

Xiaozhu Wang

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

2,674
citations

201385

27
h-index

205818

48
g-index

78
all docs

78
docs citations

78
times ranked

3889
citing authors

#	ARTICLE	IF	CITATIONS
1	Two Dobzhansky-Muller Genes Interact to Cause Hybrid Lethality in <i>Drosophila</i> . <i>Science</i> , 2006, 314, 1292-1295.	6.0	357
2	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
3	Transcriptome-Wide Identification of Novel Imprinted Genes in Neonatal Mouse Brain. <i>PLoS ONE</i> , 2008, 3, e3839.	1.1	170
4	Function and Evolution of DNA Methylation in <i>Nasonia vitripennis</i> . <i>PLoS Genetics</i> , 2013, 9, e1003872.	1.5	162
5	Paternally expressed genes predominate in the placenta. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10705-10710.	3.3	137
6	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
7	Using next-generation RNA sequencing to identify imprinted genes. <i>Heredity</i> , 2014, 113, 156-166.	1.2	108
8	A Survey for Novel Imprinted Genes in the Mouse Placenta by mRNA-seq. <i>Genetics</i> , 2011, 189, 109-122.	1.2	89
9	A genome-wide approach to identifying novel-imprinted genes. <i>Human Genetics</i> , 2008, 122, 625-634.	1.8	70
10	Paternally biased X inactivation in mouse neonatal brain. <i>Genome Biology</i> , 2010, 11, R79.	13.9	64
11	Genomic responses to selection for tame/aggressive behaviors in the silver fox (<i>Vulpes vulpes</i>) Tj ETQq1 1 0.784314 rgBT /Overle 10398-10403.	3.3	64
12	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
13	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
14	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
15	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
16	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
17	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
18	Chromosome-wide profiling of X-chromosome inactivation and epigenetic states in fetal brain and placenta of the opossum, <i>Monodelphis domestica</i> . <i>Genome Research</i> , 2014, 24, 70-83.	2.4	48

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19	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
20	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
21	Random X inactivation in the mule and horse placenta. <i>Genome Research</i> , 2012, 22, 1855-1863.	2.4	38
22	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
23	OCS2: genome re-annotation of the jewel wasp <i>Nasonia vitripennis</i> . <i>BMC Genomics</i> , 2016, 17, 678.	1.2	35
24	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
25	Contrasting Methods of Quantifying Fine Structure of Human Recombination. <i>Annual Review of Genomics and Human Genetics</i> , 2010, 11, 45-64.	2.5	32
26	The Genetic Architecture of the Genome-Wide Transcriptional Response to ER Stress in the Mouse. <i>PLoS Genetics</i> , 2015, 11, e1004924.	1.5	32
27	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
28	GWAS Analysis Indicated Importance of NF- κ B Signaling Pathway in Host Resistance Against Motile <i>Aeromonas Septicemia</i> Disease in Catfish. <i>Marine Biotechnology</i> , 2019, 21, 335-347.	1.1	30
29	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
30	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
31	Complement regulatory protein genes in channel catfish and their involvement in disease defense response. <i>Developmental and Comparative Immunology</i> , 2015, 53, 33-41.	1.0	23
32	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
33	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
34	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
35	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
36	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

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37	Genomic imprinting does not reduce the dosage of UBE3A in neurons. <i>Epigenetics and Chromatin</i> , 2017, 10, 27.	1.8	15
38	Whole-Genome Shotgun Metagenomic Sequencing Reveals Distinct Gut Microbiome Signatures of Obese Cats. <i>Microbiology Spectrum</i> , 2022, 10, e0083722.	1.2	15
39	TIVAN: tissue-specific <i>cis</i> -eQTL single nucleotide variant annotation and prediction. <i>Bioinformatics</i> , 2019, 35, 1573-1575.	1.8	14
40	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
41	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
42	Genome Assembly of the A-Group Wolbachia in <i>Nasonia oneida</i> Using Linked-Reads Technology. <i>Genome Biology and Evolution</i> , 2019, 11, 3008-3013.	1.1	10
43	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
44	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
45	Identification of novel GPCR partners of the central melanocortin signaling. <i>Molecular Metabolism</i> , 2021, 53, 101317.	3.0	9
46	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
47	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
48	Genome-wide histone state profiling of fibroblasts from the opossum, <i>Monodelphis domestica</i> , identifies the first marsupial-specific imprinted gene. <i>BMC Genomics</i> , 2014, 15, 89.	1.2	6
49	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
50	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
51	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
52	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
53	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
54	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

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55	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
56	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
57	Genomic Imprinting in Invasive Trophoblast in Mammalian Interspecies Hybrids.. <i>Biology of Reproduction</i> , 2010, 83, 102-102.	1.2	4
58	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
59	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
60	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
61	Comparative Transcriptome and Endophytic Bacterial Community Analysis of <i>Morchella conica</i> SH. <i>Frontiers in Microbiology</i> , 2021, 12, 682356.	1.5	3
62	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
63	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
64	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
65	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
66	Role of macronutrient intake in the epigenetics of obesity. <i>Biochemical Society Transactions</i> , 2022, 50, 487-497.	1.6	2
67	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
68	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
69	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