

Sheng-Yong Xu

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Genome-wide identification and low-salinity stress analysis of the Hsp70 gene family in swimming crab (<i>Portunus trituberculatus</i>). <i>International Journal of Biological Macromolecules</i> , 2022, 208, 126-135.	7.5	13
2	Ecological impacts of sea-crossing bridge construction on local sediment microbiome in East China. <i>Regional Studies in Marine Science</i> , 2022, , 102363.	0.7	1
3	Chromosome-scale genome assembly of brown-spotted flathead &Platycephalus& sp.1 provides insights into demersal adaptation in flathead fish. <i>Zoological Research</i> , 2021, 42, 660-665.	2.1	2
4	Chromosome-Level Genome Assembly and Annotation of a Sciaenid Fish, <i>Argyrosomus japonicus</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
5	The complete mitochondrial genome of <i>Platycephalus</i> sp.1 (Teleostei, Platycephalidae) obtained by whole genome sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1941-1943.	0.4	0
6	The complete mitochondrial genome of <i>Hemitripterus villosus</i> (Pallas, 1814) from Zhoushan archipelago. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2622-2623.	0.4	1
7	Whole genome survey and genetic markers development of crocodile flathead <i>Cociella crocodilus</i>. <i>Animal Genetics</i> , 2021, 52, 891-895.	1.7	8
8	The complete mitochondrial genome of <i>Jaydia lineata</i> (Perciformes, Apogonidae) obtained by next-generation sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2507-2508.	0.4	4
9	The complete mitochondrial genome of <i>Hexagrammos agrammus</i> (Scorpaeniformes:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2509-2511.	0.4	0
10	Comprehensive whole genome survey analyses of male and female brown-spotted flathead fish <i>Platycephalus</i> sp.1. <i>Genomics</i> , 2020, 112, 4742-4748.	2.9	10
11	The complete mitochondrial genome of <i>Hapalogenys analis</i> (Perciformes, Haemulidea) except for control region, obtained by whole genome sequencing. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2807-2808.	0.4	1
12	Whole genome survey analysis and microsatellite motif identification of <i>Sebastes marmoratus</i>. <i>Bioscience Reports</i> , 2020, 40, .	2.4	18
13	Comparative analysis of the complete mitochondrial genomes of three rockfishes (Scorpaeniformes,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 2020, 40, .	2.4	12
14	Population genomics reveals possible genetic evidence for parallel evolution of <i>Sebastes marmoratus</i> in the northwestern Pacific Ocean. <i>Open Biology</i> , 2019, 9, 190028.	3.6	8
15	Whole genome resequencing data for three rockfish species of <i>Sebastes</i> . <i>Scientific Data</i> , 2019, 6, 97.	5.3	12
16	Using species distribution model to predict the impact of climate change on the potential distribution of Japanese whiting <i>Sillago japonica</i> . <i>Ecological Indicators</i> , 2019, 104, 333-340.	6.3	71
17	Population genetic structure and selective pressure on the mitochondrial ATP6 gene of the Japanese sand lance <i>Ammodytes personatus</i> Girard. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2019, 99, 1409-1416.	0.8	6
18	Evidence for intra-mitochondrial variation in population genetic structure of <i>Platycephalus</i> sp.1 In the Northwestern Pacific. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2019, 30, 281-288.	0.7	9

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19	Thermal adaptation of Japanese sand lance (<i>Ammodytes personatus</i>) in different ocean currents revealed by the cytochrome-b gene. <i>Marine and Freshwater Research</i> , 2019, 70, 1484.	1.3	1
20	Development of genome-wide SNPs for population genetics and population assignment of <i>Sebastes marmoratus</i> . <i>Conservation Genetics Resources</i> , 2018, 10, 575-578.	0.8	2
21	A draft genome assembly of the Chinese sillago (<i>Sillago sinica</i>), the first reference genome for Sillaginidae fishes. <i>GigaScience</i> , 2018, 7, .	6.4	30
22	Local adaptation shapes pattern of mitochondrial population structure in <i>Sebastes marmoratus</i> . <i>Environmental Biology of Fishes</i> , 2017, 100, 763-774.	1.0	15
23	Genomic evidence for local adaptation in the ovoviparous marine fish <i>Sebastes marmoratus</i> with a background of population homogeneity. <i>Scientific Reports</i> , 2017, 7, 1562.	3.3	32
24	Analysis of the diet of finless porpoise (<i>Neophocaena asiaeorientalis sunameri</i>) based on prey morphological characters and DNA barcoding. <i>Conservation Genetics Resources</i> , 2016, 8, 523-531.	0.8	18
25	The low mitochondrial diversities in lizardfish <i>Saurida elongate</i> : Recent population expansion and selection. <i>Biochemical Systematics and Ecology</i> , 2016, 68, 44-50.	1.3	3
26	Genetic variation in scaly hair-fin anchovy <i>Setipinna tenuifilis</i> (Engraulidae) based on the mitochondrial DNA control region. <i>Mitochondrial DNA</i> , 2014, 25, 223-230.	0.6	4
27	Unexpected complex horizontal gene transfer in teleost fish. <i>Environmental Epigenetics</i> , 0, , .	1.8	0
28	Genomic Comparison and Genetic Marker Identification of the White-Spotted Bamboo Shark <i>Chiloscyllium plagiosum</i> . <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	1