

# Jian Xu

## List of Publications by Year in descending order

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46  
papers

1,903  
citations

471509

17  
h-index

265206

42  
g-index

51  
all docs

51  
docs citations

51  
times ranked

1833  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence and genetic diversity of the common carp, <i>Cyprinus carpio</i> . <i>Nature Genetics</i> , 2014, 46, 1212-1219.	21.4	576
2	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
3	Development and evaluation of the first high-throughput SNP array for common carp ( <i>Cyprinus</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 135	2.8	135
4	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
5	Characterization of Common Carp Transcriptome: Sequencing, De Novo Assembly, Annotation and Comparative Genomics. <i>PLoS ONE</i> , 2012, 7, e35152.	2.5	121
6	Comparative Transcriptome Analysis Reveals the Genetic Basis of Skin Color Variation in Common Carp. <i>PLoS ONE</i> , 2014, 9, e108200.	2.5	89
7	Genome-Wide SNP Discovery from Transcriptome of Four Common Carp Strains. <i>PLoS ONE</i> , 2012, 7, e48140.	2.5	73
8	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
9	From asymmetrical to balanced genomic diversification during rediploidization: Subgenomic evolution in allotetraploid fish. <i>Science Advances</i> , 2020, 6, eaaz7677.	10.3	59
10	Transcriptome Sequencing and Analysis of Wild Amur Ide ( <i>Leuciscus waleckii</i> ) Inhabiting an Extreme Alkaline-Saline Lake Reveals Insights into Stress Adaptation. <i>PLoS ONE</i> , 2013, 8, e59703.	2.5	51
11	Draft genome of the Northern snakehead, <i>Channa argus</i> . <i>GigaScience</i> , 2017, 6, 1-5.	6.4	45
12	Identification of Novel Immunogenic Proteins from <i>Mycoplasma bovis</i> and Establishment of an Indirect ELISA Based on Recombinant E1 Beta Subunit of the Pyruvate Dehydrogenase Complex. <i>PLoS ONE</i> , 2014, 9, e88328.	2.5	38
13	Gene expression changes leading extreme alkaline tolerance in Amur ide ( <i>Leuciscus waleckii</i> ) inhabiting soda lake. <i>BMC Genomics</i> , 2013, 14, 682.	2.8	36
14	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
15	Genome Wide Identification, Phylogeny, and Expression of Aquaporin Genes in Common Carp ( <i>Cyprinus</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 135	2.5	27
16	Research advances and future perspectives of genomics and genetic improvement in allotetraploid common carp. <i>Reviews in Aquaculture</i> , 2022, 14, 957-978.	9.0	23
17	Phylogeny and Evolution of Multiple Common Carp ( <i>Cyprinus carpio</i> L.) Populations Clarified by Phylogenetic Analysis Based on Complete Mitochondrial Genomes. <i>Marine Biotechnology</i> , 2015, 17, 565-575.	2.4	22
18	Genomic, Transcriptomic, and Epigenomic Features Differentiate Genes That Are Relevant for Muscular Polyunsaturated Fatty Acids in the Common Carp. <i>Frontiers in Genetics</i> , 2019, 10, 217.	2.3	20

#	ARTICLE	IF	CITATIONS
19	Complete mitochondrial genome of <i>Leuciscus waleckii</i> (Cypriniformes: Cyprinidae: Leuciscus). Mitochondrial DNA, 2013, 24, 126-128.	0.6	18
20	Adaptive evolution of low-salinity tolerance and hypoosmotic regulation in a euryhaline teleost, <i>Takifugu obscurus</i> . Marine Biology, 2020, 167, 1.	1.5	16
21	Transcriptional differences provide insight into environmental acclimatization in wild amur ide ( <i>Leuciscus waleckii</i> ) during spawning migration from alkalized lake to freshwater river. Genomics, 2019, 111, 267-276.	2.9	15
22	Transcriptional Profiling Reveals Differential Gene Expression of Amur Ide ( <i>Leuciscus waleckii</i> ) during Spawning Migration. International Journal of Molecular Sciences, 2015, 16, 13959-13972.	4.1	13
23	Construction of the BAC Library of Small Abalone ( <i>Haliotis diversicolor</i> ) for Gene Screening and Genome Characterization. Marine Biotechnology, 2016, 18, 49-56.	2.4	13
24	Phylogenetic and Evolutionary Analyses of the Frizzled Gene Family in Common Carp ( <i>Cyprinus carpio</i> ) Provide Insights into Gene Expansion from Whole-Genome Duplications. PLoS ONE, 2015, 10, e0144037.	2.5	12
25	Comparative transcriptome analysis between aquatic and aerial breathing organs of <i>Channa argus</i> to reveal the genetic basis underlying bimodal respiration. Marine Genomics, 2016, 29, 89-96.	1.1	12
26	Patterns of Geographical and Potential Adaptive Divergence in the Genome of the Common Carp ( <i>Cyprinus carpio</i> ). Frontiers in Genetics, 2019, 10, 660.	2.3	12
27	A Drive to Driven Model of Mapping Intraspecific Interaction Networks. IScience, 2019, 22, 109-122.	4.1	11
28	Genomics in the common carp. , 2016, , 247-274.		9
29	Development and evaluation of a high-throughput single nucleotide polymorphism multiplex assay for assigning pedigrees in common carp. Aquaculture Research, 2017, 48, 1866-1876.	1.8	9
30	Duplication and differentiation of common carp ( <i>Cyprinus carpio</i> ) myoglobin genes revealed by BAC analysis. Gene, 2014, 548, 210-216.	2.2	8
31	The complete mitochondrial genome of <i>Cobitis lutheri</i> (Cypriniformes: Cobitidae: Cobitis). Mitochondrial DNA, 2015, 26, 875-876.	0.6	8
32	Complete mitochondrial genome of Northern Sheatfish ( <i>Silurus soldatovi</i> ). Mitochondrial DNA, 2015, 26, 891-892.	0.6	7
33	Performance of genome prediction for morphological and growth-related traits in Yellow River carp. Aquaculture, 2021, 536, 736463.	3.5	7
34	Population genetic analysis of aquaculture salmonid populations in China using a 57K rainbow trout SNP array. PLoS ONE, 2018, 13, e0202582.	2.5	6
35	Genomic features of common carp that are relevant for resistance against <i>Aeromonas hydrophila</i> infection. Aquaculture, 2022, 547, 737512.	3.5	6
36	Genomic Analysis of Glutathione S-transferases (GST) Family in Common Carp: Identification, Phylogeny and Expression. Pakistan Journal of Zoology, 2017, 49, 1437-1448.	0.2	5

#	ARTICLE	IF	CITATIONS
37	Genome-wide association study and gene editing reveals the causal gene responsible for abnormal red skin color in Yellow River carp. <i>Aquaculture</i> , 2022, 560, 738530.	3.5	5
38	Transcriptomic analysis reveals the genes involved in tetrodotoxin (TTX) accumulation, translocation, and detoxification in the pufferfish <i>Takifugu rubripes</i> . <i>Chemosphere</i> , 2022, , 134962.	8.2	4
39	Transcriptome Analysis Reveals Molecular Underpinnings of Common Carp ( <i>Cyprinus carpio</i> ) Under Hypoxia Stress. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	4
40	Genome-wide identification of endosialin family of C-type lectins in common carp ( <i>Cyprinus carpio</i> ) and their response following <i>Aeromonas hydrophila</i> infection. <i>Developmental and Comparative Immunology</i> , 2022, 129, 104338.	2.3	3
41	Complete mitochondrial genome of <i>Sarcocheilichthys lacustris</i> (Cypriniformes, Cyprinidae). <i>Mitochondrial DNA</i> , 2015, 26, 765-766.	0.6	2
42	The complete mitochondrial genome of Russian sturgeon ( <i>Acipenser gueldenstaedti</i> ). <i>Mitochondrial DNA</i> , 2016, 27, 986-987.	0.6	2
43	Complete mitochondrial genome of yellowfin goby ( <i>Acanthogobius hasta</i> ). <i>Mitochondrial DNA</i> , 2016, 27, 1231-1232.	0.6	1
44	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
45	Diversification of the duplicated Rab1a genes in a hypoxia-tolerant fish, common carp ( <i>Cyprinus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 54-62.	1.6	0
46	The complete mitochondrial genome of <i>Channa marulius</i> (Perciformes: Channidae: Channa). <i>Mitochondrial DNA</i> , 2016, 27, 1148-1149.	0.6	0