Qiong Shi

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	The Sinocyclocheilus cavefish genome provides insights into cave adaptation. BMC Biology, 2016, 14, 1.	3.8	292
3	Genome Sequencing of the Perciform Fish Larimichthys crocea Provides Insights into Molecular and Genetic Mechanisms of Stress Adaptation. PLoS Genetics, 2015, 11, e1005118.	3.5	230
4	The seahorse genome and the evolution of its specialized morphology. Nature, 2016, 540, 395-399.	27.8	186
5	The genome and transcriptome of Japanese flounder provide insights into flatfish asymmetry. Nature Genetics, 2017, 49, 119-124.	21.4	178
6	The pearl oyster Pinctada fucata martensii genome and multi-omic analyses provide insights into biomineralization. GigaScience, 2017, 6, 1-12.	6.4	160
7	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. Nature Communications, 2014, 5, 5594.	12.8	135
8	Draft genome of the Chinese mitten crab, Eriocheir sinensis. GigaScience, 2016, 5, 5.	6.4	106
9	Transcriptome analysis reveals the molecular mechanisms underlying growth superiority in a novel grouper hybrid (Epinephelus fuscogutatus♀ × E. lanceolatusâ™,). BMC Genetics, 2016, 17, 24.	2.7	94
10	Cone Snails: A Big Store of Conotoxins for Novel Drug Discovery. Toxins, 2017, 9, 397.	3.4	93
11	The Asian arowana (Scleropages formosus) genome provides new insights into the evolution of an early lineage of teleosts. Scientific Reports, 2016, 6, 24501.	3.3	89
12	Research advances in the genomics and applications for molecular breeding of aquaculture animals. Aquaculture, 2020, 526, 735357.	3.5	80
13	The Distribution of Tryptophan-Dependent Indole-3-Acetic Acid Synthesis Pathways in Bacteria Unraveled by Large-Scale Genomic Analysis. Molecules, 2019, 24, 1411.	3.8	76
14	Draft genome of the protandrous Chinese black porgy, Acanthopagrus schlegelii. GigaScience, 2018, 7, 1-7.	6.4	70
15	Draft genome of the Peruvian scallop Argopecten purpuratus. GigaScience, 2018, 7, .	6.4	60
16	High-throughput identification of novel conotoxins from the Chinese tubular cone snail (Conus) Tj ETQq0 0 0 rg	BT /Overlc	ock 10 Tf 50 1

17	Genome and Transcriptome Sequencing of the Astaxanthin-Producing Green Microalga, <i>Haematococcus pluvialis</i> . Genome Biology and Evolution, 2019, 11, 166-173.	2.5	52
18	High-quality genome assembly of channel catfish, Ictalurus punctatus. GigaScience, 2016, 5, 39.	6.4	45

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19	Draft genome of the Northern snakehead, Channa argus. GigaScience, 2017, 6, 1-5.	6.4	45
20	Fish-T1K (Transcriptomes of 1,000 Fishes) Project: large-scale transcriptome data for fish evolution studies. GigaScience, 2016, 5, 18.	6.4	44
21	Construction of a High-Density Linkage Map and QTL Fine Mapping for Growth- and Sex-Related Traits in Channel Catfish (Ictalurus punctatus). Frontiers in Genetics, 2019, 10, 251.	2.3	44
22	The American Paddlefish Genome Provides Novel Insights into Chromosomal Evolution and Bone Mineralization in Early Vertebrates. Molecular Biology and Evolution, 2021, 38, 1595-1607.	8.9	44
23	A genome-wide association study on growth traits in orange-spotted grouper (Epinephelus coioides) with RAD-seq genotyping. Science China Life Sciences, 2018, 61, 934-946.	4.9	42
24	Chromosomeâ€level genome assembly for the largemouth bass <i>Micropterus salmoides</i> provides insights into adaptation to fresh and brackish water. Molecular Ecology Resources, 2021, 21, 301-315.	4.8	42
25	Construction of high-density genetic linkage maps for orange-spotted grouper Epinephelus coioidesusing multiplexed shotgun genotyping. BMC Genetics, 2013, 14, 113.	2.7	39
26	Draft genome of the lined seahorse, Hippocampus erectus. GigaScience, 2017, 6, 1-6.	6.4	38
27	Comparative Transcriptomic Study of Muscle Provides New Insights into the Growth Superiority of a Novel Grouper Hybrid. PLoS ONE, 2016, 11, e0168802.	2.5	38
28	Draft genomes of two Atlantic bay scallop subspecies Argopecten irradians irradians and A. i. concentricus. Scientific Data, 2020, 7, 99.	5.3	37
29	Draft Genome and Complete Hox-Cluster Characterization of the Sterlet (Acipenser ruthenus). Frontiers in Genetics, 2019, 10, 776.	2.3	34
30	Construction of high-density genetic linkage maps and QTL mapping in the golden pompano. Aquaculture, 2018, 482, 90-95.	3.5	32
31	Genome-Wide Mapping of Growth-Related Quantitative Trait Loci in Orange-Spotted Grouper (Epinephelus coioides) Using Double Digest Restriction-Site Associated DNA Sequencing (ddRADseq). International Journal of Molecular Sciences, 2016, 17, 501.	4.1	31
32	A chromosome-level genome assembly of the oriental river prawn, <i>Macrobrachium nipponense</i> . GigaScience, 2021, 10, .	6.4	28
33	Construction of the High-Density Genetic Linkage Map and Chromosome Map of Large Yellow Croaker (Larimichthys crocea). International Journal of Molecular Sciences, 2015, 16, 26237-26248.	4.1	27
34	From Marine Venoms to Drugs: Efficiently Supported by a Combination of Transcriptomics and Proteomics. Marine Drugs, 2017, 15, 103.	4.6	27
35	High-Throughput Identification of Antimicrobial Peptides from Amphibious Mudskippers. Marine Drugs, 2017, 15, 364.	4.6	26
36	Genome and population sequencing of a chromosome-level genome assembly of the Chinese tapertail anchovy (Coilia nasus) provides novel insights into migratory adaptation. GigaScience, 2020, 9, .	6.4	26

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37	Whole genome sequencing of a snailfish from the Yap Trench (~7,000 m) clarifies the molecular mechanisms underlying adaptation to the deep sea. PLoS Genetics, 2021, 17, e1009530.	3.5	26
38	Whole Genome Sequencing of the Giant Grouper (Epinephelus lanceolatus) and High-Throughput Screening of Putative Antimicrobial Peptide Genes. Marine Drugs, 2019, 17, 503.	4.6	25
39	Identification and characterization of lipid metabolism-related microRNAs in the liver of genetically improved farmed tilapia (GIFT, Oreochromis niloticus) by deep sequencing. Fish and Shellfish Immunology, 2017, 69, 227-235.	3.6	24
40	Genome resequencing of the orange-spotted grouper (Epinephelus coioides) for a genome-wide association study on ammonia tolerance. Aquaculture, 2019, 512, 734332.	3.5	24
41	Deciphering the Microbial Taxonomy and Functionality of Two Diverse Mangrove Ecosystems and Their Potential Abilities To Produce Bioactive Compounds. MSystems, 2020, 5, .	3.8	23
42	Molecular Evolution of Aralkylamine N-Acetyltransferase in Fish: A Genomic Survey. International Journal of Molecular Sciences, 2016, 17, 51.	4.1	22
43	Mudskippers and Their Genetic Adaptations to an Amphibious Lifestyle. Animals, 2018, 8, 24.	2.3	22
44	Whole Genome Sequencing of the Blue Tilapia (Oreochromis aureus) Provides a Valuable Genetic Resource for Biomedical Research on Tilapias. Marine Drugs, 2019, 17, 386.	4.6	22
45	Divergence, evolution and adaptation in ray-finned fish genomes. Science China Life Sciences, 2019, 62, 1003-1018.	4.9	22
46	Comparative Transcriptomic Studies on a Cadmium Hyperaccumulator Viola baoshanensis and Its Non-Tolerant Counterpart V. inconspicua. International Journal of Molecular Sciences, 2019, 20, 1906.	4.1	22
47	High Throughput Identification of Antimicrobial Peptides from Fish Gastrointestinal Microbiota. Toxins, 2017, 9, 266.	3.4	21
48	High Throughput Identification of Novel Conotoxins from the Vermivorous Oak Cone Snail (Conus) Tj ETQq0 0	0 rgβŢ /Ov 4.1	erlock 10 Tf 5
49	Transcriptomic evidence of adaptive tolerance to high environmental ammonia in mudskippers. Genomics, 2018, 110, 404-413.	2.9	21
50	High-Throughput Identification of Putative Antimicrobial Peptides from Multi-Omics Data of the Lined Seahorse (Hippocampus erectus). Marine Drugs, 2020, 18, 30.	4.6	19
51	Genome-wide association improves genomic selection for ammonia tolerance in the orange-spotted grouper (Epinephelus coioides). Aquaculture, 2021, 533, 736214.	3.5	19
52	De novo assembly and comparative transcriptome analysis of the foot from Chinese green mussel (Perna viridis) in response to cadmium stimulation. PLoS ONE, 2017, 12, e0176677.	2.5	18
53	Mitochondrial genome sequencing of a vermivorous cone snail Conus quercinus supports the correlative analysis between phylogenetic relationships and dietary types of Conus species. PLoS ONE, 2018, 13, e0193053	2.5	18

54High-Throughput Identification and Analysis of Novel Conotoxins from Three Vermivorous Cone4.61854Snails by Transcriptome Sequencing. Marine Drugs, 2019, 17, 193.4.618

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55	A chromosome-level genome assembly of the striped catfish (Pangasianodon hypophthalmus). Genomics, 2021, 113, 3349-3356.	2.9	18
56	Whole-Genome Sequencing of the Giant Devil Catfish, Bagarius yarrelli. Genome Biology and Evolution, 2019, 11, 2071-2077.	2.5	17
57	Dynamic genetic differentiation drives the widespread structural and functional convergent evolution of snake venom proteinaceous toxins. BMC Biology, 2022, 20, 4.	3.8	17
58	Screening and Validation of Highly-Efficient Insecticidal Conotoxins from a Transcriptome-Based Dataset of Chinese Tubular Cone Snail. Toxins, 2017, 9, 214.	3.4	16
59	A comparative transcriptomic study on developmental gonads provides novel insights into sex change in the protandrous black porgy (Acanthopagrus schlegelii). Genomics, 2019, 111, 277-283.	2.9	16
60	Comparative Genomics Studies on the dmrt Gene Family in Fish. Frontiers in Genetics, 2020, 11, 563947.	2.3	16
61	The first Conus genome assembly reveals a primary genetic central dogma of conopeptides in C. betulinus. Cell Discovery, 2021, 7, 11.	6.7	16
62	Phylogenetic Analysis of Core Melanin Synthesis Genes Provides Novel Insights Into the Molecular Basis of Albinism in Fish. Frontiers in Genetics, 2021, 12, 707228.	2.3	16
63	Whole genome sequencing of Chinese clearhead icefish, Protosalanx hyalocranius. GigaScience, 2017, 6, 1-6.	6.4	15
64	A Genomic Survey of Angiotensin-Converting Enzymes Provides Novel Insights into Their Molecular Evolution in Vertebrates. Molecules, 2018, 23, 2923.	3.8	15
65	Genome Assembly for a Yunnan-Guizhou Plateau "3E―Fish, Anabarilius grahami (Regan), and Its Evolutionary and Genetic Applications. Frontiers in Genetics, 2018, 9, 614.	2.3	15
66	Molecular responses of an estuarine oyster to multiple metal contamination in Southern China revealed by RNA-seq. Science of the Total Environment, 2020, 701, 134648.	8.0	15
67	Melatonin is Involved in Sex Change of the Ricefield Eel, Monopterus albus Zuiew. Reviews in Fish Biology and Fisheries, 2005, 15, 23-36.	4.9	14
68	Prediction of Toxin Genes from Chinese Yellow Catfish Based on Transcriptomic and Proteomic Sequencing. International Journal of Molecular Sciences, 2016, 17, 556.	4.1	14
69	A Genomic Survey of SCPP Family Genes in Fishes Provides Novel Insights into the Evolution of Fish Scales. International Journal of Molecular Sciences, 2017, 18, 2432.	4.1	14
70	Identification of Candidate Genes for the Plateau Adaptation of a Tibetan Amphipod, Gammarus lacustris, Through Integration of Genome and Transcriptome Sequencing. Frontiers in Genetics, 2019, 10, 53.	2.3	14
71	A chromosome-level genome assembly of the Asian arowana, Scleropages formosus. Scientific Data, 2016, 3, 160105.	5.3	13
72	Transcriptomic Characterization of the South American Freshwater Stingray Potamotrygon motoro Venom Apparatus. Toxins, 2018, 10, 544.	3.4	13

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73	Whole-Genome Sequencing of Chinese Yellow Catfish Provides a Valuable Genetic Resource for High-Throughput Identification of Toxin Genes. Toxins, 2018, 10, 488.	3.4	13
74	The complete mitochondrial genome of the intertidal spider (Desis jiaxiangi) provides novel insights into the adaptive evolution of the mitogenome and the evolution of spiders. Bmc Ecology and Evolution, 2021, 21, 72.	1.6	13
75	A Comparative Genomic and Transcriptomic Survey Provides Novel Insights into N-Acetylserotonin Methyltransferase (ASMT) in Fish. Molecules, 2017, 22, 1653.	3.8	12
76	High Throughput Identification of Antihypertensive Peptides from Fish Proteome Datasets. Marine Drugs, 2018, 16, 365.	4.6	12
77	The Complete Mitochondrial Genome of Glyptothorax macromaculatus Provides a Well-Resolved Molecular Phylogeny of the Chinese Sisorid Catfishes. Genes, 2018, 9, 282.	2.4	12
78	Whole Genome Sequencing of Chinese White Dolphin (Sousa chinensis) for High-Throughput Screening of Antihypertensive Peptides. Marine Drugs, 2019, 17, 504.	4.6	12
79	Molecular Evolution of Tryptophan Hydroxylases in Vertebrates: A Comparative Genomic Survey. Genes, 2019, 10, 203.	2.4	12
80	Toll protein family structure, evolution and response of the whiteleg shrimp (<i>Litopenaeusvannamei</i>) to exogenous iridescent virus. Journal of Fish Diseases, 2021, 44, 1131-1145.	1.9	11
81	Identification and characterization of a novel defensin from Asian green mussel Perna viridis. Fish and Shellfish Immunology, 2018, 74, 242-249.	3.6	10
82	An SNP-Based Genetic Map and QTL Mapping for Growth Traits in the Red-Spotted Grouper (Epinephelus) Tj ETQ)q0.0.0 rgE 2.4	3T /Overlock
83	Genome Sequencing of the Japanese Eel (Anguilla japonica) for Comparative Genomic Studies on tbx4 and a tbx4 Gene Cluster in Teleost Fishes. Marine Drugs, 2019, 17, 426.	4.6	9
84	Molecular cloning of two kcnk3 genes from the Northern snakehead (Channa argus) for quantification of their transcriptions in response to fasting and refeeding. General and Comparative Endocrinology, 2019, 281, 49-57.	1.8	9
85	The First Genome Survey of the Antarctic Krill (Euphausia superba) Provides a Valuable Genetic Resource for Polar Biomedical Research. Marine Drugs, 2020, 18, 185.	4.6	9
86	Construction of a chromosome-level genome assembly for genome-wide identification of growth-related quantitative trait loci in <i>Sinocyclocheilus grahami</i> (Cypriniformes,) Tj ETQq0 0 C) rg £,∏ /Ov€	erloxck 10 Tf 5
87	Transcriptome sequencing of the gill and barbel of Southern catfish (Silurus meridionalis) revealed immune responses and novel rhamnose-binding lectins (RBLs). Genomics, 2019, 111, 222-230.	2.9	8
88	Characterization of two kcnk3 genes in Nile tilapia (Oreochromis niloticus): Molecular cloning, tissue distribution, and transcriptional changes in various salinity of seawater. Genomics, 2020, 112, 2213-2222.	2.9	8
89	Characterization of five caspase genes and their transcriptional changes in response to exogenous iridescent virus challenge in the whiteleg shrimp (Litopenaeus vannamei). Aquaculture, 2021, 534, 736192.	3.5	8

⁹⁰A Chromosome-Level Genome Assembly of the Mandarin Fish (Siniperca chuatsi). Frontiers in Genetics,
2021, 12, 671650.2.38

#	Article	IF	CITATIONS
91	Putative Antimicrobial Peptides in Fish: Using Zebrafish as a Representative. Protein and Peptide Letters, 2020, 27, 1059-1067.	0.9	8

Pathogen of Vibrio harveyi infection and C-type lectin proteins in whiteleg shrimp (Litopenaeus) Tj ETQq0 0 0 rgBT (Overlock 10 Tf 50 70

93	A Comparative Genomic Survey Provides Novel Insights into Molecular Evolution of l-Aromatic Amino Acid Decarboxylase in Vertebrates. Molecules, 2018, 23, 917.	3.8	7
94	High-throughput identification of heavy metal binding proteins from the byssus of chinese green mussel (Perna viridis) by combination of transcriptome and proteome sequencing. PLoS ONE, 2019, 14, e0216605.	2.5	7
95	China is initiating the Aquatic 10-100-1,000 Genomics Program. Science China Life Sciences, 2017, 60, 329-332.	4.9	6
96	A Comparative Metagenomics Study on Gastrointestinal Microbiota in Amphibious Mudskippers and Other Vertebrate Animals. Animals, 2019, 9, 660.	2.3	6
97	Comparative transcriptome analyses of venom glands from three scorpionfishes. Genomics, 2019, 111, 231-241.	2.9	6
98	A Comparative Genomics Study on the Molecular Evolution of Serotonin/Melatonin Biosynthesizing Enzymes in Vertebrates. Frontiers in Molecular Biosciences, 2020, 7, 11.	3.5	6
99	Genome-wide identification of a novel elovl4 gene and its transcription in response to nutritional and osmotic regulations in rabbitfish (Siganus canaliculatus). Aquaculture, 2020, 529, 735666.	3.5	6
100	Temporal dynamics of teleost populations during the Pleistocene: a report from publicly available genome data. BMC Genomics, 2021, 22, 490.	2.8	6
101	The complete mitochondrial genome sequence of a cavefish <i>Sinocyclocheilus anshuiensis</i> (Cypriniformes: Cyprinidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4256-4258.	0.7	5
102	A Transcriptomic Survey of Ion Channel-Based Conotoxins in the Chinese Tubular Cone Snail (Conus) Tj ETQq0 0	0 rgBT /O 4:6	verlock 10 T
103	Assessing the genetic diversity of the critically endangered Chinese sturgeon Acipenser sinensis using mitochondrial markers and genome-wide single-nucleotide polymorphisms from RAD-seq. Science China Life Sciences, 2018, 61, 1090-1098.	4.9	5
104	Characterization of two kcnk3 genes in rabbitfish (Siganus canaliculatus): Molecular cloning, distribution patterns and their potential roles in fatty acids metabolism and osmoregulation. General and Comparative Endocrinology, 2020, 296, 113546.	1.8	5
105	Genome and Transcriptome Sequencing of casper and roy Zebrafish Mutants Provides Novel Genetic Clues for Iridophore Loss. International Journal of Molecular Sciences, 2020, 21, 2385.	4.1	5

106	Complete Genome Sequence of a Marine Bacterium, Pseudomonas pseudoalcaligenes Strain S1, with High Mercury Resistance and Bioaccumulation Capacity. Genome Announcements, 2016, 4, .	0.8	4
107	Insights into Body Size Evolution: A Comparative Transcriptome Study on Three Species of Asian Sisoridae Catfish. International Journal of Molecular Sciences, 2019, 20, 944.	4.1	4

¹⁰⁸High throughput screening of small immune peptides and antimicrobial peptides from the Fish-T1K
database. Genomics, 2019, 111, 215-221.2.94

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109	Molecular evolution of melatonin receptor genes (mtnr) in vertebrates and its shedding light on mtnr1c. Gene, 2021, 769, 145256.	2.2	4
110	Genome-wide identification and characterization of 14-3-3 genes in fishes. Gene, 2021, 791, 145721.	2.2	4
111	Special issue on fish transcriptomics. Genomics, 2019, 111, 213-214.	2.9	3
112	Comprehensive Transcriptional Changes in the Liver of Kanglang White Minnow (Anabarilius grahami) in Response to the Infection of Parasite Ichthyophthirius multifiliis. Animals, 2020, 10, 681.	2.3	3
113	Spider Silks: An Overview of Their Component Proteins for Hydrophobicity and Biomedical Applications. Protein and Peptide Letters, 2021, 28, 255-269.	0.9	3
114	A chromosome-level genome assembly of the jade perch (Scortum barcoo). Scientific Data, 2022, 9, .	5.3	3
115	The complete mitochondrial genome sequence of the giant mudskipper, Periophthalmodon schlosseri (Perciformes: gobiidae). Mitochondrial DNA Part B: Resources, 2016, 1, 599-600.	0.4	2
116	A genomic survey on the immune differences among <i>Sinocyclocheilus</i> fishes. Communicative and Integrative Biology, 2016, 9, e1255833.	1.4	2
117	The complete mitochondrial genome of horned Golden-line barbell, Sinocyclocheilus rhinocerous (Cypriniformes, Cyprinidae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 269-270.	0.7	2
118	Whole-Genome Sequencing of Sinocyclocheilus maitianheensis Reveals Phylogenetic Evolution and Immunological Variances in Various Sinocyclocheilus Fishes. Frontiers in Genetics, 2021, 12, 736500.	2.3	2
119	The complete mitochondrial genome of Florida gar (<i>Lepisosteus platyrhincus</i>). Mitochondrial DNA Part B: Resources, 2016, 1, 128-129.	0.4	1
120	The complete mitochondrial genome of Eastern paradise fish (Polynemus dubius). Mitochondrial DNA Part B: Resources, 2016, 1, 132-133.	0.4	1
121	Draft Genome of the Mirrorwing Flyingfish (Hirundichthys speculiger). Frontiers in Genetics, 2021, 12, 695700.	2.3	1
122	Homeostasis Regulation by Potassium Channel Subfamily K Member 3 (KCNK3) in Various Fishes. Frontiers in Marine Science, 2021, 8, .	2.5	1
123	Evolutionary Genomics Reveals Multiple Functions of Arylalkylamine N-Acetyltransferase in Fish. Frontiers in Genetics, 2022, 13, .	2.3	1
124	The complete mitochondrial genome of the yellow-spotted triggerfish (Pseudobalistes fuscus). Mitochondrial DNA Part B: Resources, 2016, 1, 558-559.	0.4	0
125	A new species of bandy-bandy (Vermicella: Serpentes: Elapidae) from the Weipa region, Cape York, Australia. Zootaxa, 2018, 4446, 1.	0.5	0
126	Whole-Genome Sequencing and Genome-Wide Studies of Spiny Head Croaker (Collichthys lucidus) Reveals Potential Insights for Well-Developed Otoliths in the Family Sciaenidae. Frontiers in Genetics, 2021, 12, 730255.	2.3	0

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127	High-Throughput Identification of Antihypertensive Peptides (AHTPs) and Characterization of AHTP-Derived Genes in the Lined Seahorse (Hippocampus erectus). Frontiers in Marine Science, 0, 9, .	2.5	Ο