

Qiong Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11396240/publications.pdf>

Version: 2024-02-01

24
papers

24,875
citations

411340

20
h-index

685536

24
g-index

25
all docs

25
docs citations

25
times ranked

35492
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and Characterization of a Novel Species of Genus Akkermansia with Metabolic Health Effects in a Diet-Induced Obesity Mouse Model. <i>Cells</i> , 2022, 11, 2084.	1.8	5
2	Akkermansia muciniphila Protects Against Psychological Disorder-Induced Gut Microbiota-Mediated Colonic Mucosal Barrier Damage and Aggravation of Colitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 723856.	1.8	34
3	Growth performance, nutrient digestibility, and fecal microbial composition of weaned pigs fed multi-enzyme supplemented diets. <i>Journal of Animal Science</i> , 2020, 98, .	0.2	11
4	Review, Evaluation, and Directions for Gene-Targeted Assembly for Ecological Analyses of Metagenomes. <i>Frontiers in Genetics</i> , 2019, 10, 957.	1.1	8
5	Effect of LSU and ITS genetic markers and reference databases on analyses of fungal communities. <i>Biology and Fertility of Soils</i> , 2019, 55, 79-88.	2.3	33
6	NifH-Harboring Bacterial Community Composition across an Alaskan Permafrost Thaw Gradient. <i>Frontiers in Microbiology</i> , 2016, 7, 1894.	1.5	35
7	Clusters of Antibiotic Resistance Genes Enriched Together Stay Together in Swine Agriculture. <i>MBio</i> , 2016, 7, e02214-15.	1.8	201
8	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
9	Fungal identification using a Bayesian classifier and the Warcup training set of internal transcribed spacer sequences. <i>Mycologia</i> , 2016, 108, 1-5.	0.8	178
10	Xander: employing a novel method for efficient gene-targeted metagenomic assembly. <i>Microbiome</i> , 2015, 3, 32.	4.9	83
11	Hunting Down Frame Shifts: Ecological Analysis of Diverse Functional Gene Sequences. <i>Frontiers in Microbiology</i> , 2015, 6, 1267.	1.5	3
12	Evaluation of the Ion Torrent Personal Genome Machine for Gene-Targeted Studies Using Amplicons of the Nitrogenase Gene <i>nifH</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 4536-4545.	1.4	26
13	Ribosomal Database Project: data and tools for high throughput rRNA analysis. <i>Nucleic Acids Research</i> , 2014, 42, D633-D642.	6.5	3,768
14	Pyrosequencing reveals higher impact of silver nanoparticles than Ag ⁺ on the microbial community structure of activated sludge. <i>Water Research</i> , 2014, 48, 317-325.	5.3	155
15	A gene-targeted approach to investigate the intestinal butyrate-producing bacterial community. <i>Microbiome</i> , 2013, 1, 8.	4.9	129
16	Tropical agricultural land management influences on soil microbial communities through its effect on soil organic carbon. <i>Soil Biology and Biochemistry</i> , 2013, 65, 33-38.	4.2	189
17	Ecological Patterns of <i>nifH</i> Genes in Four Terrestrial Climatic Zones Explored with Targeted Metagenomics Using FrameBot, a New Informatics Tool. <i>MBio</i> , 2013, 4, e00592-13.	1.8	279
18	FunGene: the functional gene pipeline and repository. <i>Frontiers in Microbiology</i> , 2013, 4, 291.	1.5	518

#	ARTICLE	IF	CITATIONS
19	Using the RDP Classifier to Predict Taxonomic Novelty and Reduce the Search Space for Finding Novel Organisms. PLoS ONE, 2012, 7, e32491.	1.1	153
20	Bacterial community comparisons by taxonomy-supervised analysis independent of sequence alignment and clustering. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14637-14642.	3.3	87
21	Bacterial Communities in the Rhizosphere of Biofuel Crops Grown on Marginal Lands as Evaluated by 16S rRNA Gene Pyrosequences. Bioenergy Research, 2010, 3, 20-27.	2.2	40
22	Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. Nucleic Acids Research, 2010, 38, e200-e200.	6.5	808
23	Comparative Analysis of Pyrosequencing and a Phylogenetic Microarray for Exploring Microbial Community Structures in the Human Distal Intestine. PLoS ONE, 2009, 4, e6669.	1.1	719
24	Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. Applied and Environmental Microbiology, 2007, 73, 5261-5267.	1.4	17,125