

# Xinyun Li

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

1,893  
citations

279798

23  
h-index

315739

38  
g-index

70  
all docs

70  
docs citations

70  
times ranked

2235  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	5.5	32
2	Epigenomics analysis of miRNA cis-regulatory elements in pig muscle and fat tissues. <i>Genomics</i> , 2022, 114, 110276.	2.9	7
3	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> , 2022, 11, 383-396.	3.8	30
4	Detection of Four Porcine Enteric Coronaviruses Using CRISPR-Cas12a Combined with Multiplex Reverse Transcriptase Loop-Mediated Isothermal Amplification Assay. <i>Viruses</i> , 2022, 14, 833.	3.3	12
5	Identification of the CKM Gene as a Potential Muscle-Specific Safe Harbor Locus in Pig Genome. <i>Genes</i> , 2022, 13, 921.	2.4	2
6	An Inexpensive CRISPR-Based Point-of-Care Test for the Identification of Meat Species and Meat Products. <i>Genes</i> , 2022, 13, 912.	2.4	9
7	Enhancer-promoter interaction maps provide insights into skeletal muscle-related traits in pig genome. <i>BMC Biology</i> , 2022, 20, .	3.8	13
8	rMVP: A Memory-efficient, Visualization-enhanced, and Parallel-accelerated Tool for Genome-wide Association Study. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 619-628.	6.9	396
9	A compendium and comparative epigenomics analysis of cis-regulatory elements in the pig genome. <i>Nature Communications</i> , 2021, 12, 2217.	12.8	63
10	Genome-wide association and transcriptome studies identify candidate genes and pathways for feed conversion ratio in pigs. <i>BMC Genomics</i> , 2021, 22, 294.	2.8	11
11	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.	3.9	8
12	Improvement, identification, and target prediction for miRNAs in the porcine genome by using massive, public high-throughput sequencing data. <i>Journal of Animal Science</i> , 2021, 99, .	0.5	2
13	Identifying candidate genes associated with sperm morphology abnormalities using weighted single-step GWAS in a Duroc boar population. <i>Theriogenology</i> , 2020, 141, 9-15.	2.1	18
14	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.	3.0	22
15	CRISPR screening of porcine sgRNA library identifies host factors associated with Japanese encephalitis virus replication. <i>Nature Communications</i> , 2020, 11, 5178.	12.8	40
16	Identification of ACTB Gene as a Potential Safe Harbor Locus in Pig Genome. <i>Molecular Biotechnology</i> , 2020, 62, 589-597.	2.4	4
17	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.	4.8	11
18	LncRNAs are regulated by chromatin states and affect the skeletal muscle cell differentiation. <i>Cell Proliferation</i> , 2020, 53, e12879.	5.3	12

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19	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.	3.8	54
20	A gene prioritization method based on a swine multi-omics knowledgebase and a deep learning model. <i>Communications Biology</i> , 2020, 3, 502.	4.4	36
21	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.	2.0	0
22	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.	5.3	14
23	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.	2.2	3
24	KAML: improving genomic prediction accuracy of complex traits using machine learning determined parameters. <i>Genome Biology</i> , 2020, 21, 146.	8.8	51
25	Genome-Wide Patterns of Homozygosity and Relevant Characterizations on the Population Structure in PiÅ©train Pigs. <i>Genes</i> , 2020, 11, 577.	2.4	10
26	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.	2.3	11
27	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.	6.3	9
28	miR-208b modulating skeletal muscle development and energy homoeostasis through targeting distinct targets. <i>RNA Biology</i> , 2020, 17, 743-754.	3.1	23
29	Weighted single-step GWAS identified candidate genes associated with semen traits in a Duroc boar population. <i>BMC Genomics</i> , 2019, 20, 797.	2.8	27
30	Identification of Glyceraldehyde-3-Phosphate Dehydrogenase Gene as an Alternative Safe Harbor Locus in Pig Genome. <i>Genes</i> , 2019, 10, 660.	2.4	7
31	Genome-Wide Association Study Reveals Candidate Genes for Growth Relevant Traits in Pigs. <i>Frontiers in Genetics</i> , 2019, 10, 302.	2.3	42
32	Identification and Conservation Analysis of Cis-Regulatory Elements in Pig Liver. <i>Genes</i> , 2019, 10, 348.	2.4	7
33	Identifying Selection Signatures for Backfat Thickness in Yorkshire Pigs Highlights New Regions Affecting Fat Metabolism. <i>Genes</i> , 2019, 10, 254.	2.4	14
34	Widespread Existence of Quorum Sensing Inhibitors in Marine Bacteria: Potential Drugs to Combat Pathogens with Novel Strategies. <i>Marine Drugs</i> , 2019, 17, 275.	4.6	31
35	Quantification of allelic differential expression using a simple Fluorescence primer PCR-RFLP-based method. <i>Scientific Reports</i> , 2019, 9, 6334.	3.3	1
36	H3K27me3 Depletion during Differentiation Promotes Myogenic Transcription in Porcine Satellite Cells. <i>Genes</i> , 2019, 10, 231.	2.4	13

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37	The DNA Methylation Status of Wnt and Tgf $\beta$ 2 Signals Is a Key Factor on Functional Regulation of Skeletal Muscle Satellite Cell Development. <i>Frontiers in Genetics</i> , 2019, 10, 220.	2.3	15
38	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.	6.4	8
39	A miR-18a binding-site polymorphism in CDC42 3'UTR affects CDC42 mRNA expression in placentas and is associated with litter size in pigs. <i>Mammalian Genome</i> , 2019, 30, 34-41.	2.2	12
40	sRNAprimerDB: comprehensive primer design and search web service for small non-coding RNAs. <i>Bioinformatics</i> , 2019, 35, 1566-1572.	4.1	18
41	Neuronal Signal Transduction-Involved Genes in Pig Hypothalamus Affect Feed Efficiency as Revealed by Transcriptome Analysis. <i>BioMed Research International</i> , 2018, 2018, 1-10.	1.9	24
42	Transcriptional Profiling of Leucocyte Count Variation from Porcine Peripheral Blood Reveals Differential Gene Expression. <i>BioMed Research International</i> , 2018, 2018, 1-11.	1.9	3
43	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.	1.8	18
44	Prostate Luminal Progenitor Cells in Development and Cancer. <i>Trends in Cancer</i> , 2018, 4, 769-783.	7.4	54
45	Transcriptome Analysis of Potential miRNA Involved in Adipogenic Differentiation of C2C12 Myoblasts. <i>Lipids</i> , 2018, 53, 375-386.	1.7	18
46	A survey of transcriptome complexity in <i>Sus scrofa</i> using single-molecule long-read sequencing. <i>DNA Research</i> , 2018, 25, 421-437.	3.4	83
47	Transcriptome Analysis of Adipose Tissue Indicates That the cAMP Signaling Pathway Affects the Feed Efficiency of Pigs. <i>Genes</i> , 2018, 9, 336.	2.4	26
48	Population size may shape the accumulation of functional mutations following domestication. <i>BMC Evolutionary Biology</i> , 2018, 18, 4.	3.2	15
49	Synergistic effects of TGF $\beta$ 2, WNT9a, and FGFR4 signals attenuate satellite cell differentiation during skeletal muscle development. <i>Aging Cell</i> , 2018, 17, e12788.	6.7	39
50	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.	3.3	41
51	CRISPR-offinder: 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.	6.4	44
52	Fibroblast Growth Factor 21 Promotes C2C12 Cells Myogenic Differentiation by Enhancing Cell Cycle Exit. <i>BioMed Research International</i> , 2017, 2017, 1-9.	1.9	11
53	Candidate Gene Identification of Feed Efficiency and Coat Color Traits in a C57BL/6J $\times$ Kunming F2 Mice Population Using Genome-Wide Association Study. <i>BioMed Research International</i> , 2017, 2017, 1-7.	1.9	6
54	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, 1010-1021.	6.4	6

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55	Natural Functional SNPs in miR-155 Alter Its Expression Level, Blood Cell Counts, and Immune Responses. <i>Frontiers in Immunology</i> , 2016, 7, 295.	4.8	13
56	Cellular Localization and Regulation of Expression of the PLET1 Gene in Porcine Placenta. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2048.	4.1	8
57	Transcriptome Analysis Reveals that Vitamin A Metabolism in the Liver Affects Feed Efficiency in Pigs. <i>C3: Genes, Genomes, Genetics</i> , 2016, 6, 3615-3624.	1.8	37
58	miR-124 attenuates Japanese encephalitis virus replication by targeting DNM2. <i>Virology Journal</i> , 2016, 13, 105.	3.4	19
59	Metabolomic investigation of porcine muscle and fatty tissue after Clenbuterol treatment using gas chromatography/mass spectrometry. <i>Journal of Chromatography A</i> , 2016, 1456, 242-248.	3.7	18
60	Characterization of the Promoter Regions of Two Sheep Keratin-Associated Protein Genes for Hair Cortex-Specific Expression. <i>PLoS ONE</i> , 2016, 11, e0153936.	2.5	12
61	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.	3.3	137
62	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, 7976-7994.	4.1	15
63	miRNA Transcriptome of Hypertrophic Skeletal Muscle with Overexpressed Myostatin Propeptide. <i>BioMed Research International</i> , 2014, 2014, 1-19.	1.9	12
64	The Inflammation-Related Gene S100A12 Is Positively Regulated by C/EBP $\beta$ and AP-1 in Pigs. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13802-13816.	4.1	8
65	Interactome Mapping Reveals Important Pathways in Skeletal Muscle Development of Pigs. <i>International Journal of Molecular Sciences</i> , 2014, 15, 21788-21802.	4.1	3
66	Pseudorabies viral replication is inhibited by a novel target of miR-21. <i>Virology</i> , 2014, 456-457, 319-328.	2.4	40
67	Molecular characterization, induced expression, and transcriptional regulation of porcine S100A12 gene. <i>Molecular Immunology</i> , 2010, 47, 1601-1607.	2.2	16
68	Characterization analysis and polymorphism detection of the porcine Myd88 gene. <i>Genetics and Molecular Biology</i> , 2009, 32, 295-300.	1.3	5
69	Understanding <i>Haemophilus parasuis</i> infection in porcine spleen through a transcriptomics approach. <i>BMC Genomics</i> , 2009, 10, 64.	2.8	59