

# 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

51  
docs citations

51  
times ranked

6427  
citing authors

#	ARTICLE	IF	CITATIONS
1	Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice. ISME Journal, 2010, 4, 232-241.	4.4	845
2	Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. Scientific Reports, 2015, 5, 14405.	1.6	499
3	A gut microbiota-targeted dietary intervention for amelioration of chronic inflammation underlying metabolic syndrome. FEMS Microbiology Ecology, 2014, 87, 357-367.	1.3	338
4	Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. EBioMedicine, 2015, 2, 968-984.	2.7	306
5	The Bamboo-Eating Giant Panda Harbors a Carnivore-Like Gut Microbiota, with Excessive Seasonal Variations. MBio, 2015, 6, e00022-15.	1.8	282
6	Accelerated dysbiosis of gut microbiota during aggravation of DSS-induced colitis by a butyrate-producing bacterium. Scientific Reports, 2016, 6, 27572.	1.6	164
7	Thauera and Azoarcus as functionally important genera in a denitrifying quinoline-removal bioreactor as revealed by microbial community structure comparison. FEMS Microbiology Ecology, 2006, 55, 274-286.	1.3	149
8	Back to the Future of Soil Metagenomics. Frontiers in Microbiology, 2016, 7, 73.	1.5	120
9	Endotoxin Producers Overgrowing in Human Gut Microbiota as the Causative Agents for Nonalcoholic Fatty Liver Disease. MBio, 2020, 11, .	1.8	96
10	Performance and bacterial compositions of aged refuse reactors treating mature landfill leachate. Bioresource Technology, 2012, 103, 71-77.	4.8	76
11	Versatile aromatic compound-degrading capacity and microdiversity of Thauera strains isolated from a coking wastewater treatment bioreactor. Journal of Industrial Microbiology and Biotechnology, 2010, 37, 927-934.	1.4	75
12	Linkage between N <sub>2</sub> O emission and functional gene abundance in an intensively managed calcareous fluvo-aquic soil. Scientific Reports, 2017, 7, 43283.	1.6	54
13	New subgroup of Bacteroidetes and diverse microorganisms in Tibetan plateau glacial ice provide a biological record of environmental conditions. FEMS Microbiology Ecology, 2009, 67, 21-29.	1.3	47
14	The abundance of fecal Faecalibacterium prausnitzii in relation to obesity and gender in Chinese adults. Archives of Microbiology, 2014, 196, 73-77.	1.0	47
15	Structural differentiation of bacterial communities in indole-degrading bioreactors under denitrifying and sulfate-reducing conditions. Research in Microbiology, 2010, 161, 687-693.	1.0	44
16	Genomic Microdiversity of <i>Bifidobacterium pseudocatenulatum</i> Underlying Differential Strain-Level Responses to Dietary Carbohydrate Intervention. MBio, 2017, 8, .	1.8	43
17	A diverse bacterial community in an anoxic quinoline-degrading bioreactor determined by using pyrosequencing and clone library analysis. Applied Microbiology and Biotechnology, 2011, 91, 425-434.	1.7	40
18	Microorganisms in the Malan ice core and their relation to climatic and environmental changes. Global Biogeochemical Cycles, 2006, 20, n/a-n/a.	1.9	39

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19	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
20	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
21	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
22	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
23	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
24	Towards sustainable agriculture: rhizosphere microbiome engineering. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7141-7160.	1.7	28
25	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
26	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
27	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
28	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
29	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
30	Oxygen-depletion by rapid ammonia oxidation regulates kinetics of N <sub>2</sub> O, NO and N <sub>2</sub> production in an ammonium fertilised agricultural soil. <i>Soil Biology and Biochemistry</i> , 2021, 163, 108460.	4.2	17
31	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
32	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
33	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
34	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
35	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
36	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

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37	Enhanced N <sub>2</sub> 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
38	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
39	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
40	Diversity of 16S rDNA and environmental factor influencing microorganisms in Malan ice core. <i>Science Bulletin</i> , 2003, 48, 1146-1151.	1.7	9
41	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
42	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
43	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
44	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
45	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
46	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
47	<sup>68</sup> 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