

Zhe-Xue Quan

List of Publications by Year in descending order

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78
papers

3,699
citations

126907

33
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138484

58
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83
all docs

83
docs citations

83
times ranked

4678
citing authors

#	ARTICLE	IF	CITATIONS
1	The gut microbiome and microbial metabolites in acute myocardial infarction. <i>Journal of Genetics and Genomics</i> , 2022, 49, 569-578.	3.9	11
2	<i>Thalassolituus alkanivorans</i> sp. nov., a hydrocarbon-utilizing bacterium isolated from the Mariana Trench. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	7
3	Abundance and Niche Differentiation of Comammox in the Sludges of Wastewater Treatment Plants That Use the Anaerobic–Anoxic–Aerobic Process. <i>Life</i> , 2022, 12, 954.	2.4	1
4	<i>Methylophaga pinxianii</i> sp. nov., isolated from the Mariana Trench. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	5
5	The complete genome of extracellular protease-producing <i>Deinococcus</i> sp. D7000 isolated from the hadal region of Mariana Trench Challenger Deep. <i>Marine Genomics</i> , 2021, 57, 100832.	1.1	4
6	Abundance and niche specificity of different types of complete ammonia oxidizers (comammox) in salt marshes covered by different plants. <i>Science of the Total Environment</i> , 2021, 768, 144993.	8.0	39
7	Horizontal Gene Transfer of Genes Encoding Copper-Containing Membrane-Bound Monooxygenase (CuMMO) and Soluble Di-iron Monooxygenase (SDIMO) in Ethane- and Propane-Oxidizing <i>Rhodococcus</i> Bacteria. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0022721.	3.1	5
8	Cross-phytgroup assessment of foliar epiphytic mycobiomes. <i>Environmental Microbiology</i> , 2021, 23, 6210-6222.	3.8	4
9	Comparison of Fecal Collection Methods on Variation in Gut Metagenomics and Untargeted Metabolomics. <i>MSphere</i> , 2021, 6, e0063621.	2.9	12
10	Salinity gradients shape the nitrifier community composition in Nanliu River Estuary sediments and the ecophysiology of comammox <i>Nitrospira inopinata</i> . <i>Science of the Total Environment</i> , 2021, 795, 148768.	8.0	22
11	Ammonium promoting methane oxidation by stimulating the Type Ia methane-oxidizing bacteria in tidal flat sediments of the Yangtze River estuary. <i>Science of the Total Environment</i> , 2021, 793, 148470.	8.0	5
12	Archaeal nitrification is constrained by copper complexation with organic matter in municipal wastewater treatment plants. <i>ISME Journal</i> , 2020, 14, 335-346.	9.8	62
13	Dynamics of Skin Mycobiome in Infants. <i>Frontiers in Microbiology</i> , 2020, 11, 1790.	3.5	20
14	Use of Newly Designed Primers for Quantification of Complete Ammonia-Oxidizing (Comammox) Bacterial Clades and Strict Nitrite Oxidizers in the Genus <i>Nitrospira</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	38
15	Temperature and salinity drive comammox community composition in mangrove ecosystems across southeastern China. <i>Science of the Total Environment</i> , 2020, 742, 140456.	8.0	47
16	Design of targeted primers based on 16S rRNA sequences in meta-transcriptomic datasets and identification of a novel taxonomic group in the Asgard archaea. <i>BMC Microbiology</i> , 2020, 20, 25.	3.3	13
17	Age and Mothers: Potent Influences of Children’s Skin Microbiota. <i>Journal of Investigative Dermatology</i> , 2019, 139, 2497-2505.e6.	0.7	46
18	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184

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19	Distribution of comammox and canonical ammonia-oxidizing bacteria in tidal flat sediments of the Yangtze River estuary at different depths over four seasons. <i>Journal of Applied Microbiology</i> , 2019, 127, 533-543.	3.1	33
20	<i>Roseicella frigidaeris</i> gen. nov., sp. nov., isolated from an air-conditioning system. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1384-1389.	1.7	12
21	<i>Rhodophycicola porphyridii</i> gen. nov., sp. nov., isolated from a red alga, <i>Porphyridium marinum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1656-1661.	1.7	19
22	<i>Oceaniradius stylonematis</i> gen. nov., sp. nov., isolated from a red alga, <i>Stylonema cornu-cervi</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1967-1973.	1.7	16
23	Ubiquity and Diversity of Complete Ammonia Oxidizers (Comammox). <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	146
24	Microbial Communities and Diversities in Mudflat Sediments Analyzed Using a Modified Metatranscriptomic Method. <i>Frontiers in Microbiology</i> , 2018, 9, 93.	3.5	20
25	Draft Genome Sequence of <i>n</i> -Alkane-Utilizing <i>Acinetobacter</i> sp. Strain BS1, Isolated from Ethane Oxidation Culture. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
26	A Modified Low-quantity RNA-Seq Method for Microbial Community and Diversity Analysis Using Small Subunit Ribosomal RNA. <i>Bio-protocol</i> , 2018, 8, e2828.	0.4	0
27	Effects of <i>Spartina alterniflora</i> Invasion on the Abundance, Diversity, and Community Structure of Sulfate Reducing Bacteria along a Successional Gradient of Coastal Salt Marshes in China. <i>Wetlands</i> , 2017, 37, 221-232.	1.5	36
28	An improved protocol with a highly degenerate primer targeting copper-containing membrane-bound monooxygenase genes for community analysis of methane- and ammonia-oxidizing bacteria. <i>FEMS Microbiology Ecology</i> , 2017, 93, fiw244.	2.7	35
29	Assessment of molecular detection of anaerobic ammonium-oxidizing (anammox) bacteria in different environmental samples using PCR primers based on 16S rRNA and functional genes. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7689-7702.	3.6	21
30	MIPE: A metagenome-based community structure explorer and SSU primer evaluation tool. <i>PLoS ONE</i> , 2017, 12, e0174609.	2.5	7
31	Modified RNA-seq method for microbial community and diversity analysis using rRNA in different types of environmental samples. <i>PLoS ONE</i> , 2017, 12, e0186161.	2.5	15
32	Tagged Highly Degenerate Primer (THDP)-PCR for Community Analysis of Methane- and Ammonia-oxidizing Bacteria Based on Copper-containing Membrane-bound Monooxygenases (CuMMO). <i>Bio-protocol</i> , 2017, 7, e2354.	0.4	0
33	Responses of soil nitrogen fixation to <i>Spartina alterniflora</i> invasion and nitrogen addition in a Chinese salt marsh. <i>Scientific Reports</i> , 2016, 6, 20384.	3.3	48
34	The Influence of Age and Gender on Skin-Associated Microbial Communities in Urban and Rural Human Populations. <i>PLoS ONE</i> , 2015, 10, e0141842.	2.5	181
35	Communities of ammonia oxidizers at different stages of <i>Spartina alterniflora</i> invasion in salt marshes of Yangtze River estuary. <i>Journal of Microbiology</i> , 2015, 53, 311-320.	2.8	19
36	Influence of Azo Dye Concentration on Activated Sludge Bacterial Community in the Presence of Functionalized Polyurethane Foam. <i>Applied Biochemistry and Biotechnology</i> , 2015, 175, 2574-2588.	2.9	10

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37	Complete genome sequence of <i>Methylophilus</i> sp. TWE2 isolated from methane oxidation enrichment culture of tap-water. <i>Journal of Biotechnology</i> , 2015, 211, 121-122.	3.8	9
38	The First Complete Genome Sequence of the Class Fimbriimonadia in the Phylum Armatimonadetes. <i>PLoS ONE</i> , 2014, 9, e100794.	2.5	16
39	Community size and composition of ammonia oxidizers and denitrifiers in an alluvial intertidal wetland ecosystem. <i>Frontiers in Microbiology</i> , 2014, 5, 371.	3.5	28
40	Analysis of microbial diversity by pyrosequencing the small-subunit ribosomal RNA without PCR amplification. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3777-3789.	3.6	16
41	Unveiling abundance and distribution of planktonic <i>Bacteria</i> and <i>Archaea</i> in a polynya in <i>Amundsen Sea</i> , <i>Antarctica</i> . <i>Environmental Microbiology</i> , 2014, 16, 1566-1578.	3.8	38
42	Greenhouse gas emissions following an invasive plant eradication program. <i>Ecological Engineering</i> , 2014, 73, 229-237.	3.6	12
43	Responses of bacterial and fungal communities to an elevation gradient in a subtropical montane forest of China. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 2219-2230.	3.6	86
44	Bacterial and fungal diversity in the starter production process of Fen liquor, a traditional Chinese liquor. <i>Journal of Microbiology</i> , 2013, 51, 430-438.	2.8	61
45	Analysis of the bacterial communities associated with different drinking water treatment processes. <i>World Journal of Microbiology and Biotechnology</i> , 2013, 29, 1573-1584.	3.6	48
46	Methyl Coenzyme M Reductase A (<i>mcrA</i>) Gene-Based Investigation of Methanogens in the Mudflat Sediments of Yangtze River Estuary, China. <i>Microbial Ecology</i> , 2013, 66, 257-267.	2.8	49
47	Effects of <i>Spartina alterniflora</i> invasion on the communities of methanogens and sulfate-reducing bacteria in estuarine marsh sediments. <i>Frontiers in Microbiology</i> , 2013, 4, 243.	3.5	82
48	Hydrazine Synthase, a Unique Phylomarker with Which To Study the Presence and Biodiversity of Anammox Bacteria. <i>Applied and Environmental Microbiology</i> , 2012, 78, 752-758.	3.1	228
49	Removal of viruses and disinfection by-products at two drinking water treatment plants in southern China. <i>Desalination and Water Treatment</i> , 2012, 48, 221-231.	1.0	6
50	Metagenome Analysis of a Complex Community Reveals the Metabolic Blueprint of Anammox Bacterium <i>Candidatus Jettenia asiatica</i> . <i>Frontiers in Microbiology</i> , 2012, 3, 366.	3.5	86
51	Bacterial succession during 500 years of soil development under agricultural use. <i>Ecological Research</i> , 2012, 27, 793-807.	1.5	32
52	Coverage evaluation of universal bacterial primers using the metagenomic datasets. <i>BMC Microbiology</i> , 2012, 12, 66.	3.3	165
53	Abundance and composition of ammonia-oxidizing bacteria and archaea in different types of soil in the Yangtze River estuary. <i>Journal of Zhejiang University: Science B</i> , 2012, 13, 769-782.	2.8	36
54	Description of <i>Fimbriimonas ginsengisoli</i> gen. nov., sp. nov. within the Fimbriimonadia class nov., of the phylum Armatimonadetes. <i>Antonie Van Leeuwenhoek</i> , 2012, 102, 307-317.	1.7	58

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55	Comparison of Bacterial and Fungal Communities Between Natural and Planted Pine Forests in Subtropical China. <i>Current Microbiology</i> , 2012, 64, 34-42.	2.2	27
56	Bacterial and fungal diversity in the traditional Chinese liquor fermentation process. <i>International Journal of Food Microbiology</i> , 2011, 146, 31-37.	4.7	154
57	<i>Flavobacterium dongtanense</i> sp. nov., isolated from the rhizosphere of a wetland reed. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 343-346.	1.7	23
58	<i>Altererythrobacter dongtanensis</i> sp. nov., isolated from a tidal flat. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 2035-2039.	1.7	38
59	Molecular epidemiology of <i>Cryptococcus neoformans</i> species complex isolates from HIV-positive and HIV-negative patients in southeast China. <i>Frontiers of Medicine in China</i> , 2010, 4, 117-126.	0.1	13
60	<i>Pseudomonas caeni</i> sp. nov., a denitrifying bacterium isolated from the sludge of an anaerobic ammonium-oxidizing bioreactor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2594-2598.	1.7	58
61	Rhizosphere effects on soil bacterial abundance and diversity in the Yellow River Deltaic ecosystem as influenced by petroleum contamination and soil salinization. <i>Soil Biology and Biochemistry</i> , 2009, 41, 2535-2542.	8.8	104
62	The bacterial diversity in an anaerobic ammonium-oxidizing (anammox) reactor community. <i>Systematic and Applied Microbiology</i> , 2009, 32, 278-289.	2.8	124
63	Could nested PCR be applicable for the study of microbial diversity?. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 1447-1452.	3.6	14
64	<i>Henriciella marina</i> gen. nov., sp. nov., a novel member of the family Hyphomonadaceae isolated from the East Sea. <i>Journal of Microbiology</i> , 2009, 47, 156-161.	2.8	28
65	Bacterial diversity of water and sediment in the Changjiang estuary and coastal area of the East China Sea. <i>FEMS Microbiology Ecology</i> , 2009, 70, 236-248.	2.7	185
66	Analyses of microbial consortia in the starter of Fen Liquor. <i>Letters in Applied Microbiology</i> , 2009, 48, 478-485.	2.2	51
67	Diversity of ammonium-oxidizing bacteria in a granular sludge anaerobic ammonium-oxidizing (anammox) reactor. <i>Environmental Microbiology</i> , 2008, 10, 3130-3139.	3.8	283
68	<i>Marinobacter goseongensis</i> sp. nov., from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2866-2870.	1.7	22
69	<i>Pedobacter agri</i> sp. nov., from soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 1640-1643.	1.7	47
70	<i>Joostella marina</i> gen. nov., sp. nov., a novel member of the family Flavobacteriaceae isolated from the East Sea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 1388-1392.	1.7	40
71	<i>Chryseobacterium caeni</i> sp. nov., isolated from bioreactor sludge. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 141-145.	1.7	46
72	<i>Sulfitobacter litoralis</i> sp. nov., a marine bacterium isolated from the East Sea, Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 692-695.	1.7	42

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73	<i>Pseudoalteromonas marina</i> sp. nov., a marine bacterium isolated from tidal flats of the Yellow Sea, and reclassification of <i>Pseudoalteromonas sagamiensis</i> as <i>Algicola sagamiensis</i> comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 12-18.	1.7	44
74	<i>Vibrio litoralis</i> sp. nov., isolated from a Yellow Sea tidal flat in Korea. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 562-565.	1.7	23
75	<i>Oceanisphaera donghaensis</i> sp. nov., a halophilic bacterium from the East Sea, Korea. International Journal of Systematic and Evolutionary Microbiology, 2006, 56, 895-898.	1.7	19
76	<i>Rhizobium daejeonense</i> sp. nov. isolated from a cyanide treatment bioreactor. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 2543-2549.	1.7	86
77	Toxicity and degradation of metal-complexed cyanide by a bacterial consortium under sulfate-reducing conditions. Biotechnology Letters, 2004, 26, 1007-1011.	2.2	7
78	Enhancement of sulfate reduction activity using granular sludge in anaerobic treatment of acid mine drainage. Biotechnology Letters, 2003, 25, 503-508.	2.2	16