

Baohua Chen

List of Publications by Year in descending order

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31
papers

851
citations

623734

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times ranked

721
citing authors

#	ARTICLE	IF	CITATIONS
1	The allotetraploid origin and asymmetrical genome evolution of the common carp <i>Cyprinus carpio</i> . <i>Nature Communications</i> , 2019, 10, 4625.	12.8	156
2	An ultra-high density linkage map and QTL mapping for sex and growth-related traits of common carp (<i>Cyprinus carpio</i>). <i>Scientific Reports</i> , 2016, 6, 26693.	3.3	126
3	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
4	Genomic selection for parasitic ciliate <i>Cryptocaryon irritans</i> resistance in large yellow croaker. <i>Aquaculture</i> , 2021, 531, 735786.	3.5	63
5	The sequencing and de novo assembly of the <i>Larimichthys crocea</i> genome using PacBio and Hi-C technologies. <i>Scientific Data</i> , 2019, 6, 188.	5.3	50
6	Transcriptome analysis reveals the temporal gene expression patterns in skin of large yellow croaker (<i>Larimichthys crocea</i>) in response to <i>Cryptocaryon irritans</i> infection. <i>Fish and Shellfish Immunology</i> , 2020, 99, 462-472.	3.6	49
7	Chromosome-Level Assembly of the Chinese Seabass (<i>Lateolabrax maculatus</i>) Genome. <i>Frontiers in Genetics</i> , 2019, 10, 275.	2.3	33
8	Population Genomics Reveals Genetic Divergence and Adaptive Differentiation of Chinese Sea Bass (<i>Lateolabrax maculatus</i>). <i>Marine Biotechnology</i> , 2018, 20, 45-59.	2.4	30
9	The sequence and de novo assembly of <i>Takifugu bimaculatus</i> genome using PacBio and Hi-C technologies. <i>Scientific Data</i> , 2019, 6, 187.	5.3	29
10	GWAS identified candidate variants and genes associated with acute heat tolerance of large yellow croaker. <i>Aquaculture</i> , 2021, 540, 736696.	3.5	29
11	Genetic Mapping of Head Size Related Traits in Common Carp (<i>Cyprinus carpio</i>). <i>Frontiers in Genetics</i> , 2018, 9, 448.	2.3	27
12	Genome-Scale Association Study of Abnormal Scale Pattern in Yellow River Carp Identified Previously Known Causative Gene in European Mirror Carp. <i>Marine Biotechnology</i> , 2018, 20, 573-583.	2.4	24
13	Genome-wide identification, phylogeny, and expression of fibroblast growth genes in common carp. <i>Gene</i> , 2016, 578, 225-231.	2.2	20
14	Construction of a High-Density Genetic Linkage Map and QTL Mapping for Growth-Related Traits in <i>Takifugu bimaculatus</i> . <i>Marine Biotechnology</i> , 2020, 22, 130-144.	2.4	19
15	Transcriptional differences provide insight into environmental acclimatization in wild amur ide (<i>Leuciscus waleckii</i>) during spawning migration from alkalized lake to freshwater river. <i>Genomics</i> , 2019, 111, 267-276.	2.9	15
16	Construction of the BAC Library of Small Abalone (<i>Haliotis diversicolor</i>) for Gene Screening and Genome Characterization. <i>Marine Biotechnology</i> , 2016, 18, 49-56.	2.4	13
17	Identification and Expression Analysis of Long Non-coding RNA in Large Yellow Croaker (<i>Larimichthys</i>) Tj ETQq1 1 0,784314 rgBT /Overl	2.3	13
18	Chromosome-level genome of <i>Poropuntius huangchuchieni</i> provides a diploid progenitor-like reference genome for the allotetraploid <i>Cyprinus carpio</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 1658-1669.	4.8	13

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19	Patterns of Geographical and Potential Adaptive Divergence in the Genome of the Common Carp (<i>Cyprinus carpio</i>). <i>Frontiers in Genetics</i> , 2019, 10, 660.	2.3	12
20	Genome-wide identification and characterization of olfactory receptor genes in common carp (<i>Cyprinus carpio</i>). <i>Gene</i> , 2021, 777, 145468.	2.2	11
21	Development and Evaluation of a High-Throughput Single-Nucleotide Polymorphism Array for Large Yellow Croaker (<i>Larimichthys crocea</i>). <i>Frontiers in Genetics</i> , 2020, 11, 571751.	2.3	10
22	Fine-Scale Population Genetic Structure and Parapatric Cryptic Species of Kuruma Shrimp (<i>Marsupenaeus japonicus</i>), Along the Northwestern Pacific Coast of China. <i>Frontiers in Genetics</i> , 2020, 11, 118.	2.3	8
23	Population genetic analysis of aquaculture salmonid populations in China using a 57K rainbow trout SNP array. <i>PLoS ONE</i> , 2018, 13, e0202582.	2.5	6
24	Genomic Analysis of Glutathione S-transferases (GST) Family in Common Carp: Identification, Phylogeny and Expression. <i>Pakistan Journal of Zoology</i> , 2017, 49, 1437-1448.	0.2	5
25	Mitogenomic Perspectives on the Adaptation to Extreme Alkaline Environment of Amur ide (<i>Leuciscus</i>) Tj ETQq1 1 0.784314 3gBT /Over 2.4	0.784314	3
26	The complete mitochondrial genome of Russian sturgeon (<i>Acipenser gueldenstaedti</i>). <i>Mitochondrial DNA</i> , 2016, 27, 986-987.	0.6	2
27	Intraspecific mitochondrial variations between <i>Rhinogobio typus</i> from the Yellow River and Yangtze River. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3536-3537.	0.7	2
28	Genetic analysis of whole mitochondrial genome of <i>Lateolabrax maculatus</i> (Perciformes: Moronidae) indicates the presence of two populations along the Chinese coast. <i>Zoologia</i> , 0, 37, 1-12.	0.5	2
29	Complete mitochondrial genome of yellowfin goby (<i>Acanthogobius hasta</i>). <i>Mitochondrial DNA</i> , 2016, 27, 1231-1232.	0.6	1
30	Complete mitochondrial genomes of two ornamental fishes. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2531-2532.	0.7	1
31	Genome-wide genetic analysis of cultured rainbow trout (<i>Oncorhynchus mykiss</i>) populations in China. <i>Journal of Fishery Sciences of China</i> , 2018, 25, 485.	0.2	1