

# Zhe-Xue Quan

## List of Publications by Year in descending order

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78  
papers

3,699  
citations

126907

33  
h-index

138484

58  
g-index

83  
all docs

83  
docs citations

83  
times ranked

4678  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
5	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
6	Coverage evaluation of universal bacterial primers using the metagenomic datasets. <i>BMC Microbiology</i> , 2012, 12, 66.	3.3	165
7	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
8	Ubiquity and Diversity of Complete Ammonia Oxidizers (Comammox). <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	146
9	The bacterial diversity in an anaerobic ammonium-oxidizing (anammox) reactor community. <i>Systematic and Applied Microbiology</i> , 2009, 32, 278-289.	2.8	124
10	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
11	<i>Rhizobium daejeonense</i> sp. nov. isolated from a cyanide treatment bioreactor. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 2543-2549.	1.7	86
12	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
13	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
14	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
15	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
16	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
17	<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
18	Description of <i>Fimbriimonas ginsengisoli</i> gen. nov., sp. nov. within the <i>Fimbriimonadia</i> class nov., of the phylum <i>Armatimonadetes</i> . <i>Antonie Van Leeuwenhoek</i> , 2012, 102, 307-317.	1.7	58

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19	Analyses of microbial consortia in the starter of Fen Liquor. Letters in Applied Microbiology, 2009, 48, 478-485.	2.2	51
20	Methyl Coenzyme M Reductase A (mcrA) Gene-Based Investigation of Methanogens in the Mudflat Sediments of Yangtze River Estuary, China. Microbial Ecology, 2013, 66, 257-267.	2.8	49
21	Analysis of the bacterial communities associated with different drinking water treatment processes. World Journal of Microbiology and Biotechnology, 2013, 29, 1573-1584.	3.6	48
22	Responses of soil nitrogen fixation to <i>Spartina alterniflora</i> invasion and nitrogen addition in a Chinese salt marsh. Scientific Reports, 2016, 6, 20384.	3.3	48
23	<i>Pedobacter agri</i> sp. nov., from soil. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1640-1643.	1.7	47
24	Temperature and salinity drive comammox community composition in mangrove ecosystems across southeastern China. Science of the Total Environment, 2020, 742, 140456.	8.0	47
25	<i>Chryseobacterium caeni</i> sp. nov., isolated from bioreactor sludge. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 141-145.	1.7	46
26	Age and Mothers: Potent Influences of Children's Skin Microbiota. Journal of Investigative Dermatology, 2019, 139, 2497-2505.e6.	0.7	46
27	<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
28	<i>Sulfitobacter litoralis</i> sp. nov., a marine bacterium isolated from the East Sea, Korea. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 692-695.	1.7	42
29	<i>Joostella marina</i> gen. nov., sp. nov., a novel member of the family Flavobacteriaceae isolated from the East Sea. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1388-1392.	1.7	40
30	Abundance and niche specificity of different types of complete ammonia oxidizers (comammox) in salt marshes covered by different plants. Science of the Total Environment, 2021, 768, 144993.	8.0	39
31	<i>Altererythrobacter dongtanensis</i> sp. nov., isolated from a tidal flat. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 2035-2039.	1.7	38
32	Unveiling abundance and distribution of planktonic <i>Bacteroidetes</i> and <i>Archaea</i> in a polynya in <i>Amundsen Sea</i> , <i>Antarctica</i> . Environmental Microbiology, 2014, 16, 1566-1578.	3.8	38
33	Use of Newly Designed Primers for Quantification of Complete Ammonia-Oxidizing (Comammox) Bacterial Clades and Strict Nitrite Oxidizers in the Genus <i>Nitrospira</i> . Applied and Environmental Microbiology, 2020, 86, .	3.1	38
34	Abundance and composition of ammonia-oxidizing bacteria and archaea in different types of soil in the Yangtze River estuary. Journal of Zhejiang University: Science B, 2012, 13, 769-782.	2.8	36
35	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. Wetlands, 2017, 37, 221-232.	1.5	36
36	An improved protocol with a highly degenerate primer targeting copper-containing membrane-bound monooxygenase genes for community analysis of methane- and ammonia-oxidizing bacteria. FEMS Microbiology Ecology, 2017, 93, fiw244.	2.7	35

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37	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
38	Bacterial succession during 500 years of soil development under agricultural use. <i>Ecological Research</i> , 2012, 27, 793-807.	1.5	32
39	<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
40	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
41	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
42	<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
43	<i>Vibrio litoralis</i> sp. nov., isolated from a Yellow Sea tidal flat in Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 562-565.	1.7	23
44	<i>Marinobacter goseongensis</i> sp. nov., from seawater. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2008, 58, 2866-2870.	1.7	22
45	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
46	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
47	Microbial Communities and Diversities in Mudflat Sediments Analyzed Using a Modified Metatranscriptomic Method. <i>Frontiers in Microbiology</i> , 2018, 9, 93.	3.5	20
48	Dynamics of Skin Mycobiome in Infants. <i>Frontiers in Microbiology</i> , 2020, 11, 1790.	3.5	20
49	<i>Oceanisphaera donghaensis</i> sp. nov., a halophilic bacterium from the East Sea, Korea. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 895-898.	1.7	19
50	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
51	<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
52	Enhancement of sulfate reduction activity using granular sludge in anaerobic treatment of acid mine drainage. <i>Biotechnology Letters</i> , 2003, 25, 503-508.	2.2	16
53	The First Complete Genome Sequence of the Class Fimbriimonadia in the Phylum Armatimonadetes. <i>PLoS ONE</i> , 2014, 9, e100794.	2.5	16
54	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

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55	<i>Oceaniradius stylonematis</i> gen. nov., sp. nov., isolated from a red alga, <i>Stylonema cornu-cervi</i> . International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1967-1973.	1.7	16
56	Modified RNA-seq method for microbial community and diversity analysis using rRNA in different types of environmental samples. PLoS ONE, 2017, 12, e0186161.	2.5	15
57	Could nested PCR be applicable for the study of microbial diversity?. World Journal of Microbiology and Biotechnology, 2009, 25, 1447-1452.	3.6	14
58	Molecular epidemiology of <i>Cryptococcus neoformans</i> species complex isolates from HIV-positive and HIV-negative patients in southeast China. Frontiers of Medicine in China, 2010, 4, 117-126.	0.1	13
59	Design of targeted primers based on 16S rRNA sequences in meta-transcriptomic datasets and identification of a novel taxonomic group in the Asgard archaea. BMC Microbiology, 2020, 20, 25.	3.3	13
60	Greenhouse gas emissions following an invasive plant eradication program. Ecological Engineering, 2014, 73, 229-237.	3.6	12
61	Comparison of Fecal Collection Methods on Variation in Gut Metagenomics and Untargeted Metabolomics. MSphere, 2021, 6, e0063621.	2.9	12
62	<i>Roseicella frigidaeris</i> gen. nov., sp. nov., isolated from an air-conditioning system. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 1384-1389.	1.7	12
63	The gut microbiome and microbial metabolites in acute myocardial infarction. Journal of Genetics and Genomics, 2022, 49, 569-578.	3.9	11
64	Influence of Azo Dye Concentration on Activated Sludge Bacterial Community in the Presence of Functionalized Polyurethane Foam. Applied Biochemistry and Biotechnology, 2015, 175, 2574-2588.	2.9	10
65	Complete genome sequence of <i>Methylophilus</i> sp. TWE2 isolated from methane oxidation enrichment culture of tap-water. Journal of Biotechnology, 2015, 211, 121-122.	3.8	9
66	Toxicity and degradation of metal-complexed cyanide by a bacterial consortium under sulfate-reducing conditions. Biotechnology Letters, 2004, 26, 1007-1011.	2.2	7
67	MIPE: A metagenome-based community structure explorer and SSU primer evaluation tool. PLoS ONE, 2017, 12, e0174609.	2.5	7
68	<i>Thalassolituus alkanivorans</i> sp. nov., a hydrocarbon-utilizing bacterium isolated from the Mariana Trench. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	7
69	Removal of viruses and disinfection by-products at two drinking water treatment plants in southern China. Desalination and Water Treatment, 2012, 48, 221-231.	1.0	6
70	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. Applied and Environmental Microbiology, 2021, 87, e0022721.	3.1	5
71	Ammonium promoting methane oxidation by stimulating the Type Ia methane-oxidizing bacteria in tidal flat sediments of the Yangtze River estuary. Science of the Total Environment, 2021, 793, 148470.	8.0	5
72	<i>Methylophaga pinxianii</i> sp. nov., isolated from the Mariana Trench. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	5

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73	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
74	Cross-phytgroup assessment of foliar epiphytic mycobiomes. <i>Environmental Microbiology</i> , 2021, 23, 6210-6222.	3.8	4
75	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
76	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
77	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
78	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