

# Jianguo Lu

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

2,094  
citations

279798

23  
h-index

243625

44  
g-index

53  
all docs

53  
docs citations

53  
times ranked

3245  
citing authors

#	ARTICLE	IF	CITATIONS
1	Geographic Scale Influences the Interactivities Between Determinism and Stochasticity in the Assembly of Sedimentary Microbial Communities on the South China Sea Shelf. <i>Microbial Ecology</i> , 2023, 85, 121-136.	2.8	5
2	Modeling thermal conductivity of soils during a freezing process. <i>Heat and Mass Transfer</i> , 2022, 58, 283-293.	2.1	14
3	Identification of pigment genes (melanin, carotenoid and pteridine) associated with skin color variant in red tilapia using transcriptome analysis. <i>Aquaculture</i> , 2022, 547, 737429.	3.5	27
4	Bacterial, archaeal, and fungal community structure and interrelationships of deep-sea shrimp intestine and the surrounding sediment. <i>Environmental Research</i> , 2022, 205, 112461.	7.5	5
5	Hydro-thermal characteristics and deformation behaviors of silty clay subjected to freeze-thaw cycles. <i>Arabian Journal of Geosciences</i> , 2022, 15, 1.	1.3	4
6	Chromosome-level Genome Assembly of <i>Acanthopagrus latus</i> Provides Insights into Salinity Stress Adaptation of Sparidae. <i>Marine Biotechnology</i> , 2022, 24, 655-660.	2.4	2
7	Gene expression profiles provide insights into the survival strategies in deep-sea mussel ( <i>Bathymodiolus platifrons</i> ) of different developmental stages. <i>BMC Genomics</i> , 2022, 23, 311.	2.8	2
8	A time-course transcriptome analysis of gonads from yellow catfish ( <i>Pelteobagrus fulvidraco</i> ) reveals genes associated with gonad development. <i>BMC Genomics</i> , 2022, 23, .	2.8	3
9	Transcriptome Profiling Reveals the Sexual Dimorphism of Gene Expression Patterns during Gonad Differentiation in the Half-Smooth Tongue Sole ( <i>Cynoglossus semilaevis</i> ). <i>Marine Biotechnology</i> , 2021, 23, 18-30.	2.4	17
10	The application of genome editing technology in fish. <i>Marine Life Science and Technology</i> , 2021, 3, 326-346.	4.6	9
11	Geochemical and microbial insights into vertical distributions of genetic potential of N-cycling processes in deep-sea sediments. <i>Ecological Indicators</i> , 2021, 125, 107461.	6.3	9
12	Hypoosmotic stress induced functional alternations of intestinal barrier integrity, inflammatory reactions, and neurotransmission along gut-brain axis in the yellowfin seabream ( <i>Acanthopagrus latus</i> ). <i>Journal of Experimental Biology</i> , 2021, 244, 197-207.	10.0	10
13	Comparative Genome Analysis of <i>Bacillus amyloliquefaciens</i> Focusing on Phylogenomics, Functional Traits, and Prevalence of Antimicrobial and Virulence Genes. <i>Frontiers in Genetics</i> , 2021, 12, 724217.	2.3	4
14	Seasonal variations in soil physicochemical properties and microbial community structure influenced by <i>Spartina alterniflora</i> invasion and <i>Kandelia obovata</i> restoration. <i>Science of the Total Environment</i> , 2021, 797, 149213.	8.0	25
15	Characterization of tissue-associated bacterial community of two <i>Bathymodiolus</i> species from the adjacent cold seep and hydrothermal vent environments. <i>Science of the Total Environment</i> , 2021, 796, 149046.	8.0	7
16	Construction of High-Density Genetic Map and Mapping of Sex-Related Loci in the Yellow Catfish ( <i>Pelteobagrus fulvidraco</i> ). <i>Marine Biotechnology</i> , 2020, 22, 31-40.	2.4	8
17	Gonadal Transcriptome Analysis of Sex-Related Genes in the Protandrous Yellowfin Seabream ( <i>Acanthopagrus latus</i> ). <i>Frontiers in Genetics</i> , 2020, 11, 709.	2.3	14
18	Response of gut microbiota and immune function to hypoosmotic stress in the yellowfin seabream ( <i>Acanthopagrus latus</i> ). <i>Science of the Total Environment</i> , 2020, 745, 140976.	8.0	23

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19	Identification and Comparison of microRNAs in the Gonad of the Yellowfin Seabream ( <i>Acanthopagrus</i> ) Tj ETQq1 1 0.784314 rgBT /Over	4.1	19
20	Hypoosmotic stress induced tissue-specific immune responses of yellowfin seabream ( <i>Acanthopagrus</i> ) Tj ETQq0 0 0.784314 rgBT /Over	3.6	27
21	Dysbiosis of gut microbiota by dietary exposure of three graphene-family materials in zebrafish ( <i>Danio</i> ) Tj ETQq1 1 0.784314 rgBT /Over	7.5	51
22	Individual and combined effects of ammonia-N and sulfide on the immune function and intestinal microbiota of Pacific white shrimp <i>Litopenaeus vannamei</i> . <i>Fish and Shellfish Immunology</i> , 2019, 92, 230-240.	3.6	31
23	Evaluation of calculation models for the unfrozen water content of freezing soils. <i>Journal of Hydrology</i> , 2019, 575, 976-985.	5.4	39
24	Fitting methods and seasonality effects on the assessment of pelagic fish communities in Daya Bay, China. <i>Ecological Indicators</i> , 2019, 103, 346-354.	6.3	4
25	Effects of starch-coating of magnetite nanoparticles on cellular uptake, toxicity and gene expression profiles in adult zebrafish. <i>Science of the Total Environment</i> , 2018, 622-623, 930-941.	8.0	40
26	Toxicity and Transcriptome Sequencing (RNA-seq) Analyses of Adult Zebrafish in Response to Exposure Carboxymethyl Cellulose Stabilized Iron Sulfide Nanoparticles. <i>Scientific Reports</i> , 2018, 8, 8083.	3.3	44
27	Sexually Dimorphic Gene Expression Associated with Growth and Reproduction of Tongue Sole ( <i>Cynoglossus semilaevis</i> ) Revealed by Brain Transcriptome Analysis. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1402.	4.1	15
28	The channel catfish genome sequence provides insights into the evolution of scale formation in teleosts. <i>Nature Communications</i> , 2016, 7, 11757.	12.8	231
29	Joint detection of copy number variations in parent-offspring trios. <i>Bioinformatics</i> , 2016, 32, 1130-1137.	4.1	18
30	Complete mitochondrial genome of the <i>Triplophysa bombifrons</i> and <i>Triplophysa strauchii</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4710-4711.	0.7	2
31	Complete mitochondrial genome of the <i>Lampetra japonica</i> . <i>Mitochondrial DNA</i> , 2016, 27, 1293-1294.	0.6	0
32	Mitochondrial DNA sequence of <i>Lampetra morri</i> . <i>Mitochondrial DNA</i> , 2016, 27, 1391-1392.	0.6	1
33	Complete mitochondrial genome of the <i>Lampetra reissneri</i> . <i>Mitochondrial DNA</i> , 2016, 27, 1395-1396.	0.6	2
34	ALLMAPS: robust scaffold ordering based on multiple maps. <i>Genome Biology</i> , 2015, 16, 3.	8.8	340
35	Transcriptomic Analyses Reveal Novel Genes with Sexually Dimorphic Expression in Yellow Catfish ( <i>Pelteobagrus fulvidraco</i> ) Brain. <i>Marine Biotechnology</i> , 2015, 17, 613-623.	2.4	27
36	Gonadal transcriptomic analysis of yellow catfish ( <i>Pelteobagrus fulvidraco</i> ): identification of sex-related genes and genetic markers. <i>Physiological Genomics</i> , 2014, 46, 798-807.	2.3	46

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37	Comparative genomic analysis of catfish linkage group 8 reveals two homologous chromosomes in zebrafish and other teleosts with extensive inter-chromosomal rearrangements. <i>BMC Genomics</i> , 2013, 14, 387.	2.8	14
38	Efficient assembly and annotation of the transcriptome of catfish by RNA-Seq analysis of a doubled haploid homozygote. <i>BMC Genomics</i> , 2012, 13, 595.	2.8	109
39	Second-Generation Genetic Linkage Map of Catfish and Its Integration with the BAC-Based Physical Map. <i>C3: Genes, Genomes, Genetics</i> , 2012, 2, 1233-1241.	1.8	41
40	Alternative complement pathway of channel catfish ( <i>Ictalurus punctatus</i> ): Molecular characterization, mapping and expression analysis of factors Bf/C2 and Df. <i>Fish and Shellfish Immunology</i> , 2012, 32, 186-195.	3.6	25
41	RNA-seq analysis of mucosal immune responses reveals signatures of intestinal barrier disruption and pathogen entry following <i>Edwardsiella ictaluri</i> infection in channel catfish, <i>Ictalurus punctatus</i> . <i>Fish and Shellfish Immunology</i> , 2012, 32, 816-827.	3.6	210
42	Profiling of gene duplication patterns of sequenced teleost genomes: evidence for rapid lineage-specific genome expansion mediated by recent tandem duplications. <i>BMC Genomics</i> , 2012, 13, 246.	2.8	100
43	DNA Barcoding of Catfish: Species Authentication and Phylogenetic Assessment. <i>PLoS ONE</i> , 2011, 6, e17812.	2.5	65
44	Molecular responses of calreticulin genes to iron overload and bacterial challenge in channel catfish ( <i>Ictalurus punctatus</i> ). <i>Developmental and Comparative Immunology</i> , 2011, 35, 267-272.	2.3	35
45	Microfibrillar-associated protein 4 (MFAP4) genes in catfish play a novel role in innate immune responses. <i>Developmental and Comparative Immunology</i> , 2011, 35, 568-579.	2.3	47
46	Generation of genome-scale gene-associated SNPs in catfish for the construction of a high-density SNP array. <i>BMC Genomics</i> , 2011, 12, 53.	2.8	122
47	A pilot study for channel catfish whole genome sequencing and de novo assembly. <i>BMC Genomics</i> , 2011, 12, 629.	2.8	25
48	The catfish genome database cBARBEL: an informatic platform for genome biology of ictalurid catfish. <i>Nucleic Acids Research</i> , 2011, 39, D815-D821.	14.5	28
49	Alternative splicing in teleost fish genomes: same-species and cross-species analysis and comparisons. <i>Molecular Genetics and Genomics</i> , 2010, 283, 531-539.	2.1	61
50	Assembly of 500,000 inter-specific catfish expressed sequence tags and large scale gene-associated marker development for whole genome association studies. <i>Genome Biology</i> , 2010, 11, R8.	9.6	83
51	Molecular characterization of complement factor I reveals constitutive expression in channel catfish. <i>Fish and Shellfish Immunology</i> , 2009, 27, 529-534.	3.6	17