

Jianwei Chen

List of Publications by Year in descending order

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33
papers

1,247
citations

566801

15
h-index

414034

32
g-index

41
all docs

41
docs citations

41
times ranked

1582
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity, prevalence, and expression of cyanase genes (<i>cynS</i>) in planktonic marine microorganisms. <i>ISME Journal</i> , 2022, 16, 602-605.	4.4	15
2	A Bacterial Genome and Culture Collection of Gut Microbial in Weanling Piglet. <i>Microbiology Spectrum</i> , 2022, 10, e0241721.	1.2	3
3	A Novel Isolate of Spherical Multicellular Magnetotactic Prokaryotes Has Two Magnetosome Gene Clusters and Synthesizes Both Magnetite and Greigite Crystals. <i>Microorganisms</i> , 2022, 10, 925.	1.6	1
4	The microbial diversity in industrial effluents makes high-throughput sequencing-based source tracking of the effluents possible. <i>Environmental Research</i> , 2022, 212, 113640.	3.7	5
5	Inulin supplementation ameliorates hyperuricemia and modulates gut microbiota in Uox-knockout mice. <i>European Journal of Nutrition</i> , 2021, 60, 2217-2230.	1.8	74
6	Revealing an Invasion Risk of Fish Species in Qingdao Underwater World by Environmental DNA Metabarcoding. <i>Journal of Ocean University of China</i> , 2021, 20, 124-136.	0.6	6
7	Comparison of different sequencing strategies for assembling chromosome-level genomes of extremophiles with variable GC content. <i>IScience</i> , 2021, 24, 102219.	1.9	3
8	Draft Genomes and Comparative Analysis of Seven Mangrove Rhizosphere-Associated Fungi Isolated From <i>Kandelia obovata</i> and <i>Acanthus ilicifolius</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	2
9	Reduced microbial stability in the active layer is associated with carbon loss under alpine permafrost degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	138
10	Metaproteomics reveals nutrient availability shaping distinct microbial community and metabolic niche in the nutrient-depleted and replete layers of an oligotrophic euphotic zone. <i>Science of the Total Environment</i> , 2021, 774, 145123.	3.9	4
11	Thymic T-Cell Production Is Associated With Changes in the Gut Microbiota in Young Chicks. <i>Frontiers in Immunology</i> , 2021, 12, 700603.	2.2	4
12	eDNA metabarcoding as a promising conservation tool for monitoring fish diversity in a coastal wetland of the Pearl River Estuary compared to bottom trawling. <i>Science of the Total Environment</i> , 2020, 702, 134704.	3.9	85
13	Chromosome-Level Comprehensive Genome of Mangrove Sediment-Derived Fungus <i>Penicillium variabile</i> HXQ-H-1. <i>Journal of Fungi (Basel, Switzerland)</i> , 2020, 6, 7.	1.5	6
14	Deciphering the Microbial Taxonomy and Functionality of Two Diverse Mangrove Ecosystems and Their Potential Abilities To Produce Bioactive Compounds. <i>MSystems</i> , 2020, 5, .	1.7	23
15	Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments. <i>GigaScience</i> , 2020, 9, .	3.3	5
16	Interactions of commensal and pathogenic microorganisms with the mucus layer in the colon. <i>Gut Microbes</i> , 2020, 11, 680-690.	4.3	45
17	Fungal Dysbiosis Aggravates Pouchitis in a Rat Model of Ileal Pouch Anal Anastomosis. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 1831-1842.	0.9	2
18	Dynamics of bacteriophages in gut of giant pandas reveal a potential regulation of dietary intake on bacteriophage composition. <i>Science of the Total Environment</i> , 2020, 734, 139424.	3.9	6

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19	MALDI-TOF Characterization of Protein Expression Mutation During Morphological Changes of Bacteria Under the Impact of Antibiotics. <i>Analytical Chemistry</i> , 2019, 91, 2352-2359.	3.2	14
20	Hypothalamus-pituitary-gonad axis transcriptome profiling for sex differentiation in <i>Acipenser sinensis</i> . <i>Scientific Data</i> , 2019, 6, 87.	2.4	12
21	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. <i>Molecular Ecology Resources</i> , 2019, 19, 944-956.	2.2	27
22	A survey of the sperm whale (<i>Physeter catodon</i>) commensal microbiome. <i>PeerJ</i> , 2019, 7, e7257.	0.9	15
23	Dynamics of Gut Microbiome in Giant Panda Cubs Reveal Transitional Microbes and Pathways in Early Life. <i>Frontiers in Microbiology</i> , 2018, 9, 3138.	1.5	30
24	A Microbiota-Derived Bacteriocin Targets the Host to Confer Diarrhea Resistance in Early-Weaned Piglets. <i>Cell Host and Microbe</i> , 2018, 24, 817-832.e8.	5.1	184
25	Population genomic data reveal genes related to important traits of quail. <i>GigaScience</i> , 2018, 7, .	3.3	38
26	The draft genome of blunt snout bream (<i>Megalobrama amblycephala</i>) reveals the development of intermuscular bone and adaptation to herbivorous diet. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	95
27	Gradual Changes of Gut Microbiota in Weaned Miniature Piglets. <i>Frontiers in Microbiology</i> , 2016, 7, 1727.	1.5	164
28	Genetic regulation and manipulation for natural product discovery. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 2953-2965.	1.7	13
29	Degradation Network Reconstruction in Uric Acid and Ammonium Amendments in Oil-Degrading Marine Microcosms Guided by Metagenomic Data. <i>Frontiers in Microbiology</i> , 2015, 6, 1270.	1.5	18
30	Identification and Functional Analysis of Genome Mutations in a Fluoride-Resistant <i>Streptococcus mutans</i> Strain. <i>PLoS ONE</i> , 2015, 10, e0122630.	1.1	52
31	Bacterial population and biodegradation potential in chronically crude oil-contaminated marine sediments are strongly linked to temperature. <i>Scientific Reports</i> , 2015, 5, 11651.	1.6	91
32	Conversion of Uric Acid into Ammonium in Oil-Degrading Marine Microbial Communities: a Possible Role of Halomonads. <i>Microbial Ecology</i> , 2015, 70, 724-740.	1.4	14
33	Complete genome sequence of <i>Bacillus</i> sp. YP1, a polyethylene-degrading bacterium from waxworm's gut. <i>Journal of Biotechnology</i> , 2015, 200, 77-78.	1.9	51