

Xiaojun Zhang

List of Publications by Year in descending order

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47
papers

3,751
citations

257101

24
h-index

214527

47
g-index

51
all docs

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docs citations

51
times ranked

6427
citing authors

#	ARTICLE	IF	CITATIONS
1	Enhanced N ₂ O emission rate in field soil undergoing conventional intensive fertilization is attributed to the shifts of denitrifying guilds. <i>Pedosphere</i> , 2021, 31, 145-156.	2.1	13
2	Synthesis, Preclinical Evaluation, and First-in-Human PET Study of Quinoline-Containing PSMA Tracers with Decreased Renal Excretion. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 4179-4195.	2.9	16
3	Towards sustainable agriculture: rhizosphere microbiome engineering. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7141-7160.	1.7	28
4	Oxygen-depletion by rapid ammonia oxidation regulates kinetics of N ₂ O, NO and N ₂ production in an ammonium fertilised agricultural soil. <i>Soil Biology and Biochemistry</i> , 2021, 163, 108460.	4.2	17
5	⁶⁸ Ga-DOTA-DiPSMA PET/CT Imaging: Biodistribution, Dosimetry, and Preliminary Application in Prostate Cancer. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 811972.	2.0	1
6	Cross-Feeding between Members of <i>Thauera</i> spp. and <i>Rhodococcus</i> spp. Drives Quinoline-Denitrifying Degradation in a Hypoxic Bioreactor. <i>MSphere</i> , 2020, 5, .	1.3	3
7	Endotoxin Producers Overgrowing in Human Gut Microbiota as the Causative Agents for Nonalcoholic Fatty Liver Disease. <i>MBio</i> , 2020, 11, .	1.8	96
8	Response of treatment performance and microbial community structure to the temporary suspension of an industrial anaerobic bioreactor. <i>Science of the Total Environment</i> , 2019, 646, 229-237.	3.9	22
9	Non-synchronous Structural and Functional Dynamics During the Coalescence of Two Distinct Soil Bacterial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 1125.	1.5	13
10	Variability in the Response of Bacterial Community Assembly to Environmental Selection and Biotic Factors Depends on the Immigrated Bacteria, as Revealed by a Soil Microcosm Experiment. <i>MSystems</i> , 2019, 4, .	1.7	4
11	Divergence of Granular Sludges and Microbial Communities in Two Types of Anaerobic Reactors Treating Different Wastewaters. <i>Journal of Microbiology and Biotechnology</i> , 2019, 29, 633-644.	0.9	3
12	The Advanced Anaerobic Expanded Granular Sludge Bed (AnaEG) Possessed Temporally and Spatially Stable Treatment Performance and Microbial Community in Treating Starch Processing Wastewater. <i>Frontiers in Microbiology</i> , 2018, 9, 589.	1.5	14
13	Rapid Succession of Actively Transcribing Denitrifier Populations in Agricultural Soil During an Anoxic Spell. <i>Frontiers in Microbiology</i> , 2018, 9, 3208.	1.5	12
14	Change in microbial community in landfill refuse contaminated with antibiotics facilitates denitrification more than the increase in ARG over long-term. <i>Scientific Reports</i> , 2017, 7, 41230.	1.6	34
15	Genomic Microdiversity of <i>Bifidobacterium pseudocatenulatum</i> Underlying Differential Strain-Level Responses to Dietary Carbohydrate Intervention. <i>MBio</i> , 2017, 8, .	1.8	43
16	Linkage between N ₂ O emission and functional gene abundance in an intensively managed calcareous fluvo-aquic soil. <i>Scientific Reports</i> , 2017, 7, 43283.	1.6	54
17	Time-resolved analysis of a denitrifying bacterial community revealed a core microbiome responsible for the anaerobic degradation of quinoline. <i>Scientific Reports</i> , 2017, 7, 14778.	1.6	20
18	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	1.5	120

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19	Effect of effluent recirculation rate on the performance of anaerobic bio-filter treating coal gasification wastewater under co-digestion conditions. <i>RSC Advances</i> , 2016, 6, 87926-87934.	1.7	15
20	Accelerated dysbiosis of gut microbiota during aggravation of DSS-induced colitis by a butyrate-producing bacterium. <i>Scientific Reports</i> , 2016, 6, 27572.	1.6	164
21	Diminution of the gut resistome after a gut microbiota-targeted dietary intervention in obese children. <i>Scientific Reports</i> , 2016, 6, 24030.	1.6	33
22	Draft genome sequence of <i>Thauera</i> sp. DTG from a denitrifying quinoline degrading microbial consortium. <i>Applied Environmental Biotechnology</i> , 2016, 1, 38.	1.0	5
23	Draft genome sequence of <i>Thauera</i> sp. DTG from a denitrifying quinoline degrading microbial consortium. <i>Applied Environmental Biotechnology</i> , 2016, 1, 38-43.	1.0	1
24	Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. <i>Scientific Reports</i> , 2015, 5, 14405.	1.6	499
25	Bacteria in the injection water differently impacts the bacterial communities of production wells in high-temperature petroleum reservoirs. <i>Frontiers in Microbiology</i> , 2015, 6, 505.	1.5	19
26	The Bamboo-Eating Giant Panda Harbors a Carnivore-Like Gut Microbiota, with Excessive Seasonal Variations. <i>MBio</i> , 2015, 6, e00022-15.	1.8	282
27	Novel Mass Bio System (MBS) and its potential application in advanced treatment of coal gasification wastewater. <i>RSC Advances</i> , 2015, 5, 88692-88702.	1.7	25
28	Crude oil degradation by bacterial consortia under four different redox and temperature conditions. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 1451-1461.	1.7	14
29	Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. <i>EBioMedicine</i> , 2015, 2, 968-984.	2.7	306
30	A gut microbiota-targeted dietary intervention for amelioration of chronic inflammation underlying metabolic syndrome. <i>FEMS Microbiology Ecology</i> , 2014, 87, 357-367.	1.3	338
31	The abundance of fecal <i>Faecalibacterium prausnitzii</i> in relation to obesity and gender in Chinese adults. <i>Archives of Microbiology</i> , 2014, 196, 73-77.	1.0	47
32	A fullerene colloidal suspension stimulates the growth and denitrification ability of wastewater treatment sludge-derived bacteria. <i>Chemosphere</i> , 2014, 108, 411-417.	4.2	24
33	Fate of invading bacteria in soil and survival of transformants after simulated uptake of transgenes, as evaluated by a model system based on lindane degradation. <i>Research in Microbiology</i> , 2012, 163, 200-210.	1.0	9
34	Performance and bacterial compositions of aged refuse reactors treating mature landfill leachate. <i>Bioresource Technology</i> , 2012, 103, 71-77.	4.8	76
35	A diverse bacterial community in an anoxic quinoline-degrading bioreactor determined by using pyrosequencing and clone library analysis. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 425-434.	1.7	40
36	Versatile aromatic compound-degrading capacity and microdiversity of <i>Thauera</i> strains isolated from a coking wastewater treatment bioreactor. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2010, 37, 927-934.	1.4	75

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37	Decomposition of Bt transgenic rice residues and response of soil microbial community in rapeseed-rice cropping system. <i>Plant and Soil</i> , 2010, 336, 279-290.	1.8	38
38	Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. <i>ISME Journal</i> , 2010, 4, 232-241.	4.4	845
39	Structural differentiation of bacterial communities in indole-degrading bioreactors under denitrifying and sulfate-reducing conditions. <i>Research in Microbiology</i> , 2010, 161, 687-693.	1.0	44
40	New subgroup of Bacteroidetes and diverse microorganisms in Tibetan plateau glacial ice provide a biological record of environmental conditions. <i>FEMS Microbiology Ecology</i> , 2009, 67, 21-29.	1.3	47
41	Development of group-specific PCR-DGGE fingerprinting for monitoring structural changes of <i>Thauera</i> spp. in an industrial wastewater treatment plant responding to operational perturbations. <i>Journal of Microbiological Methods</i> , 2008, 75, 231-236.	0.7	38
42	A Constructed Alkaline Consortium and Its Dynamics in Treating Alkaline Black Liquor with Very High Pollution Load. <i>PLoS ONE</i> , 2008, 3, e3777.	1.1	29
43	Cloning of Environmental Genomic Fragments as Physical Markers for Monitoring Microbial Populations in Coking Wastewater Treatment System. <i>Microbial Ecology</i> , 2007, 53, 163-172.	1.4	11
44	Microorganisms in the Malan ice core and their relation to climatic and environmental changes. <i>Global Biogeochemical Cycles</i> , 2006, 20, n/a-n/a.	1.9	39
45	<i>Thauera</i> and <i>Azoarcus</i> as functionally important genera in a denitrifying quinoline-removal bioreactor as revealed by microbial community structure comparison. <i>FEMS Microbiology Ecology</i> , 2006, 55, 274-286.	1.3	149
46	Diversity of 16S rDNA and environmental factor influencing microorganisms in Malan ice core. <i>Science Bulletin</i> , 2003, 48, 1146-1151.	1.7	9
47	Analysis of the characteristics of microorganisms packed in the ice core of Malan Glacier, Tibet, China. <i>Science in China Series D: Earth Sciences</i> , 2001, 44, 369-374.	0.9	14