# Zhanjiang Liu

List of Publications by Year
in descending order



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|---|---|---|---|
| 124 papers | 6,855 citations | 47006 47 h-index | 69250 77 g-index |
| 168 all docs | 168 docs citations | 168 times ranked | 4776 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Application of second-generation sequencing (SGS) and third generation sequencing (TGS) in aquaculture breeding program. Aquaculture, 2022, 548, 737633. | 3.5 | 12 |
| 2 | Allelically and Differentially Expressed Genes After Infection of Edwardsiella ictaluri in Channel Catfish as Determined by Bulk Segregant RNA-Seq. Marine Biotechnology, 2022, 24, 174-189. | 2.4 | 2 |
| 3 | Identification of an Epigenetically Marked Locus within the Sex Determination Region of Channel Catfish. International Journal of Molecular Sciences, 2022, 23, 5471. | 4.1 | 7 |
| 4 | Feminization of channel catfish with 17Î²-oestradiol involves methylation and expression of a specific set of genes independent of the sex determination region. Epigenetics, 2022, 17, 1820-1837. | 2.7 | 5 |
| 5 | Crosstalk between dopamine and insulin signaling in growth control of the oyster. General and Comparative Endocrinology, 2021, 313, 113895. | 1.8 | 7 |
| 6 | Genomic Prediction of Columnaris Disease Resistance in Catfish. Marine Biotechnology, 2020, 22, 145-151. | 2.4 | 6 |
| 7 | The Y chromosome sequence of the channel catfish suggests novel sex determination mechanisms in teleost fish. BMC Biology, 2019, 17, 6. | 3.8 | 91 |
| 8 | Post-transcriptional regulation through alternative splicing after infection with Flavobacterium columnare in channel catfish (Ictalurus punctatus). Fish and Shellfish Immunology, 2019, 91, 188-193. | 3.6 | 25 |
| 9 | GWAS Analysis Indicated Importance of NF-ÎºB Signaling Pathway in Host Resistance Against Motile Aeromonas Septicemia Disease in Catfish. Marine Biotechnology, 2019, 21, 335-347. | 2.4 | 30 |
| 10 | FOXO genes in channel catfish and their response after bacterial infection. Developmental and Comparative Immunology, 2019, 97, 38-44. | 2.3 | 11 |
| 11 | Polyadenylation sites and their characteristics in the genome of channel catfish (Ictalurus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Genomics and Proteomics, 2019, 30, 248-255. | 1.0 | 0 |
| 12 | Consumption of florfenicol-medicated feed alters the composition of the channel catfish intestinal microbiota including enriching the relative abundance of opportunistic pathogens. Aquaculture, 2019, 501, 111-118. | 3.5 | 39 |
| 13 | Heat stress induced alternative splicing in catfish as determined by transcriptome analysis. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2019, 29, 166-172. | 1.0 | 36 |
| 14 | JAK and STAT members in channel catfish: Identification, phylogenetic analysis and expression profiling after Edwardsiella ictaluri infection. Developmental and Comparative Immunology, 2018, 81, 334-341. | 2.3 | 27 |
| 15 | Historical demography of common carp estimated from individuals collected from various parts of the world using the pairwise sequentially markovian coalescent approach. Genetica, 2018, 146, 235-241. | 1.1 | 11 |
| 16 | Comparative genome analysis of 52 fish species suggests differential associations of repetitive elements with their living aquatic environments. BMC Genomics, 2018, 19, 141. | 2.8 | 89 |
| 17 | Transcriptome analysis reveals enrichment of genes associated with auditory system in swimbladder of channel catfish. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2018, 27, 30-39. | 1.0 | 8 |
| 18 | Comparative transcriptome analysis reveals conserved branching morphogenesis related genes involved in chamber formation of catfish swimbladder. Physiological Genomics, 2018, 50, 67-76. | 2.3 | 6 |

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|---|---|---|---|
| 19 | Identification of novel genes significantly affecting growth in catfish through GWAS analysis. Molecular Genetics and Genomics, 2018, 293, 587-599. | 2.1 | 53 |
| 20 | Genome sequence of walking catfish (Clarias batrachus) provides insights into terrestrial adaptation. BMC Genomics, 2018, 19, 952. | 2.8 | 36 |
| 21 | The annotation of repetitive elements in the genome of channel catfish (Ictalurus punctatus). PLoS ONE, 2018, 13, e0197371. | 2.5 | 13 |
| 22 | Chemokine C-C motif ligand 33 is a key regulator of teleost fish barbel development. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5018-E5027. | 7.1 | 29 |
| 23 | Comparative transcriptome analysis of the swimbladder reveals expression signatures in response to low oxygen stress in channel catfish,Ictalurus punctatus. Physiological Genomics, 2018, 50, 636-647. | 2.3 | 22 |
| 24 | Genome-wide association analysis of intra-specific QTL associated with the resistance for enteric septicemia of catfish. Molecular Genetics and Genomics, 2018, 293, 1365-1378. | 2.1 | 19 |
| 25 | Increased Alternative Splicing as a Host Response to Edwardsiella ictaluri Infection in Catfish. Marine Biotechnology, 2018, 20, 729-738. | 2.4 | 55 |
| 26 | GWAS analysis using interspecific backcross progenies reveals superior blue catfish alleles responsible for strong resistance against enteric septicemia of catfish. Molecular Genetics and Genomics, 2018, 293, 1107-1120. | 2.1 | 28 |
| 27 | A Review of Molecular Responses of Catfish to Bacterial Diseases and Abiotic Stresses. Frontiers in Physiology, 2018, 9, 1113. | 2.8 | 36 |
| 28 | Identification of NF-ÎºB related genes in channel catfish and their expression profiles in mucosal tissues after columnaris bacterial infection. Developmental and Comparative Immunology, 2017, 70, 27-38. | 2.3 | 17 |
| 29 | Development of a 690â€‰K SNP array in catfish and its application for genetic mapping and validation of the reference genome sequence. Scientific Reports, 2017, 7, 40347. | 3.3 | 50 |
| 30 | Aquaculture genomics, genetics and breeding in the United States: current status, challenges, and priorities for future research. BMC Genomics, 2017, 18, 191. | 2.8 | 155 |
| 31 | The NCK and ABI adaptor genes in catfish and their involvement in ESC disease response. Developmental and Comparative Immunology, 2017, 73, 119-123. | 2.3 | 8 |
| 32 | Genome-Wide Association Study Reveals Multiple Novel QTL Associated with Low Oxygen Tolerance in Hybrid Catfish. Marine Biotechnology, 2017, 19, 379-390. | 2.4 | 58 |
| 33 | The chemokinome superfamily: II. The 64 CC chemokines in channel catfish and their involvement in disease and hypoxia responses. Developmental and Comparative Immunology, 2017, 73, 97-108. | 2.3 | 36 |
| 34 | Large-scale SNP discovery and construction of a high-density genetic map of Colossoma macropomum through genotyping-by-sequencing. Scientific Reports, 2017, 7, 46112. | 3.3 | 32 |
| 35 | DExD/H-box RNA helicase genes are differentially expressed between males and females during the critical period of male sex differentiation in channel catfish. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 22, 109-119. | 1.0 | 8 |
| 36 | A deletion in the Hermanskyâ€"Pudlak syndrome 4 (Hps4) gene appears to be responsible for albinism in channel catfish. Molecular Genetics and Genomics, 2017, 292, 663-670. | 2.1 | 26 |

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|---|---|---|---|
| 37 | The chemokinome superfamily in channel catfish: I. CXC subfamily and their involvement in disease defense and hypoxia responses. Fish and Shellfish Immunology, 2017, 60, 380-390. | 3.6 | 42 |
| 38 | A Genome-Wide Association Study Reveals That Genes with Functions for Bone Development Are Associated with Body Conformation in Catfish. Marine Biotechnology, 2017, 19, 570-578. | 2.4 | 53 |
| 39 | The CC and CXC chemokine receptors in channel catfish (Ictalurus punctatus) and their involvement in disease and hypoxia responses. Developmental and Comparative Immunology, 2017, 77, 241-251. | 2.3 | 32 |
| 40 | Effects of strain and body weight on low-oxygen tolerance of channel catfish (Ictalurus punctatus). Aquaculture International, 2017, 25, 1645-1652. | 2.2 | 5 |
| 41 | Genomic organization and evolution of olfactory receptors and trace amine-associated receptors in channel catfish, Ictalurus punctatus. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 644-651. | 2.4 | 15 |
| 42 | Taste receptors and gustatory associated G proteins in channel catfish, Ictalurus punctatus. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 21, 1-9. | 1.0 | 4 |
| 43 | GWAS analysis of QTL for enteric septicemia of catfish and their involved genes suggest evolutionary conservation of a molecular mechanism of disease resistance. Molecular Genetics and Genomics, 2017, 292, 231-242. | 2.1 | 59 |
| 44 | Identification, annotation and expression analysis of 29 Rho GTPase genes from channel catfish (Ictalurus punctatus) after bacterial infections. Developmental and Comparative Immunology, 2017, 67, 445-451. | 2.3 | 9 |
| 45 | Genomic Basis of Adaptive Evolution: The Survival of Amur Ide (Leuciscuswaleckii) in an Extremely Alkaline Environment. Molecular Biology and Evolution, 2017, 34, 145-159. | 8.9 | 66 |
| 46 | Analysis of apolipoprotein genes and their involvement in disease response of channel catfish after bacterial infection. Developmental and Comparative Immunology, 2017, 67, 464-470. | 2.3 | 31 |
| 47 | Multiple across-strain and within-strain QTLs suggest highly complex genetic architecture for hypoxia tolerance in channel catfish. Molecular Genetics and Genomics, 2017, 292, 63-76. | 2.1 | 61 |
| 48 | Next generation sequencing yields the complete mitochondrial genome of the striped raphael catfish,Platydoras armatulus(Siluriformes: Doradidae). Mitochondrial DNA, 2016, 27, 1-2. | 0.6 | 1 |
| 49 | A Genome-Wide Association Study Identifies Multiple Regions Associated with Head Size in Catfish. G3: Genes, Genomes, Genetics, 2016, 6, 3389-3398. | 1.8 | 70 |
| 50 | The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. Nature Communications, 2016, 7, 11757. | 12.8 | 231 |
| 51 | Transcriptome Display During Testicular Differentiation of Channel Catfish (Ictalurus punctatus) as Revealed by RNA-Seq Analysis. Biology of Reproduction, 2016, 95, 19-19. | 2.7 | 35 |
| 52 | Expression of Bcl-2 genes in channel catfish after bacterial infection and hypoxia stress. Developmental and Comparative Immunology, 2016, 65, 79-90. | 2.3 | 42 |
| 53 | Ribosomal protein genes are highly enriched among genes with allele-specific expression in the interspecific F1 hybrid catfish. Molecular Genetics and Genomics, 2016, 291, 1083-1093. | 2.1 | 5 |
| 54 | Genome-wide identification of Hsp70 genes in channel catfish and their regulated expression after bacterial infection. Fish and Shellfish Immunology, 2016, 49, 154-162. | 3.6 | 40 |

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|---|---|---|---|
| 55 | Septin genes in channel catfish (Ictalurus punctatus) and their involvement in disease defense responses. Fish and Shellfish Immunology, 2016, 49, 110-121. | 3.6 | 10 |
| 56 | Phosphoinositide 3-kinase family in channel catfish and their regulated expression after bacterial infection. Fish and Shellfish Immunology, 2016, 49, 364-373. | 3.6 | 11 |
| 57 | Comparative transcriptome analysis of papilla and skin in the sea cucumber,Apostichopus japonicus. PeerJ, 2016, 4, e1779. | 2.0 | 13 |
| 58 | Identification and Characterization of MicroRNAs from Longitudinal Muscle and Respiratory Tree in Sea Cucumber (Apostichopus japonicus) Using High-Throughput Sequencing. PLoS ONE, 2015, 10, e0134899. | 2.5 | 7 |
| 59 | Identification and expression analysis of 26 oncogenes of the receptor tyrosine kinase family in channel catfish after bacterial infection and hypoxic stress. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 14, 16-25. | 1.0 | 4 |
| 60 | Identification, phylogeny and expression analysis of suppressors of cytokine signaling in channel catfish. Molecular Immunology, 2015, 64, 276-284. | 2.2 | 32 |
| 61 | The serpin superfamily in channel catfish: Identification, phylogenetic analysis and expression profiling in mucosal tissues after bacterial infections. Developmental and Comparative Immunology, 2015, 49, 267-277. | 2.3 | 18 |
| 62 | Complement regulatory protein genes in channel catfish and their involvement in disease defense response. Developmental and Comparative Immunology, 2015, 53, 33-41. | 2.3 | 23 |
| 63 | Construction of a high-density, high-resolution genetic map and its integration with BAC-based physical map in channel catfish. DNA Research, 2015, 22, 39-52. | 3.4 | 89 |
| 64 | A genome-wide association study in catfish reveals the presence of functional hubs of related genes within QTLs for columnaris disease resistance. BMC Genomics, 2015, 16, 196. | 2.8 | 117 |
| 65 | Hsp90, Hsp60 and sHsp families of heat shock protein genes in channel catfish and their expression after bacterial infections. Fish and Shellfish Immunology, 2015, 44, 642-651. | 3.6 | 64 |
| 66 | 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. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 13, 60-69. | 1.0 | 24 |
| 67 | Expression of tumor suppressor genes in channel catfish after bacterial infections. Developmental and Comparative Immunology, 2015, 48, 171-177. | 2.3 | 11 |
| 68 | Identification and Analysis of Genome-Wide SNPs Provide Insight into Signatures of Selection and Domestication in Channel Catfish (Ictalurus punctatus). PLoS ONE, 2014, 9, e109666. | 2.5 | 55 |
| 69 | Genome-Wide Identification of Hsp40 Genes in Channel Catfish and Their Regulated Expression after Bacterial Infection. PLoS ONE, 2014, 9, e115752. | 2.5 | 31 |
| 70 | The complete mitochondrial genome of the armored catfish,Hypostomus plecostomus(Siluriformes:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf | 0.6 | 5 |
| 71 | Generation of physical map contig-specific sequences. Frontiers in Genetics, 2014, 5, 243. | 2.3 | 2 |
| 72 | Development of the catfish 250K SNP array for genome-wide association studies. BMC Research Notes, 2014, 7, 135. | 1.4 | 87 |

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|---|---|---|---|
| 73 | Transciptome Analysis of the Gill and Swimbladder of Takifugu rubripes by RNA-Seq. PLoS ONE, 2014, 9, e85505. | 2.5 | 25 |
| 74 | Transcriptional regulation of hypoxia inducible factors alpha (HIF-Î±) and their inhibiting factor (FIH-1) of channel catfish (Ictalurus punctatus) under hypoxia. Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology, 2014, 169, 38-50. | 1.6 | 84 |
| 75 | Expression of nitric oxide synthase (NOS) genes in channel catfish is highly regulated and time dependent after bacterial challenges. Developmental and Comparative Immunology, 2014, 45, 74-86. | 2.3 | 40 |
| 76 | Channel catfish hemoglobin genes: Identification, phylogenetic and syntenic analysis, and specific induction in response to heat stress. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2014, 9, 11-22. | 1.0 | 12 |
| 77 | Pathogen recognition receptors in channel catfish: IV. Identification, phylogeny and expression analysis of peptidoglycan recognition proteins. Developmental and Comparative Immunology, 2014, 46, 291-299. | 2.3 | 31 |
| 78 | Genome sequence and genetic diversity of the common carp, Cyprinus carpio. Nature Genetics, 2014, 46, 1212-1219. | 21.4 | 576 |
| 79 | Analysis of 52 Rab GTPases from channel catfish and their involvement in immune responses after bacterial infections. Developmental and Comparative Immunology, 2014, 45, 21-34. | 2.3 | 30 |
| 80 | The cytochrome P450 genes of channel catfish: Their involvement in disease defense responses as revealed by meta-analysis of RNA-Seq data sets. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 2813-2828. | 2.4 | 30 |
| 81 | SNP Discovery from Transcriptome of the Swimbladder of Takifugu rubripes. PLoS ONE, 2014, 9, e92502. | 2.5 | 14 |
| 82 | Characterization and Expression Analysis of MicroRNAs in the Tube Foot of Sea Cucumber Apostichopus japonicus. PLoS ONE, 2014, 9, e111820. | 2.5 | 8 |
| 83 | Bulk segregant RNA-seq reveals expression and positional candidate genes and allele-specific expression for disease resistance against enteric septicemia of catfish. BMC Genomics, 2013, 14, 929. | 2.8 | 79 |
| 84 | Whole genome comparative analysis of channel catfish (Ictalurus punctatus) with four model fish species. BMC Genomics, 2013, 14, 780. | 2.8 | 17 |
| 85 | Four lysozymes (one c-type and three g-type) in catfish are drastically butÂdifferentially induced after bacterial infection. Fish and Shellfish Immunology, 2013, 35, 136-145. | 3.6 | 40 |
| 86 | Pathogen recognition receptors in channel catfish: III Phylogeny and expression analysis of Toll-like receptors. Developmental and Comparative Immunology, 2013, 40, 185-194. | 2.3 | 112 |
| 87 | RNA-Seq reveals expression signatures of genes involved in oxygen transport, protein synthesis, folding, and degradation in response to heat stress in catfish. Physiological Genomics, 2013, 45, 462-476. | 2.3 | 134 |
| 88 | Male-Biased Genes in Catfish as Revealed by RNA-Seq Analysis of the Testis Transcriptome. PLoS ONE, 2013, 8, e68452. | 2.5 | 71 |
| 89 | Efficient assembly and annotation of the transcriptome of catfish by RNA-Seq analysis of a doubled haploid homozygote. BMC Genomics, 2012, 13, 595. | 2.8 | 109 |
| 90 | Second-Generation Genetic Linkage Map of Catfish and Its Integration with the BAC-Based Physical Map. G3: Genes, Genomes, Genetics, 2012, 2, 1233-1241. | 1.8 | 41 |

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|---|---|---|---|
| 91 | Rapid development of molecular resources for a freshwater mussel, Villosa lienosa (Bivalvia:Unionidae), using an RNA-seq-based approach. Freshwater Science, 2012, 31, 695-708. | 1.8 | 31 |
| 92 | Pathogen recognition receptors in channel catfish: I. Identification, phylogeny and expression of NOD-like receptors. Developmental and Comparative Immunology, 2012, 37, 77-86. | 2.3 | 98 |
| 93 | Pathogen recognition receptors in channel catfish: II. Identification, phylogeny and expression of retinoic acid-inducible gene I (RIG-I)-like receptors (RLRs). Developmental and Comparative Immunology, 2012, 37, 381-389. | 2.3 | 86 |
| 94 | Transcriptomic signatures of attachment, NF-ÎºB suppression and IFN stimulation in the catfish gill following columnaris bacterial infection. Developmental and Comparative Immunology, 2012, 38, 169-180. | 2.3 | 163 |
| 95 | RNA-seq analysis of mucosal immune responses reveals signatures of intestinal barrier disruption and pathogen entry following Edwardsiella ictaluri infection in channel catfish, Ictalurus punctatus. Fish and Shellfish Immunology, 2012, 32, 816-827. | 3.6 | 210 |
| 96 | Development of genomic resources in support of sequencing, assembly, and annotation of the catfish genome. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2011, 6, 11-17. | 1.0 | 20 |
| 97 | Generation of genome-scale gene-associated SNPs in catfish for the construction of a high-density SNP array. BMC Genomics, 2011, 12, 53. | 2.8 | 122 |
| 98 | Library Construction for next Generation Sequencing. , 2010, , 57-67. | | 3 |
| 99 | Alternative splicing in teleost fish genomes: same-species and cross-species analysis and comparisons. Molecular Genetics and Genomics, 2010, 283, 531-539. | 2.1 | 61 |
| 100 | Identification and Characterization of Full-Length cDNAs in Channel Catfish (Ictalurus punctatus) and Blue Catfish (Ictalurus furcatus). PLoS ONE, 2010, 5, e11546. | 2.5 | 40 |
| 101 | Construction of Genetic Linkage Maps and Comparative Genome Analysis of Catfish Using Gene-Associated Markers. Genetics, 2009, 181, 1649-1660. | 2.9 | 104 |
| 102 | NOD-like subfamily of the nucleotide-binding domain and leucine-rich repeat containing family receptors and their expression in channel catfish. Developmental and Comparative Immunology, 2009, 33, 991-999. | 2.3 | 121 |
| 103 | Microarray analysis of gene expression in the blue catfish liver reveals early activation of the MHC class I pathway after infection with Edwardsiella ictaluri. Molecular Immunology, 2008, 45, 553-566. | 2.2 | 129 |
| 104 | A BAC-based physical map of the channel catfish genome. Genomics, 2007, 90, 380-388. | 2.9 | 72 |
| 105 | Expression analysis of the acute phase response in channel catfish (Ictalurus punctatus) after infection with a Gram-negative bacterium. Developmental and Comparative Immunology, 2007, 31, 1183-1196. | 2.3 | 170 |
| 106 | Evolution of CC chemokines in teleost fish: a case study in gene duplication and implications for immune diversity. Immunogenetics, 2007, 59, 613-623. | 2.4 | 134 |
| 107 | Repeat structure of the catfish genome: a genomic and transcriptomic assessment of Tc1-like transposon elements in channel catfish (Ictalurus punctatus). Genetica, 2007, 131, 81-90. | 1.1 | 35 |
| 108 | Comparison of domestic and wild channel catfish (Ictalurus punctatus) populations provides no evidence for genetic impact. Aquaculture, 2006, 252, 133-146. | 3.5 | 52 |

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|---|---|---|---|
| 109 | Characterization of 23 CC chemokine genes and analysis of their expression in channel catfish (Ictalurus punctatus). Developmental and Comparative Immunology, 2006, 30, 783-796. | 2.3 | 84 |
| 110 | The catfish liver-expressed antimicrobial peptide 2 (LEAP-2) gene is expressed in a wide range of tissues and developmentally regulated. Molecular Immunology, 2006, 43, 367-377. | 2.2 | 118 |
| 111 | Molecular systematics of bisexual Artemia populations. Aquaculture Research, 2006, 37, 671-680. | 1.8 | 22 |
| 112 | Catfish CC chemokines: genomic clustering, duplications, and expression after bacterial infection with Edwardsiella ictaluri. Molecular Genetics and Genomics, 2006, 275, 297-309. | 2.1 | 64 |
| 113 | Constitutive expression of three novel catfish CXC chemokines: homeostatic chemokines in teleost fish. Molecular Immunology, 2005, 42, 1355-1366. | 2.2 | 84 |
| 114 | Bioinformatic Mining of Type I Microsatellites from Expressed Sequence Tags of Channel Catfish (Ictalurus punctatus). Marine Biotechnology, 2004, 6, 364-377. | 2.4 | 139 |
| 115 | Multiple CC chemokines in channel catfish and blue catfish as revealed by analysis of expressed sequence tags. Immunogenetics, 2004, 56, 379-87. | 2.4 | 56 |
| 116 | Dress-out and fillet yields of channel catfish, Ictalurus punctatus, blue catfish, Ictalurus furcatus, and their F1, F2 and backcross hybrids. Aquaculture, 2003, 228, 81-90. | 3.5 | 77 |
| 117 | An AFLP-Based Genetic Linkage Map of Channel Catfish (Ictalurus punctatus) Constructed by Using an Interspecific Hybrid Resource Family. Genetics, 2003, 165, 687-694. | 2.9 | 153 |
| 118 | Molecular characterization and differential expression of the myostatin gene in channel catfish (Ictalurus punctatus). Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1575, 99-107. | 2.4 | 94 |
| 119 | Effects of Insert Size on Transposition Efficiency of the Sleeping Beauty Transposon in Mouse Cells. Marine Biotechnology, 2001, 3, 241-245. | 2.4 | 54 |
| 120 | Channel Catfish Follicle-Stimulating Hormone and Luteinizing Hormone: Complementary DNA Cloning and Expression During Ovulation. Marine Biotechnology, 2001, 3, 0590-0599. | 2.4 | 33 |
| 121 | Comparison of Manual Stripping and Pen Spawning for Production of Channel Catfish Ã— Blue Catfish Hybrids and Aquarium Spawning of Channel Catfish. North American Journal of Aquaculture, 2000, 62, 260-265. | 1.4 | 46 |
| 122 | The skeletal muscle Î±-actin gene of channel catfish (Ictalurus punctatus) and its association with piscine specific SINE elements. Gene, 2000, 252, 173-181. | 2.2 | 41 |
| 123 | Development of Amplified Fragment Length Polymorphism (AFLP) Markers Suitable for Genetic Linkage Mapping of Catfish. Transactions of the American Fisheries Society, 1999, 128, 317-327. | 1.4 | 43 |
| 124 | Development of Polymorphic EST Markers Suitable for Genetic Linkage Mapping of Catfish. Marine Biotechnology, 1999, 1, 437-447. | 2.4 | 51 |