Chenhong Li

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The Tree of Life and a New Classification of Bony Fishes. PLOS Currents, 2013, 5, .	1.4	526
2	Comprehensive phylogeny of ray-finned fishes (Actinopterygii) based on transcriptomic and genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6249-6254.	7.1	445
3	A practical approach to phylogenomics: the phylogeny of ray-finned fish (Actinopterygii) as a case study. BMC Evolutionary Biology, 2007, 7, 44.	3.2	322
4	Optimal Data Partitioning and a Test Case for Ray-Finned Fishes (Actinopterygii) Based on Ten Nuclear Loci. Systematic Biology, 2008, 57, 519-539.	5.6	179
5	Capturing protein-coding genes across highly divergent species. BioTechniques, 2013, 54, 321-326.	1.8	175
6	Multi-locus phylogenetic analysis reveals the pattern and tempo of bony fish evolution. PLOS Currents, 2013, 5, .	1.4	125
7	Molecular phylogeny of Clupeiformes (Actinopterygii) inferred from nuclear and mitochondrial DNA sequences. Molecular Phylogenetics and Evolution, 2007, 44, 386-398.	2.7	89
8	DNA capture reveals transoceanic gene flow in endangered river sharks. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13302-13307.	7.1	65
9	Exon-primed intron-crossing (EPIC) markers for non-model teleost fishes. BMC Evolutionary Biology, 2010, 10, 90.	3.2	50
10	Molecular phylogeny of Squaliformes and first occurrence of bioluminescence in sharks. BMC Evolutionary Biology, 2015, 15, 162.	3.2	48
11	Monophyly and interrelationships of Snook and Barramundi (Centropomidae sensu Greenwood) and five new markers for fish phylogenetics. Molecular Phylogenetics and Evolution, 2011, 60, 463-471.	2.7	44
12	The phylogenetic placement of sinipercid fishes ("Perciformesâ€) revealed by 11 nuclear loci. Molecular Phylogenetics and Evolution, 2010, 56, 1096-1104.	2.7	43
13	Species delimitation and phylogenetic reconstruction of the sinipercids (Perciformes: Sinipercidae) based on target enrichment of thousands of nuclear coding sequences. Molecular Phylogenetics and Evolution, 2017, 111, 44-55.	2.7	33
14	Multilocus DNA barcoding – Species Identification with Multilocus Data. Scientific Reports, 2017, 7, 16601.	3.3	33
15	Phylogenomic analysis on the exceptionally diverse fish clade Gobioidei (Actinopterygii: Gobiiformes) and data-filtering based on molecular clocklikeness. Molecular Phylogenetics and Evolution, 2018, 128, 192-202.	2.7	32
16	Target gene enrichment in the cyclophyllidean cestodes, the most diverse group of tapeworms. Molecular Ecology Resources, 2016, 16, 1095-1106.	4.8	30
17	Phylogenetics of Chondrichthyes and the problem of rooting phylogenies with distant outgroups. Molecular Phylogenetics and Evolution, 2012, 63, 365-373.	2.7	29
18	EvolMarkers: a database for mining exon and intron markers for evolution, ecology and conservation studies. Molecular Ecology Resources, 2012, 12, 967-971.	4.8	26

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19	A DNA sequence-based identification checklist for Taiwanese chondrichthyans. Zootaxa, 2013, 3752, 256-78.	0.5	25
20	Historical introgression drives pervasive mitochondrial admixture between two species of pelagic sharks. Molecular Phylogenetics and Evolution, 2017, 110, 122-126.	2.7	24
21	Gene markers for exon capture and phylogenomics in rayâ€finned fishes. Ecology and Evolution, 2019, 9, 3973-3983.	1.9	19
22	Molecular systematics and phylogenetic analysis of the Asian endemic freshwater sleepers (Gobiiformes: Odontobutidae). Molecular Phylogenetics and Evolution, 2018, 121, 1-11.	2.7	18
23	Convergent evolution misled taxonomy in schizothoracine fishes (Cypriniformes: Cyprinidae). Molecular Phylogenetics and Evolution, 2019, 134, 323-337.	2.7	18
24	Exon probe sets and bioinformatics pipelines for all levels of fish phylogenomics. Molecular Ecology Resources, 2021, 21, 816-833.	4.8	18
25	A phylogenomic approach to reconstruct interrelationships of main clupeocephalan lineages with a critical discussion of morphological apomorphies. BMC Evolutionary Biology, 2018, 18, 158.	3.2	16
26	High-Quality Genome Assembly and Annotation of the Big-Eye Mandarin Fish (Siniperca knerii). G3: Genes, Genomes, Genetics, 2020, 10, 877-880.	1.8	16
27	Assexon: Assembling Exon Using Gene Capture Data. Evolutionary Bioinformatics, 2019, 15, 117693431987479.	1.2	15
28	Mitochondrial diversity and phylogeography of the Chinese perch, Siniperca chuatsi (Perciformes:) Tj ETQq0 0 () rgBT_/Ove 2 . 7	rlock 10 Tf 50 14
29	Confronting Sources of Systematic Error to Resolve Historically Contentious Relationships: A Case Study Using Gadiform Fishes (Teleostei, Paracanthopterygii, Gadiformes). Systematic Biology, 2021, 70, 739-755.	5.6	14
30	Molecular systematics of Pampus (Perciformes: Stromateidae) based on thousands of nuclear loci using target-gene enrichment. Molecular Phylogenetics and Evolution, 2019, 140, 106595.	2.7	13
31	Multiple freshwater invasions of the tapertail anchovy (Clupeiformes: Engraulidae) of the Yangtze River. Ecology and Evolution, 2019, 9, 12202-12215.	1.9	10
32	Molecular phylogenetics of the Clupeiformes based on exon-capture data and a new classification of the order. Molecular Phylogenetics and Evolution, 2022, 175, 107590.	2.7	9
33	When parasites persist: tapeworms survive host extinction and reveal waves of dispersal across Beringia. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201825.	2.6	8
34	Population structure of elongate ilisha llisha elongata along the Northwestern Pacific Coast revealed by mitochondrial control region sequences. Fisheries Science, 2016, 82, 771-785.	1.6	6
35	Exon-capture data and locus screening provide new insights into the phylogeny of flatfishes (Pleuronectoidei). Molecular Phylogenetics and Evolution, 2022, 166, 107315.	2.7	5
36	Exon-Primed Intron-Crossing (EPIC) Markers for Evolutionary Studies of Ficus and Other Taxa in the	2.1	4

Exon-Primed Intron-Crossing (EPIC) Markers for Evolutionary Studies of Ficus and Other Taxa in the Fig Family (Moraceae). Applications in Plant Sciences, 2013, 1, 1300037. 36

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#	Article	IF	CITATIONS
37	Genetic and morphological differences between yellowtail kingfish (Seriola lalandi) from the Bohai Sea, China and the Southern Ocean, Australia. Aquaculture and Fisheries, 2021, 6, 260-266.	2.2	4
38	Progress in Aquaculture Genetics and Breeding in China. Journal of the World Aquaculture Society, 2018, 49, 272-276.	2.4	3
39	Cross-species gene enrichment revealed a single population of Hilsa shad (Tenualosa ilisha) with low genetic variation in Bangladesh waters. Scientific Reports, 2021, 11, 11560.	3.3	3
40	Inline index helped in cleaning up data contamination generated during library preparation and the subsequent steps. Molecular Biology Reports, 2022, 49, 385-392.	2.3	3
41	Genetic diversity of Hilsa kelee collected from the Bay of Bengal and the Arabian Sea. Marine Biodiversity, 2020, 50, 1.	1.0	2
42	Morphological and skeletal comparison and ecological adaptability of Mandarin fish Siniperca chuatsi and big-eye Mandarin fish Siniperca kneri. Aquaculture and Fisheries, 2020, , .	2.2	1
43	Introgressive hybridization between two close speciesSiniperca chuatsiandSiniperca kneri(Percomorpharia: Sinipercidae) in the Middle Reaches of the Yangtze River. Aquatic Living Resources, 2021, 34, 2.	1.2	1
44	A high-resolution genome of an euryhaline and eurythermal rhinogoby (Rhinogobius similis Gill 1895). G3: Genes, Genomes, Genetics, 2021, , .	1.8	1
45	Conservation of genetic resources for sustainable aquaculture. Journal of the World Aquaculture Society, 2022, 53, 4-7.	2.4	1
46	Diversifying of Two Pampus Species across the Indo–Pacific Barrier and the Origin of the Genus. Diversity, 2022, 14, 180.	1.7	1
47	First report of de novo assembly and annotation from brain and blood transcriptome of an anadromous shad, Alosa sapidissima. BMC Genomic Data, 2022, 23, 22.	1.7	1
48	Population Structure, Genetic Diversity, and Conservation Strategies of a Commercially Important Sleeper Fish, Odontobutis potamophilus (Gobiiformes: Odontobutidae) Based on Gene-Capture Data. Frontiers in Genetics, 0, 13, .	2.3	1
49	A modified protocol with less clean-up steps increased efficiency and product yield of sequencing library preparation. 3 Biotech, 2022, 12, 111.	2.2	0