

Xiao-Tao Jiang

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

2,861
citations

304368

22
h-index

433756

31
g-index

32
all docs

32
docs citations

32
times ranked

3473
citing authors

#	ARTICLE	IF	CITATIONS
1	ARGs-OAP v2.0 with an expanded SARG database and Hidden Markov Models for enhancement characterization and quantification of antibiotic resistance genes in environmental metagenomes. <i>Bioinformatics</i> , 2018, 34, 2263-2270.	1.8	375
2	Illumina Sequencing of 16S rRNA Tag Revealed Spatial Variations of Bacterial Communities in a Mangrove Wetland. <i>Microbial Ecology</i> , 2013, 66, 96-104.	1.4	314
3	ARGs-OAP: online analysis pipeline for antibiotic resistance genes detection from metagenomic data using an integrated structured ARG-database. <i>Bioinformatics</i> , 2016, 32, 2346-2351.	1.8	254
4	Catalogue of antibiotic resistome and host-tracking in drinking water deciphered by a large scale survey. <i>Microbiome</i> , 2017, 5, 154.	4.9	215
5	Gut microbiota impact on the peripheral immune response in non-alcoholic fatty liver disease related hepatocellular carcinoma. <i>Nature Communications</i> , 2021, 12, 187.	5.8	209
6	Integrated biogeography of planktonic and sedimentary bacterial communities in the Yangtze River. <i>Microbiome</i> , 2018, 6, 16.	4.9	208
7	Antibiotic-mediated changes in the fecal microbiome of broiler chickens define the incidence of antibiotic resistance genes. <i>Microbiome</i> , 2018, 6, 34.	4.9	185
8	Comammox in drinking water systems. <i>Water Research</i> , 2017, 116, 332-341.	5.3	163
9	BIPES, a cost-effective high-throughput method for assessing microbial diversity. <i>ISME Journal</i> , 2011, 5, 741-749.	4.4	160
10	Antibiotic resistome in a large-scale healthy human gut microbiota deciphered by metagenomic and network analyses. <i>Environmental Microbiology</i> , 2018, 20, 355-368.	1.8	141
11	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. <i>Microbiome</i> , 2015, 3, 20.	4.9	115
12	Metagenomic and Resistome Analysis of a Full-Scale Municipal Wastewater Treatment Plant in Singapore Containing Membrane Bioreactors. <i>Frontiers in Microbiology</i> , 2019, 10, 172.	1.5	58
13	Comparison of microbial diversity determined with the same variable tag sequence extracted from two different PCR amplicons. <i>BMC Microbiology</i> , 2013, 13, 208.	1.3	55
14	MinION Nanopore Sequencing Enables Correlation between Resistome Phenotype and Genotype of Coliform Bacteria in Municipal Sewage. <i>Frontiers in Microbiology</i> , 2017, 8, 2105.	1.5	39
15	Evaluation of a Hybrid Approach Using UBLAST and BLASTX for Metagenomic Sequences Annotation of Specific Functional Genes. <i>PLoS ONE</i> , 2014, 9, e110947.	1.1	36
16	Successional dynamics and alternative stable states in a saline activated sludge microbial community over 9 years. <i>Microbiome</i> , 2021, 9, 199.	4.9	33
17	The bacterial community significantly promotes cast iron corrosion in reclaimed wastewater distribution systems. <i>Microbiome</i> , 2018, 6, 222.	4.9	32
18	Toward an Intensive Longitudinal Understanding of Activated Sludge Bacterial Assembly and Dynamics. <i>Environmental Science & Technology</i> , 2018, 52, 8224-8232.	4.6	32

#	ARTICLE	IF	CITATIONS
19	Population Dynamics of Bulking and Foaming Bacteria in a Full-scale Wastewater Treatment Plant over Five Years. <i>Scientific Reports</i> , 2016, 6, 24180.	1.6	30
20	Temporal dynamics of activated sludge bacterial communities in two diversity variant full-scale sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9379-9388.	1.7	26
21	High-Resolution Temporal and Spatial Patterns of Virome in Wastewater Treatment Systems. <i>Environmental Science & Technology</i> , 2018, 52, 10337-10346.	4.6	25
22	Effects of endocrine disrupting chemicals (EDCs) on bacterial communities in mangrove sediments. <i>Marine Pollution Bulletin</i> , 2017, 122, 122-128.	2.3	23
23	Two-Stage Clustering (TSC): A Pipeline for Selecting Operational Taxonomic Units for the High-Throughput Sequencing of PCR Amplicons. <i>PLoS ONE</i> , 2012, 7, e30230.	1.1	19
24	Passage and community changes of filterable bacteria during microfiltration of a surface water supply. <i>Environment International</i> , 2019, 131, 104998.	4.8	16
25	Cultivation-dependent and high-throughput sequencing approaches studying the co-occurrence of antibiotic resistance genes in municipal sewage system. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 8197-8207.	1.7	11
26	Seasonal Prevalence of Ammonia-Oxidizing Archaea in a Full-Scale Municipal Wastewater Treatment Plant Treating Saline Wastewater Revealed by a 6-Year Time-Series Analysis. <i>Environmental Science & Technology</i> , 2021, 55, 2662-2673.	4.6	11
27	Exploring the Shift in Structure and Function of Microbial Communities Performing Biological Phosphorus Removal. <i>PLoS ONE</i> , 2016, 11, e0161506.	1.1	9
28	Nationwide biogeography and health implications of bacterial communities in household drinking water. <i>Water Research</i> , 2022, 215, 118238.	5.3	7
29	Fecal DNA Virome Is Associated with the Development of Colorectal Neoplasia in a Murine Model of Colorectal Cancer. <i>Pathogens</i> , 2022, 11, 457.	1.2	7
30	Production and Characterization of a Cross-Reactive Monoclonal Antibody to Lipopolysaccharide. <i>Hybridoma</i> , 2009, 28, 93-99.	0.5	3