , 3, 502	6.7	10
69	Natural Functional SNPs in miR-155 Alter Its Expression Level, Blood Cell Counts, and Immune Responses. <i>Frontiers in Immunology</i> , 2016 , 7, 295	8.4	10
68	Difference in expression patterns of placental cholesterol transporters, ABCA1 and SR-BI, in Meishan and Yorkshire pigs with different placental efficiency. <i>Scientific Reports</i> , 2016 , 6, 20503	4.9	10

67	Integrated analysis of methylome, transcriptome and miRNAome of three pig breeds. <i>Epigenomics</i> , 2018 , 10, 597-612	4.4	9
66	Melatonin protects against defects induced by malathion during porcine oocyte maturation. <i>Journal of Cellular Physiology</i> , 2020 , 235, 2836-2846	7	9
65	Quantification of mature microRNAs using pincer probes and real-time PCR amplification. <i>PLoS ONE</i> , 2015 , 10, e0120160	3.7	8
64	Genome-wide analysis of expression QTL (eQTL) and allele-specific expression (ASE) in pig muscle identifies candidate genes for meat quality traits. <i>Genetics Selection Evolution</i> , 2020 , 52, 59	4.9	8
63	Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens. <i>Scientific Reports</i> , 2018 , 8, 13185	4.9	8
62	H3K27me3 Depletion during Differentiation Promotes Myogenic Transcription in Porcine Satellite Cells. <i>Genes</i> , 2019 , 10,	4.2	7
61	Single nucleotide polymorphisms in candidate genes are significantly associated with resistance to infection in goats. <i>Journal of Animal Science and Biotechnology</i> , 2019 , 10, 30	6	7
60	Characterization of porcine simple sequence repeat variation on a population scale with genome resequencing data. <i>Scientific Reports</i> , 2017 , 7, 2376	4.9	7
59	Molecular characterization and expression analysis of the porcine caveolin-3 gene. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 346, 7-13	3.4	7
58	Identifying Selection Signatures for Backfat Thickness in Yorkshire Pigs Highlights New Regions Affecting Fat Metabolism. <i>Genes</i> , 2019 , 10,	4.2	6
57	The DNA Methylation Status of Wnt and Tgf β Signals Is a Key Factor on Functional Regulation of Skeletal Muscle Satellite Cell Development. <i>Frontiers in Genetics</i> , 2019 , 10, 220	4.5	6
56	Population size may shape the accumulation of functional mutations following domestication. <i>BMC Evolutionary Biology</i> , 2018 , 18, 4	3	6
55	Genome-scale CRISPR screen identifies TMEM41B as a multi-function host factor required for coronavirus replication. <i>PLoS Pathogens</i> , 2021 , 17, e1010113	7.6	6
54	Cidec differentially regulates lipid deposition and secretion through two tissue-specific isoforms. <i>Gene</i> , 2018 , 641, 265-271	3.8	6
53	Genome-Wide Identification of Histone Modifications Involved in Placental Development in Pigs. <i>Frontiers in Genetics</i> , 2019 , 10, 277	4.5	5
52	DNA methylation changes and evolution of RNA-based duplication in <i>Sus scrofa</i> : based on a two-step strategy. <i>Epigenomics</i> , 2018 , 10, 199-218	4.4	5
51	Tris(1,3-dichloro-2-propyl) phosphate disturbs mouse embryonic development by inducing apoptosis and abnormal DNA methylation. <i>Environmental and Molecular Mutagenesis</i> , 2019 , 60, 807-815	3.2	5
50	Enhancing the antibacterial activities of sow milk via site-specific knock-in of a lactoferrin gene in pigs using CRISPR/Cas9 technology. <i>Cell and Bioscience</i> , 2020 , 10, 133	9.8	5

49	Cis-Natural Antisense Transcripts Are Mainly Co-expressed with Their Sense Transcripts and Primarily Related to Energy Metabolic Pathways during Muscle Development. <i>International Journal of Biological Sciences</i> , 2016 , 12, 1010-21	11.2	5
48	Evaluation of the effects of sequence length and microsatellite instability on single-guide RNA activity and specificity. <i>International Journal of Biological Sciences</i> , 2019 , 15, 2641-2653	11.2	5
47	Integrative analysis of transcriptomic and metabolomic profiles reveal the complex molecular regulatory network of meat quality in Enshi black pigs. <i>Meat Science</i> , 2022 , 183, 108642	6.4	5
46	Identification of Glyceraldehyde-3-Phosphate Dehydrogenase Gene as an Alternative Safe Harbor Locus in Pig Genome. <i>Genes</i> , 2019 , 10,	4.2	4
45	Identification of LncRNAs/mRNAs related to endometrium function regulated by Homeobox A10 in Ishikawa cells. <i>Cell Biology International</i> , 2015 , 39, 842-51	4.5	4
44	Genome-Wide Patterns of Homozygosity and Relevant Characterizations on the Population Structure in Piñrain Pigs. <i>Genes</i> , 2020 , 11,	4.2	4
43	Chromatin accessibility is associated with the changed expression of miRNAs that target members of the Hippo pathway during myoblast differentiation. <i>Cell Death and Disease</i> , 2020 , 11, 148	9.8	4
42	De novo assembly of mitochondrial genomes provides insights into genetic diversity and molecular evolution in wild boars and domestic pigs. <i>Genetica</i> , 2018 , 146, 277-285	1.5	4
41	The inflammation-related gene S100A12 is positively regulated by C/EBP β and AP-1 in pigs. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 13802-16	6.3	4
40	LncRNAs are regulated by chromatin states and affect the skeletal muscle cell differentiation. <i>Cell Proliferation</i> , 2020 , 53, e12879	7.9	4
39	Identification of reliable reference genes for expression studies in maternal reproductive tissues and foetal tissues of pregnant cows. <i>Reproduction in Domestic Animals</i> , 2020 , 55, 1554-1564	1.6	4
38	The complete mitochondrial genome of Mong Cai pig () in Vietnam. <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 226-227	0.5	4
37	Rapid Visual CRISPR Assay: A Naked-Eye Colorimetric Detection Method for Nucleic Acids Based on CRISPR/Cas12a and a Convolutional Neural Network.. <i>ACS Synthetic Biology</i> , 2021 ,	5.7	4
36	Novel Polymorphisms in Gene Associated with Egg-Laying Rate in Chinese Jing Hong Chicken using Genome-Wide SNP Scan. <i>Genes</i> , 2019 , 10,	4.2	3
35	Identification and Conservation Analysis of -Regulatory Elements in Pig Liver. <i>Genes</i> , 2019 , 10,	4.2	3
34	Genome-Wide Association Study and Fine Mapping Reveals Candidate Genes for Birth Weight of Yorkshire and Landrace Pigs. <i>Frontiers in Genetics</i> , 2020 , 11, 183	4.5	3
33	Dynamics of cardiomyocyte and muscle stem cell proliferation in pig. <i>Experimental Cell Research</i> , 2020 , 388, 111854	4.2	3
32	In vivo study of hepatitis B vaccine effects on inflammation and metabolism gene expression. <i>Molecular Biology Reports</i> , 2012 , 39, 3225-33	2.8	3

31	Fibroblast Growth Factor 21 Promotes C2C12 Cells Myogenic Differentiation by Enhancing Cell Cycle Exit. <i>BioMed Research International</i> , 2017 , 2017, 1648715	3	3
30	Interactome mapping reveals important pathways in skeletal muscle development of pigs. <i>International Journal of Molecular Sciences</i> , 2014 , 15, 21788-802	6.3	3
29	Integrating LCM-Based Spatio-Temporal Transcriptomics Uncovers Conceptus and Endometrial Luminal Epithelium Communication that Coordinates the Conceptus Attachment in Pigs. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
28	Genetic diversity and population structure among eight Chinese indigenous goat breeds in the Yellow River valley. <i>Small Ruminant Research</i> , 2017 , 148, 87-92	1.7	2
27	Whole-Genome Methylation Analysis Reveals Epigenetic Variation in Cloned and Donor Pigs. <i>Frontiers in Genetics</i> , 2020 , 11, 23	4.5	2
26	Candidate Gene Identification of Feed Efficiency and Coat Color Traits in a C57BL/6J [Kunming F2 Mice Population Using Genome-Wide Association Study. <i>BioMed Research International</i> , 2017 , 2017, 7132941	3	2
25	Association of β -Hydrolase D16B with Bovine Conception Rate and Sperm Plasma Membrane Lipid Composition. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
24	Identification of ACTB Gene as a Potential Safe Harbor Locus in Pig Genome. <i>Molecular Biotechnology</i> , 2020 , 62, 589-597	3	2
23	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. <i>BMC Genomics</i> , 2021 , 22, 294	4.5	2
22	The advancements, challenges, and future implications of the CRISPR/Cas9 system in swine research. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 347-360	4	2
21	Identification of new semen trait-related candidate genes in Duroc boars through genome-wide association and weighted gene co-expression network analyses. <i>Journal of Animal Science</i> , 2021 , 99,	0.7	2
20	Transcriptional Profiling of Leucocyte Count Variation from Porcine Peripheral Blood Reveals Differential Gene Expression. <i>BioMed Research International</i> , 2018 , 2018, 1496536	3	2
19	Identification of bta-miR-15a~16a cluster expression, localization and regulated target in Holsteins. <i>Molecular and Cellular Probes</i> , 2018 , 40, 8-12	3.3	2
18	An Inexpensive CRISPR-Based Point-of-Care Test for the Identification of Meat Species and Meat Products. <i>Genes</i> , 2022 , 13, 912	4.2	2
17	Whole genome variants across 57 pig breeds enable comprehensive identification of genetic signatures that underlie breed features. <i>Journal of Animal Science and Biotechnology</i> , 2020 , 11, 115	6	1
16	Identification of functional mutations at FOXP3 binding site within BIC gene that alter the expression of miR-155 in pigs. <i>Gene</i> , 2020 , 744, 144631	3.8	1
15	Ammonia Exposure Induced Cilia Dysfunction of Nasal Mucosa in the Piglets. <i>BioMed Research International</i> , 2020 , 2020, 1705387	3	1
14	Epigenomics analysis of miRNA cis-regulatory elements in pig muscle and fat tissues.. <i>Genomics</i> , 2022 , 110276	4.3	1

13	Duplex Quantitative Polymerase Chain Reaction of ISG15 and RSAD2 Increases Accuracy of Early Pregnancy Diagnosis in Dairy Cows. <i>Annals of Animal Science</i> , 2019 , 19, 383-401	2	1
12	Association of single nucleotide polymorphism in NLRC3, NLRC5, HIP1, and LRP8 genes with fecal egg counts in goats naturally infected with <i>Haemonchus contortus</i> . <i>Tropical Animal Health and Production</i> , 2020 , 52, 1583-1598	1.7	1
11	Identification of mRNAs Related to Tibial Cartilage Development of Yorkshire Piglets. <i>BioMed Research International</i> , 2019 , 2019, 2365416	3	1
10	Rv3722c Promotes Survival in Macrophages by Interacting With TRAF3. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 627798	5.9	1
9	Glycomics reveal that ST6GAL1-mediated sialylation regulates uterine lumen closure during implantation.. <i>Cell Proliferation</i> , 2021 , e13169	7.9	1
8	The assembly of caprine Y chromosome sequence reveals a unique paternal phylogenetic pattern and improves our understanding of the origin of domestic goat. <i>Ecology and Evolution</i> , 2021 , 11, 7779-7793	7.8	0
7	Excess of retrogene traffic in pig X chromosome. <i>Genetica</i> , 2019 , 147, 23-32	1.5	0
6	Genome-wide CRISPR/Cas9 screen identifies host factors important for porcine reproductive and respiratory syndrome virus replication.. <i>Virus Research</i> , 2022 , 314, 198738	6.4	0
5	Identification of the CKM Gene as a Potential Muscle-Specific Safe Harbor Locus in Pig Genome. <i>Genes</i> , 2022 , 13, 921	4.2	0
4	Quantification of allelic differential expression using a simple Fluorescence primer PCR-RFLP-based method. <i>Scientific Reports</i> , 2019 , 9, 6334	4.9	
3	Three functional mutation sites affect the immune response of pigs through altering the expression pattern and IgV domain of the CD4 protein. <i>BMC Molecular and Cell Biology</i> , 2020 , 21, 91	2.7	
2	Characterization of immune pleiotropy of ESR1 gene in pigs. <i>Immunogenetics</i> , 2020 , 72, 413-422	3.2	
1	Gene expression and chromatin conformation differs between worker bees performing different tasks.. <i>Genomics</i> , 2022 , 110362	4.3	