

# Zhanjiang Liu

## List of Publications by Year in descending order

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124  
papers

6,855  
citations

47006

47  
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69250

77  
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168  
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168  
docs citations

168  
times ranked

4776  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and genetic diversity of the common carp, <i>Cyprinus carpio</i> . <i>Nature Genetics</i> , 2014, 46, 1212-1219.	21.4	576
2	The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. <i>Nature Communications</i> , 2016, 7, 11757.	12.8	231
3	RNA-seq analysis of mucosal immune responses reveals signatures of intestinal barrier disruption and pathogen entry following <i>Edwardsiella ictaluri</i> infection in channel catfish, <i>Ictalurus punctatus</i> . <i>Fish and Shellfish Immunology</i> , 2012, 32, 816-827.	3.6	210
4	Expression analysis of the acute phase response in channel catfish ( <i>Ictalurus punctatus</i> ) after infection with a Gram-negative bacterium. <i>Developmental and Comparative Immunology</i> , 2007, 31, 1183-1196.	2.3	170
5	Transcriptomic signatures of attachment, NF- $\kappa$ B suppression and IFN stimulation in the catfish gill following columnaris bacterial infection. <i>Developmental and Comparative Immunology</i> , 2012, 38, 169-180.	2.3	163
6	Aquaculture genomics, genetics and breeding in the United States: current status, challenges, and priorities for future research. <i>BMC Genomics</i> , 2017, 18, 191.	2.8	155
7	An AFLP-Based Genetic Linkage Map of Channel Catfish ( <i>Ictalurus punctatus</i> ) Constructed by Using an Interspecific Hybrid Resource Family. <i>Genetics</i> , 2003, 165, 687-694.	2.9	153
8	Bioinformatic Mining of Type I Microsatellites from Expressed Sequence Tags of Channel Catfish ( <i>Ictalurus punctatus</i> ). <i>Marine Biotechnology</i> , 2004, 6, 364-377.	2.4	139
9	Evolution of CC chemokines in teleost fish: a case study in gene duplication and implications for immune diversity. <i>Immunogenetics</i> , 2007, 59, 613-623.	2.4	134
10	RNA-Seq reveals expression signatures of genes involved in oxygen transport, protein synthesis, folding, and degradation in response to heat stress in catfish. <i>Physiological Genomics</i> , 2013, 45, 462-476.	2.3	134
11	Microarray analysis of gene expression in the blue catfish liver reveals early activation of the MHC class I pathway after infection with <i>Edwardsiella ictaluri</i> . <i>Molecular Immunology</i> , 2008, 45, 553-566.	2.2	129
12	Generation of genome-scale gene-associated SNPs in catfish for the construction of a high-density SNP array. <i>BMC Genomics</i> , 2011, 12, 53.	2.8	122
13	NOD-like subfamily of the nucleotide-binding domain and leucine-rich repeat containing family receptors and their expression in channel catfish. <i>Developmental and Comparative Immunology</i> , 2009, 33, 991-999.	2.3	121
14	The catfish liver-expressed antimicrobial peptide 2 (LEAP-2) gene is expressed in a wide range of tissues and developmentally regulated. <i>Molecular Immunology</i> , 2006, 43, 367-377.	2.2	118
15	A genome-wide association study in catfish reveals the presence of functional hubs of related genes within QTLs for columnaris disease resistance. <i>BMC Genomics</i> , 2015, 16, 196.	2.8	117
16	Pathogen recognition receptors in channel catfish: III Phylogeny and expression analysis of Toll-like receptors. <i>Developmental and Comparative Immunology</i> , 2013, 40, 185-194.	2.3	112
17	Efficient assembly and annotation of the transcriptome of catfish by RNA-Seq analysis of a doubled haploid homozygote. <i>BMC Genomics</i> , 2012, 13, 595.	2.8	109
18	Construction of Genetic Linkage Maps and Comparative Genome Analysis of Catfish Using Gene-Associated Markers. <i>Genetics</i> , 2009, 181, 1649-1660.	2.9	104

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19	Pathogen recognition receptors in channel catfish: I. Identification, phylogeny and expression of NOD-like receptors. <i>Developmental and Comparative Immunology</i> , 2012, 37, 77-86.	2.3	98
20	Molecular characterization and differential expression of the myostatin gene in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2002, 1575, 99-107.	2.4	94
21	The Y chromosome sequence of the channel catfish suggests novel sex determination mechanisms in teleost fish. <i>BMC Biology</i> , 2019, 17, 6.	3.8	91
22	Construction of a high-density, high-resolution genetic map and its integration with BAC-based physical map in channel catfish. <i>DNA Research</i> , 2015, 22, 39-52.	3.4	89
23	Comparative genome analysis of 52 fish species suggests differential associations of repetitive elements with their living aquatic environments. <i>BMC Genomics</i> , 2018, 19, 141.	2.8	89
24	Development of the catfish 250K SNP array for genome-wide association studies. <i>BMC Research Notes</i> , 2014, 7, 135.	1.4	87
25	Pathogen recognition receptors in channel catfish: II. Identification, phylogeny and expression of retinoic acid-inducible gene I (RIG-I)-like receptors (RLRs). <i>Developmental and Comparative Immunology</i> , 2012, 37, 381-389.	2.3	86
26	Constitutive expression of three novel catfish CXC chemokines: homeostatic chemokines in teleost fish. <i>Molecular Immunology</i> , 2005, 42, 1355-1366.	2.2	84
27	Characterization of 23 CC chemokine genes and analysis of their expression in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Developmental and Comparative Immunology</i> , 2006, 30, 783-796.	2.3	84
28	Transcriptional regulation of hypoxia inducible factors alpha (HIF-1 $\alpha$ ) and their inhibiting factor (FIH-1) of channel catfish ( <i>Ictalurus punctatus</i> ) under hypoxia. <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 2014, 169, 38-50.	1.6	84
29	Bulk segregant RNA-seq reveals expression and positional candidate genes and allele-specific expression for disease resistance against enteric septicemia of catfish. <i>BMC Genomics</i> , 2013, 14, 929.	2.8	79
30	Dress-out and fillet yields of channel catfish, <i>Ictalurus punctatus</i> , blue catfish, <i>Ictalurus furcatus</i> , and their F1, F2 and backcross hybrids. <i>Aquaculture</i> , 2003, 228, 81-90.	3.5	77
31	A BAC-based physical map of the channel catfish genome. <i>Genomics</i> , 2007, 90, 380-388.	2.9	72
32	Male-Biased Genes in Catfish as Revealed by RNA-Seq Analysis of the Testis Transcriptome. <i>PLoS ONE</i> , 2013, 8, e68452.	2.5	71
33	A Genome-Wide Association Study Identifies Multiple Regions Associated with Head Size in Catfish. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3389-3398.	1.8	70
34	Genomic Basis of Adaptive Evolution: The Survival of Amur Ide ( <i>Leuciscus waleckii</i> ) in an Extremely Alkaline Environment. <i>Molecular Biology and Evolution</i> , 2017, 34, 145-159.	8.9	66
35	Catfish CC chemokines: genomic clustering, duplications, and expression after bacterial infection with <i>Edwardsiella ictaluri</i> . <i>Molecular Genetics and Genomics</i> , 2006, 275, 297-309.	2.1	64
36	Hsp90, Hsp60 and sHsp families of heat shock protein genes in channel catfish and their expression after bacterial infections. <i>Fish and Shellfish Immunology</i> , 2015, 44, 642-651.	3.6	64

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37	Alternative splicing in teleost fish genomes: same-species and cross-species analysis and comparisons. <i>Molecular Genetics and Genomics</i> , 2010, 283, 531-539.	2.1	61
38	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.	2.1	61
39	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.	2.1	59
40	Genome-Wide Association Study Reveals Multiple Novel QTL Associated with Low Oxygen Tolerance in Hybrid Catfish. <i>Marine Biotechnology</i> , 2017, 19, 379-390.	2.4	58
41	Multiple CC chemokines in channel catfish and blue catfish as revealed by analysis of expressed sequence tags. <i>Immunogenetics</i> , 2004, 56, 379-87.	2.4	56
42	Identification and Analysis of Genome-Wide SNPs Provide Insight into Signatures of Selection and Domestication in Channel Catfish ( <i>Ictalurus punctatus</i> ). <i>PLoS ONE</i> , 2014, 9, e109666.	2.5	55
43	Increased Alternative Splicing as a Host Response to <i>Edwardsiella ictaluri</i> Infection in Catfish. <i>Marine Biotechnology</i> , 2018, 20, 729-738.	2.4	55
44	Effects of Insert Size on Transposition Efficiency of the Sleeping Beauty Transposon in Mouse Cells. <i>Marine Biotechnology</i> , 2001, 3, 241-245.	2.4	54
45	A Genome-Wide Association Study Reveals That Genes with Functions for Bone Development Are Associated with Body Conformation in Catfish. <i>Marine Biotechnology</i> , 2017, 19, 570-578.	2.4	53
46	Identification of novel genes significantly affecting growth in catfish through GWAS analysis. <i>Molecular Genetics and Genomics</i> , 2018, 293, 587-599.	2.1	53
47	Comparison of domestic and wild channel catfish ( <i>Ictalurus punctatus</i> ) populations provides no evidence for genetic impact. <i>Aquaculture</i> , 2006, 252, 133-146.	3.5	52
48	Development of Polymorphic EST Markers Suitable for Genetic Linkage Mapping of Catfish. <i>Marine Biotechnology</i> , 1999, 1, 437-447.	2.4	51
49	Development of a 690K SNP array in catfish and its application for genetic mapping and validation of the reference genome sequence. <i>Scientific Reports</i> , 2017, 7, 40347.	3.3	50
50	Comparison of Manual Stripping and Pen Spawning for Production of Channel Catfish × Blue Catfish Hybrids and Aquarium Spawning of Channel Catfish. <i>North American Journal of Aquaculture</i> , 2000, 62, 260-265.	1.4	46
51	Development of Amplified Fragment Length Polymorphism (AFLP) Markers Suitable for Genetic Linkage Mapping of Catfish. <i>Transactions of the American Fisheries Society</i> , 1999, 128, 317-327.	1.4	43
52	Expression of Bcl-2 genes in channel catfish after bacterial infection and hypoxia stress. <i>Developmental and Comparative Immunology</i> , 2016, 65, 79-90.	2.3	42
53	The chemokine superfamily in channel catfish: I. CXC subfamily and their involvement in disease defense and hypoxia responses. <i>Fish and Shellfish Immunology</i> , 2017, 60, 380-390.	3.6	42
54	The skeletal muscle $\beta$ -actin gene of channel catfish ( <i>Ictalurus punctatus</i> ) and its association with piscine specific SINE elements. <i>Gene</i> , 2000, 252, 173-181.	2.2	41

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55	Second-Generation Genetic Linkage Map of Catfish and Its Integration with the BAC-Based Physical Map. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1233-1241.	1.8	41
56	Identification and Characterization of Full-Length cDNAs in Channel Catfish ( <i>Ictalurus punctatus</i> ) and Blue Catfish ( <i>Ictalurus furcatus</i> ). <i>PLoS ONE</i> , 2010, 5, e11546.	2.5	40
57	Four lysozymes (one c-type and three g-type) in catfish are drastically but differentially induced after bacterial infection. <i>Fish and Shellfish Immunology</i> , 2013, 35, 136-145.	3.6	40
58	Expression of nitric oxide synthase (NOS) genes in channel catfish is highly regulated and time dependent after bacterial challenges. <i>Developmental and Comparative Immunology</i> , 2014, 45, 74-86.	2.3	40
59	Genome-wide identification of Hsp70 genes in channel catfish and their regulated expression after bacterial infection. <i>Fish and Shellfish Immunology</i> , 2016, 49, 154-162.	3.6	40
60	Consumption of florfenicol-medicated feed alters the composition of the channel catfish intestinal microbiota including enriching the relative abundance of opportunistic pathogens. <i>Aquaculture</i> , 2019, 501, 111-118.	3.5	39
61	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.	2.3	36
62	Genome sequence of walking catfish ( <i>Clarias batrachus</i> ) provides insights into terrestrial adaptation. <i>BMC Genomics</i> , 2018, 19, 952.	2.8	36
63	A Review of Molecular Responses of Catfish to Bacterial Diseases and Abiotic Stresses. <i>Frontiers in Physiology</i> , 2018, 9, 1113.	2.8	36
64	Heat stress induced alternative splicing in catfish as determined by transcriptome analysis. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2019, 29, 166-172.	1.0	36
65	Repeat structure of the catfish genome: a genomic and transcriptomic assessment of Tc1-like transposon elements in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Genetica</i> , 2007, 131, 81-90.	1.1	35
66	Transcriptome Display During Testicular Differentiation of Channel Catfish ( <i>Ictalurus punctatus</i> ) as Revealed by RNA-Seq Analysis. <i>Biology of Reproduction</i> , 2016, 95, 19-19.	2.7	35
67	Channel Catfish Follicle-Stimulating Hormone and Luteinizing Hormone: Complementary DNA Cloning and Expression During Ovulation. <i>Marine Biotechnology</i> , 2001, 3, 0590-0599.	2.4	33
68	Identification, phylogeny and expression analysis of suppressors of cytokine signaling in channel catfish. <i>Molecular Immunology</i> , 2015, 64, 276-284.	2.2	32
69	Large-scale SNP discovery and construction of a high-density genetic map of <i>Colossoma macropomum</i> through genotyping-by-sequencing. <i>Scientific Reports</i> , 2017, 7, 46112.	3.3	32
70	The CC and CXC chemokine receptors in channel catfish ( <i>Ictalurus punctatus</i> ) and their involvement in disease and hypoxia responses. <i>Developmental and Comparative Immunology</i> , 2017, 77, 241-251.	2.3	32
71	Rapid development of molecular resources for a freshwater mussel, <i>Villosa lienosa</i> ( <i>Bivalvia:Unionidae</i> ), using an RNA-seq-based approach. <i>Freshwater Science</i> , 2012, 31, 695-708.	1.8	31
72	Genome-Wide Identification of Hsp40 Genes in Channel Catfish and Their Regulated Expression after Bacterial Infection. <i>PLoS ONE</i> , 2014, 9, e115752.	2.5	31

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73	Pathogen recognition receptors in channel catfish: IV. Identification, phylogeny and expression analysis of peptidoglycan recognition proteins. <i>Developmental and Comparative Immunology</i> , 2014, 46, 291-299.	2.3	31
74	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.	2.3	31
75	Analysis of 52 Rab GTPases from channel catfish and their involvement in immune responses after bacterial infections. <i>Developmental and Comparative Immunology</i> , 2014, 45, 21-34.	2.3	30
76	The cytochrome P450 genes of channel catfish: Their involvement in disease defense responses as revealed by meta-analysis of RNA-Seq data sets. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 2813-2828.	2.4	30
77	GWAS Analysis Indicated Importance of NF- $\kappa$ B Signaling Pathway in Host Resistance Against Motile Aeromonas Septicemia Disease in Catfish. <i>Marine Biotechnology</i> , 2019, 21, 335-347.	2.4	30
78	Chemokine C-C motif ligand 33 is a key regulator of teleost fish barbel development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5018-E5027.	7.1	29
79	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.	2.1	28
80	JAK and STAT members in channel catfish: Identification, phylogenetic analysis and expression profiling after <i>Edwardsiella ictaluri</i> infection. <i>Developmental and Comparative Immunology</i> , 2018, 81, 334-341.	2.3	27
81	A deletion in the Hermanskyâ€Pudlak syndrome 4 (Hps4) gene appears to be responsible for albinism in channel catfish. <i>Molecular Genetics and Genomics</i> , 2017, 292, 663-670.	2.1	26
82	Transcriptome Analysis of the Gill and Swimbladder of <i>Takifugu rubripes</i> by RNA-Seq. <i>PLoS ONE</i> , 2014, 9, e85505.	2.5	25
83	Post-transcriptional regulation through alternative splicing after infection with <i>Flavobacterium columnare</i> in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Fish and Shellfish Immunology</i> , 2019, 91, 188-193.	3.6	25
84	Claudin multigene family in channel catfish and their expression profiles in response to bacterial infection and hypoxia as revealed by meta-analysis of RNA-Seq datasets. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2015, 13, 60-69.	1.0	24
85	Complement regulatory protein genes in channel catfish and their involvement in disease defense response. <i>Developmental and Comparative Immunology</i> , 2015, 53, 33-41.	2.3	23
86	Molecular systematics of bisexual <i>Artemia</i> populations. <i>Aquaculture Research</i> , 2006, 37, 671-680.	1.8	22
87	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.	2.3	22
88	Development of genomic resources in support of sequencing, assembly, and annotation of the catfish genome. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2011, 6, 11-17.	1.0	20
89	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.	2.1	19
90	The serpin superfamily in channel catfish: Identification, phylogenetic analysis and expression profiling in mucosal tissues after bacterial infections. <i>Developmental and Comparative Immunology</i> , 2015, 49, 267-277.	2.3	18

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91	Whole genome comparative analysis of channel catfish ( <i>Ictalurus punctatus</i> ) with four model fish species. <i>BMC Genomics</i> , 2013, 14, 780.	2.8	17
92	Identification of NF- $\kappa$ 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.	2.3	17
93	Genomic organization and evolution of olfactory receptors and trace amine-associated receptors in channel catfish, <i>Ictalurus punctatus</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 644-651.	2.4	15
94	SNP Discovery from Transcriptome of the Swimbladder of <i>Takifugu rubripes</i> . <i>PLoS ONE</i> , 2014, 9, e92502.	2.5	14
95	The annotation of repetitive elements in the genome of channel catfish ( <i>Ictalurus punctatus</i> ). <i>PLoS ONE</i> , 2018, 13, e0197371.	2.5	13
96	Comparative transcriptome analysis of papilla and skin in the sea cucumber, <i>Apostichopus japonicus</i> . <i>PeerJ</i> , 2016, 4, e1779.	2.0	13
97	Channel catfish hemoglobin genes: Identification, phylogenetic and syntenic analysis, and specific induction in response to heat stress. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2014, 9, 11-22.	1.0	12
98	Application of second-generation sequencing (SGS) and third generation sequencing (TGS) in aquaculture breeding program. <i>Aquaculture</i> , 2022, 548, 737633.	3.5	12
99	Expression of tumor suppressor genes in channel catfish after bacterial infections. <i>Developmental and Comparative Immunology</i> , 2015, 48, 171-177.	2.3	11
100	Phosphoinositide 3-kinase family in channel catfish and their regulated expression after bacterial infection. <i>Fish and Shellfish Immunology</i> , 2016, 49, 364-373.	3.6	11
101	Historical demography of common carp estimated from individuals collected from various parts of the world using the pairwise sequentially markovian coalescent approach. <i>Genetica</i> , 2018, 146, 235-241.	1.1	11
102	FOXO genes in channel catfish and their response after bacterial infection. <i>Developmental and Comparative Immunology</i> , 2019, 97, 38-44.	2.3	11
103	Septin genes in channel catfish ( <i>Ictalurus punctatus</i> ) and their involvement in disease defense responses. <i>Fish and Shellfish Immunology</i> , 2016, 49, 110-121.	3.6	10
104	Identification, annotation and expression analysis of 29 Rho GTPase genes from channel catfish ( <i>Ictalurus punctatus</i> ) after bacterial infections. <i>Developmental and Comparative Immunology</i> , 2017, 67, 445-451.	2.3	9
105	The NCK and ABI adaptor genes in catfish and their involvement in ESC disease response. <i>Developmental and Comparative Immunology</i> , 2017, 73, 119-123.	2.3	8
106	DEXD/H-box RNA helicase genes are differentially expressed between males and females during the critical period of male sex differentiation in channel catfish. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017, 22, 109-119.	1.0	8
107	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.	1.0	8
108	Characterization and Expression Analysis of MicroRNAs in the Tube Foot of Sea Cucumber <i>Apostichopus japonicus</i> . <i>PLoS ONE</i> , 2014, 9, e111820.	2.5	8



