

Xiaozhu Wang

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

2,674
citations

201575

27
h-index

206029

48
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78
all docs

78
docs citations

78
times ranked

3889
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic and genomic architecture in eight strains of the laboratory opossum <i>Monodelphis domestica</i> . <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
2	Environment-Dependent Heterosis and Transgressive Gene Expression in Reciprocal Hybrids between the Channel Catfish <i>Ictalurus punctatus</i> and the Blue Catfish <i>Ictalurus furcatus</i> . <i>Biology</i> , 2022, 11, 117.	1.3	4
3	Role of macronutrient intake in the epigenetics of obesity. <i>Biochemical Society Transactions</i> , 2022, 50, 487-497.	1.6	2
4	Pharmacological Evaluation of Melanocortin 2 Receptor Accessory Protein 2 on Axolotl Neural Melanocortin Signaling. <i>Frontiers in Endocrinology</i> , 2022, 13, 820896.	1.5	2
5	Profiles of telomeric repeats in Insecta reveal diverse forms of telomeric motifs in Hymenoptera. <i>Life Science Alliance</i> , 2022, 5, e202101163.	1.3	16
6	Transcriptomic Analysis of Canine Osteosarcoma from a Precision Medicine Perspective Reveals Limitations of Differential Gene Expression Studies. <i>Genes</i> , 2022, 13, 680.	1.0	4
7	Whole-Genome Shotgun Metagenomic Sequencing Reveals Distinct Gut Microbiome Signatures of Obese Cats. <i>Microbiology Spectrum</i> , 2022, 10, e0083722.	1.2	15
8	Abstract A039: Transcriptomic analysis of canine osteosarcoma from a precision medicine perspective reveals limitations of differential gene expression studies. <i>Cancer Research</i> , 2022, 82, A039-A039.	0.4	0
9	Chromosome-level assembly and annotation of the blue catfish <i>Ictalurus furcatus</i> , an aquaculture species for hybrid catfish reproduction, epigenetics, and heterosis studies. <i>GigaScience</i> , 2022, 11, .	3.3	8
10	Transcriptome Analysis Reveals Key Gene Expression Changes in Blue Catfish Sperm in Response to Cryopreservation. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7618.	1.8	4
11	Comparative analysis reveals the expansion of mitochondrial DNA control region containing unusually high G-C tandem repeat arrays in <i>Nasonia vitripennis</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 166, 1246-1257.	3.6	9
12	Comparative Genomic and Transcriptomic Analyses Revealed Twenty-Six Candidate Genes Involved in the Air-Breathing Development and Function of the Bighead Catfish <i>Clarias macrocephalus</i> . <i>Marine Biotechnology</i> , 2021, 23, 90-105.	1.1	4
13	Genomic and <i>in vitro</i> pharmacodynamic analysis of rifampicin resistance in multidrug-resistant canine <i>Staphylococcus pseudintermedius</i> isolates. <i>Veterinary Dermatology</i> , 2021, 32, 219.	0.4	2
14	Comparative Transcriptome and Endophytic Bacterial Community Analysis of <i>Morchella conica</i> SH. <i>Frontiers in Microbiology</i> , 2021, 12, 682356.	1.5	3
15	Comparative Phylogenomic Analysis Reveals Evolutionary Genomic Changes and Novel Toxin Families in Endophytic <i>Liberibacter</i> Pathogens. <i>Microbiology Spectrum</i> , 2021, 9, e0050921.	1.2	6
16	Identification of novel GPCR partners of the central melanocortin signaling. <i>Molecular Metabolism</i> , 2021, 53, 101317.	3.0	9
17	Long-Read Assembly and Annotation of the Parasitoid Wasp <i>Muscidifurax raptorellus</i> , a Biological Control Agent for Filth Flies. <i>Frontiers in Genetics</i> , 2021, 12, 748135.	1.1	3
18	Hypothalamic transcriptome of tame and aggressive silver foxes (<i>Vulpes vulpes</i>) identifies gene expression differences shared across brain regions. <i>Genes, Brain and Behavior</i> , 2020, 19, e12614.	1.1	24

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19	Effectiveness of PennHIP and Orthopedic Foundation for Animals measurements of hip joint quality for breeding selection to reduce hip dysplasia in a population of purpose-bred detection dogs. <i>Journal of the American Veterinary Medical Association</i> , 2020, 257, 299-304.	0.2	6
20	Deep Transcriptomic Analysis Reveals the Dynamic Developmental Progression during Early Development of Channel Catfish (<i>Ictalurus punctatus</i>). <i>International Journal of Molecular Sciences</i> , 2020, 21, 5535.	1.8	4
21	Phylogenomic Analysis of <i>Wolbachia</i> Strains Reveals Patterns of Genome Evolution and Recombination. <i>Genome Biology and Evolution</i> , 2020, 12, 2508-2520.	1.1	19
22	Draft Genome Assemblies of Two <i>Staphylococcus pseudintermedius</i> Strains Isolated from Canine Skin Biopsy Specimens. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
23	Genome Report: Whole Genome Sequence and Annotation of the Parasitoid Jewel Wasp <i>Nasonia giraulti</i> Laboratory Strain RV2X[u]. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2565-2572.	0.8	12
24	Differential Expression of miRNAs in Hypoxia (HypoxamiRs) in Three Canine High-Grade Glioma Cell Lines. <i>Frontiers in Veterinary Science</i> , 2020, 7, 104.	0.9	12
25	Comparative Transcriptome Analysis During the Seven Developmental Stages of Channel Catfish (<i>Ictalurus punctatus</i>) and Tra Catfish (<i>Pangasianodon hypophthalmus</i>) Provides Novel Insights for Terrestrial Adaptation. <i>Frontiers in Genetics</i> , 2020, 11, 608325.	1.1	1
26	A Transient Hermaphroditic Stage in Early Male Gonadal Development in Little Yellow Croaker, <i>Larimichthys polyactis</i> . <i>Frontiers in Endocrinology</i> , 2020, 11, 542942.	1.5	9
27	Circulating tumor cell characterization of lung cancer brain metastases in the cerebrospinal fluid through single-cell transcriptome analysis. <i>Clinical and Translational Medicine</i> , 2020, 10, e246.	1.7	41
28	CRISPR/Cas9-mediated knock-in of alligator cathelicidin gene in a non-coding region of channel catfish genome. <i>Scientific Reports</i> , 2020, 10, 22271.	1.6	34
29	DNA copy number and structural variation (CNV) contributions to adult and childhood obesity. <i>Biochemical Society Transactions</i> , 2020, 48, 1819-1828.	1.6	4
30	TIVAN: tissue-specific cis-eQTL single nucleotide variant annotation and prediction. <i>Bioinformatics</i> , 2019, 35, 1573-1575.	1.8	14
31	Genome Assembly of the A-Group <i>Wolbachia</i> in <i>Nasonia oneida</i> Using Linked-Reads Technology. <i>Genome Biology and Evolution</i> , 2019, 11, 3008-3013.	1.1	10
32	GWAS Analysis Indicated Importance of NF- κ B Signaling Pathway in Host Resistance Against Motile <i>Aeromonas</i> Septicemia Disease in Catfish. <i>Marine Biotechnology</i> , 2019, 21, 335-347.	1.1	30
33	Influence of <i>Eimeria</i> spp. Infection on Chicken Jejunal Microbiota and the Efficacy of Two Alternative Products Against the Infection. <i>Avian Diseases</i> , 2019, 64, 123.	0.4	5
34	Transcriptome analysis reveals enrichment of genes associated with auditory system in swimbladder of channel catfish. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2018, 27, 30-39.	0.4	8
35	Comparative transcriptome analysis reveals conserved branching morphogenesis related genes involved in chamber formation of catfish swimbladder. <i>Physiological Genomics</i> , 2018, 50, 67-76.	1.0	6
36	Identification of novel genes significantly affecting growth in catfish through GWAS analysis. <i>Molecular Genetics and Genomics</i> , 2018, 293, 587-599.	1.0	53

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37	Genomic responses to selection for tame/aggressive behaviors in the silver fox (<i>Vulpes vulpes</i>) Tj ETQq1 10398-10403.	0.784314 3.3	rgBT /Over 64
38	Comparative transcriptome analysis of the swimbladder reveals expression signatures in response to low oxygen stress in channel catfish, <i>Ictalurus punctatus</i> . <i>Physiological Genomics</i> , 2018, 50, 636-647.	1.0	22
39	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018, 2, 1479-1491.	3.4	113
40	Genome-wide association analysis of intra-specific QTL associated with the resistance for enteric septicemia of catfish. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1365-1378.	1.0	19
41	GWAS analysis using interspecific backcross progenies reveals superior blue catfish alleles responsible for strong resistance against enteric septicemia of catfish. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1107-1120.	1.0	28
42	Identification of NF- κ B related genes in channel catfish and their expression profiles in mucosal tissues after columnaris bacterial infection. <i>Developmental and Comparative Immunology</i> , 2017, 70, 27-38.	1.0	17
43	Genome-Wide Association Study Reveals Multiple Novel QTL Associated with Low Oxygen Tolerance in Hybrid Catfish. <i>Marine Biotechnology</i> , 2017, 19, 379-390.	1.1	58
44	The chemokine superfamily: II. The 64 CC chemokines in channel catfish and their involvement in disease and hypoxia responses. <i>Developmental and Comparative Immunology</i> , 2017, 73, 97-108.	1.0	36
45	Effects of strain and body weight on low-oxygen tolerance of channel catfish (<i>Ictalurus punctatus</i>). <i>Aquaculture International</i> , 2017, 25, 1645-1652.	1.1	5
46	Genomic imprinting does not reduce the dosage of UBE3A in neurons. <i>Epigenetics and Chromatin</i> , 2017, 10, 27.	1.8	15
47	GWAS analysis of QTL for enteric septicemia of catfish and their involved genes suggest evolutionary conservation of a molecular mechanism of disease resistance. <i>Molecular Genetics and Genomics</i> , 2017, 292, 231-242.	1.0	59
48	Analysis of apolipoprotein genes and their involvement in disease response of channel catfish after bacterial infection. <i>Developmental and Comparative Immunology</i> , 2017, 67, 464-470.	1.0	31
49	Multiple across-strain and within-strain QTLs suggest highly complex genetic architecture for hypoxia tolerance in channel catfish. <i>Molecular Genetics and Genomics</i> , 2017, 292, 63-76.	1.0	61
50	OGS2: genome re-annotation of the jewel wasp <i>Nasonia vitripennis</i> . <i>BMC Genomics</i> , 2016, 17, 678.	1.2	35
51	The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. <i>Nature Communications</i> , 2016, 7, 11757.	5.8	231
52	Allele-Specific Transcriptome and Methylome Analysis Reveals Stable Inheritance and Cis-Regulation of DNA Methylation in <i>Nasonia</i> . <i>PLoS Biology</i> , 2016, 14, e1002500.	2.6	54
53	TRIM28 Controls Genomic Imprinting through Distinct Mechanisms during and after Early Genome-wide Reprogramming. <i>Cell Reports</i> , 2015, 13, 1194-1205.	2.9	39
54	Genetic and epigenetic architecture of sex-biased expression in the jewel wasps <i>Nasonia vitripennis</i> and <i>N. giraulti</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3545-54.	3.3	53

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55	The Genetic Architecture of the Genome-Wide Transcriptional Response to ER Stress in the Mouse. PLoS Genetics, 2015, 11, e1004924.	1.5	32
56	Complement regulatory protein genes in channel catfish and their involvement in disease defense response. Developmental and Comparative Immunology, 2015, 53, 33-41.	1.0	23
57	Genome-wide histone state profiling of fibroblasts from the opossum, <i>Monodelphis domestica</i> , identifies the first marsupial-specific imprinted gene. BMC Genomics, 2014, 15, 89.	1.2	6
58	Using next-generation RNA sequencing to identify imprinted genes. Heredity, 2014, 113, 156-166.	1.2	108
59	Chromosome-wide profiling of X-chromosome inactivation and epigenetic states in fetal brain and placenta of the opossum, <i>Monodelphis domestica</i> . Genome Research, 2014, 24, 70-83.	2.4	48
60	Function and Evolution of DNA Methylation in <i>Nasonia vitripennis</i> . PLoS Genetics, 2013, 9, e1003872.	1.5	162
61	Paternally expressed genes predominate in the placenta. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10705-10710.	3.3	137
62	Random X inactivation in the mule and horse placenta. Genome Research, 2012, 22, 1855-1863.	2.4	38
63	A Survey for Novel Imprinted Genes in the Mouse Placenta by mRNA-seq. Genetics, 2011, 189, 109-122.	1.2	89
64	Contrasting Methods of Quantifying Fine Structure of Human Recombination. Annual Review of Genomics and Human Genetics, 2010, 11, 45-64.	2.5	32
65	Paternally biased X inactivation in mouse neonatal brain. Genome Biology, 2010, 11, R79.	13.9	64
66	Genomic Imprinting in Invasive Trophoblast in Mammalian Interspecies Hybrids. Biology of Reproduction, 2010, 83, 102-102.	1.2	4
67	A genome-wide approach to identifying novel-imprinted genes. Human Genetics, 2008, 122, 625-634.	1.8	70
68	Transcriptome-Wide Identification of Novel Imprinted Genes in Neonatal Mouse Brain. PLoS ONE, 2008, 3, e3839.	1.1	170
69	Two Dobzhansky-Muller Genes Interact to Cause Hybrid Lethality in <i>Drosophila</i> . Science, 2006, 314, 1292-1295.	6.0	357