

Xu-Xiang Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

107
papers

6,836
citations

57758

44
h-index

62596

80
g-index

108
all docs

108
docs citations

108
times ranked

7019
citing authors

#	ARTICLE	IF	CITATIONS
1	Varied interspecies interactions between anammox and denitrifying bacteria enhanced nitrogen removal in a single-stage simultaneous anammox and denitrification system. <i>Science of the Total Environment</i> , 2022, 813, 152519.	8.0	10
2	Environmental exposure to low-dose perfluorohexanesulfonate promotes obesity and non-alcoholic fatty liver disease in mice fed a high-fat diet. <i>Environmental Science and Pollution Research</i> , 2022, 29, 49279-49290.	5.3	2
3	Metagenomic insights into the variation of bacterial communities and potential pathogenic bacteria in drinking water treatment and distribution systems. , 2022, 1, 20220015.		4
4	Recovery of gut microbiota in mice exposed to tetracycline hydrochloride and their correlation with host metabolism. <i>Ecotoxicology</i> , 2021, 30, 1620-1631.	2.4	6
5	Iron Minerals Mediated Interfacial Hydrolysis of Chloramphenicol Antibiotic under Limited Moisture Conditions. <i>Environmental Science & Technology</i> , 2021, 55, 9569-9578.	10.0	19
6	Heavy Metal Tolerance Genes Associated With Contaminated Sediments From an E-Waste Recycling River in Southern China. <i>Frontiers in Microbiology</i> , 2021, 12, 665090.	3.5	16
7	Revisiting the Microscopic Processes of Biofilm Formation on Organic Carriers: A Study under Variational Shear Stresses. <i>ACS Applied Bio Materials</i> , 2021, 4, 5529-5541.	4.6	9
8	Effects of carboxylated multi-walled carbon nanotubes on bioconcentration of pentachlorophenol and hepatic damages in goldfish. <i>Ecotoxicology</i> , 2021, 30, 1389-1398.	2.4	4
9	Technologies for bHRPs and risk control. , 2020, , 237-258.		2
10	Biological HRP in wastewater. , 2020, , 41-78.		17
11	Structural and functional alterations of gut microbiome in mice induced by chronic cadmium exposure. <i>Chemosphere</i> , 2020, 246, 125747.	8.2	58
12	Two birds with one stone: Simultaneous improvement of biofilm formation and nitrogen transformation in MBBR treating high ammonia nitrogen wastewater via exogenous N-acyl homoserine lactones. <i>Chemical Engineering Journal</i> , 2020, 386, 124001.	12.7	32
13	Bacterial enrichment in highly-selective acetate-fed bioreactors and its application in rapid biofilm formation. <i>Water Research</i> , 2020, 170, 115359.	11.3	5
14	Effects of chronic cadmium exposure at food limitation-relevant levels on energy metabolism in mice. <i>Journal of Hazardous Materials</i> , 2020, 388, 121791.	12.4	22
15	Single-Cell Sequencing Reveals Heterogeneity Effects of Bisphenol A on Zebrafish Embryonic Development. <i>Environmental Science & Technology</i> , 2020, 54, 9537-9546.	10.0	27
16	Integrated metagenomic and metatranscriptomic analyses of ultraviolet disinfection effects on antibiotic resistance genes and bacterial communities during wastewater treatment. <i>Ecotoxicology</i> , 2020, 30, 1610-1619.	2.4	5
17	Metagenomic and metatranscriptomic insights into the complex nitrogen metabolic pathways in a single-stage bioreactor coupling partial denitrification with anammox. <i>Chemical Engineering Journal</i> , 2020, 398, 125653.	12.7	66
18	Nonylphenol ethoxylates biodegradation increases estrogenicity of textile wastewater in biological treatment systems. <i>Water Research</i> , 2020, 184, 116137.	11.3	28

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19	Machine learning-aided analyses of thousands of draft genomes reveal specific features of activated sludge processes. <i>Microbiome</i> , 2020, 8, 16.	11.1	42
20	Metagenomic assembly provides a deep insight into the antibiotic resistome alteration induced by drinking water chlorination and its correlations with bacterial host changes. <i>Journal of Hazardous Materials</i> , 2019, 379, 120841.	12.4	73
21	Inhibition of Mitochondrial Fatty Acid Oxidation Contributes to Development of Nonalcoholic Fatty Liver Disease Induced by Environmental Cadmium Exposure. <i>Environmental Science & Technology</i> , 2019, 53, 13992-14000.	10.0	61
22	Aromatic compounds lead to increased abundance of antibiotic resistance genes in wastewater treatment bioreactors. <i>Water Research</i> , 2019, 166, 115073.	11.3	53
23	Combined effects of graphene oxide and zinc oxide nanoparticle on human A549 cells: bioavailability, toxicity and mechanisms. <i>Environmental Science: Nano</i> , 2019, 6, 635-645.	4.3	41
24	Abiotic and biotic processes of diclofenac in enriched nitrifying sludge: Kinetics, transformation products and reactions. <i>Science of the Total Environment</i> , 2019, 683, 80-88.	8.0	18
25	Comparative analysis of toxicity reduction of wastewater in twelve industrial park wastewater treatment plants based on battery of toxicity assays. <i>Scientific Reports</i> , 2019, 9, 3751.	3.3	19
26	Diverse aromatic-degrading bacteria present in a highly enriched autotrophic nitrifying sludge. <i>Science of the Total Environment</i> , 2019, 666, 245-251.	8.0	39
27	Towards the biofilm characterization and regulation in biological wastewater treatment. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1115-1129.	3.6	70
28	Comprehensive insights into the key components of bacterial assemblages in pharmaceutical wastewater treatment plants. <i>Science of the Total Environment</i> , 2019, 651, 2148-2157.	8.0	25
29	A comprehensive insight into the functional bacteria and genes and their roles in simultaneous denitrification and anammox system at varying substrate loadings. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 1523-1533.	3.6	32
30	Roles and correlations of functional bacteria and genes in the start-up of simultaneous anammox and denitrification system for enhanced nitrogen removal. <i>Science of the Total Environment</i> , 2019, 655, 1355-1363.	8.0	124
31	Free-living bacteria and potential bacterial pathogens in sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2455-2464.	3.6	47
32	Metagenomic analysis revealed the prevalence of antibiotic resistance genes in the gut and living environment of freshwater shrimp. <i>Journal of Hazardous Materials</i> , 2018, 350, 10-18.	12.4	90
33	Impact of salinity on antibiotic resistance genes in wastewater treatment bioreactors. <i>Chemical Engineering Journal</i> , 2018, 338, 557-563.	12.7	49
34	Microbial community structure and function in aerobic granular sludge. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3967-3979.	3.6	121
35	Metagenomic profiling of ARGs in airborne particulate matters during a severe smog event. <i>Science of the Total Environment</i> , 2018, 615, 1332-1340.	8.0	84
36	Comparison of the impacts of zinc ions and zinc nanoparticles on nitrifying microbial community. <i>Journal of Hazardous Materials</i> , 2018, 343, 166-175.	12.4	50

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37	Ultraviolet irradiation sensitizes <i>Pseudomonas aeruginosa</i> PAO1 to multiple antibiotics. <i>Environmental Science: Water Research and Technology</i> , 2018, 4, 2051-2057.	2.4	4
38	Comprehensive analyses of functional bacteria and genes in a denitrifying EGSB reactor under Cd(II) stress. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8551-8560.	3.6	18
39	Mechanisms of microbial community structure and biofouling shifts under multivalent cations stress in membrane bioreactors. <i>Journal of Hazardous Materials</i> , 2017, 327, 89-96.	12.4	18
40	Transformation of anaerobic granules into aerobic granules and the succession of bacterial community. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 7703-7713.	3.6	28
41	Cytotoxicity and Efflux Pump Inhibition Induced by Molybdenum Disulfide and Boron Nitride Nanomaterials with Sheetlike Structure. <i>Environmental Science & Technology</i> , 2017, 51, 10834-10842.	10.0	53
42	Different impacts of manure and chemical fertilizers on bacterial community structure and antibiotic resistance genes in arable soils. <i>Chemosphere</i> , 2017, 188, 455-464.	8.2	105
43	Fate of antibiotic resistance genes and their associations with bacterial community in livestock breeding wastewater and its receiving river water. <i>Water Research</i> , 2017, 124, 259-268.	11.3	255
44	Diversity, abundance, and possible sources of fecal bacteria in the Yangtze River. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 2143-2152.	3.6	28
45	High Levels of Antibiotic Resistance Genes and Their Correlations with Bacterial Community and Mobile Genetic Elements in Pharmaceutical Wastewater Treatment Bioreactors. <i>PLoS ONE</i> , 2016, 11, e0156854.	2.5	57
46	Comprehensive insights into microcystin-LR effects on hepatic lipid metabolism using cross-omics technologies. <i>Journal of Hazardous Materials</i> , 2016, 315, 126-134.	12.4	57
47	Evaluation of five microbial and four mitochondrial DNA markers for tracking human and pig fecal pollution in freshwater. <i>Scientific Reports</i> , 2016, 6, 35311.	3.3	30
48	Metagenomic analysis of bacterial community composition and antibiotic resistance genes in a wastewater treatment plant and its receiving surface water. <i>Ecotoxicology and Environmental Safety</i> , 2016, 132, 260-269.	6.0	123
49	Metagenomic insights into ultraviolet disinfection effects on antibiotic resistome in biologically treated wastewater. <i>Water Research</i> , 2016, 101, 309-317.	11.3	91
50	Influences of graphene on microbial community and antibiotic resistance genes in mouse gut as determined by high-throughput sequencing. <i>Chemosphere</i> , 2016, 144, 1306-1312.	8.2	49
51	Comparison of Cytotoxicity and Inhibition of Membrane ABC Transporters Induced by MWCNTs with Different Length and Functional Groups. <i>Environmental Science & Technology</i> , 2016, 50, 3985-3994.	10.0	56
52	Low levels of graphene and graphene oxide inhibit cellular xenobiotic defense system mediated by efflux transporters. <i>Nanotoxicology</i> , 2016, 10, 597-606.	3.0	39
53	Correlations of Gut Microbial Community Shift with Hepatic Damage and Growth Inhibition of <i>Carassius auratus</i> Induced by Pentachlorophenol Exposure. <i>Environmental Science & Technology</i> , 2015, 49, 11894-11902.	10.0	107
54	Abundance and Diversity of Bacterial Nitrifiers and Denitrifiers and Their Functional Genes in Tannery Wastewater Treatment Plants Revealed by High-Throughput Sequencing. , 2015, , 101-123.		1

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55	Bacterial Pathogens and Community Composition in Advanced Sewage Treatment Systems Revealed by Metagenomics Analysis Based on High-Throughput Sequencing. PLoS ONE, 2015, 10, e0125549.	2.5	71
56	Persistence of mitochondrial DNA markers as fecal indicators in water environments. Science of the Total Environment, 2015, 533, 383-390.	8.0	23
57	Metagenomic insights into salinity effect on diversity and abundance of denitrifying bacteria and genes in an expanded granular sludge bed reactor treating high-nitrate wastewater. Chemical Engineering Journal, 2015, 277, 116-123.	12.7	110
58	Metagenomic insights into Cr(VI) effect on microbial communities and functional genes of an expanded granular sludge bed reactor treating high-nitrate wastewater. Water Research, 2015, 76, 43-52.	11.3	192
59	Metagenomic insights into tetracycline effects on microbial community and antibiotic resistance of mouse gut. Ecotoxicology, 2015, 24, 2125-2132.	2.4	46
60	Bacterial Community Shift Drives Antibiotic Resistance Promotion during Drinking Water Chlorination. Environmental Science & Technology, 2015, 49, 12271-12279.	10.0	384
61	Correlation between microbial community structure and biofouling as determined by analysis of microbial community dynamics. Bioresource Technology, 2015, 197, 99-105.	9.6	80
62	Chemical and bioanalytical assessments on drinking water treatments by quaternized magnetic microspheres. Journal of Hazardous Materials, 2015, 285, 53-60.	12.4	10
63	Environmental fate of tetracycline resistance genes originating from swine feedlots in river water. Journal of Environmental Science and Health - Part B Pesticides, Food Contaminants, and Agricultural Wastes, 2014, 49, 624-631.	1.5	33
64	A Comprehensive Insight into Tetracycline Resistant Bacteria and Antibiotic Resistance Genes in Activated Sludge Using Next-Generation Sequencing. International Journal of Molecular Sciences, 2014, 15, 10083-10100.	4.1	60
65	A cross-omics toxicological evaluation of drinking water treated with different processes. Journal of Hazardous Materials, 2014, 271, 57-64.	12.4	3
66	A comprehensive insight into bacterial virulence in drinking water using 454 pyrosequencing and Illumina high-throughput sequencing. Ecotoxicology and Environmental Safety, 2014, 109, 15-21.	6.0	74
67	Metagenomic profiles and antibiotic resistance genes in gut microbiota of mice exposed to arsenic and iron. Chemosphere, 2014, 112, 1-8.	8.2	101
68	Abundance and Diversity of Bacterial Nitrifiers and Denitrifiers and Their Functional Genes in Tannery Wastewater Treatment Plants Revealed by High-Throughput Sequencing. PLoS ONE, 2014, 9, e113603.	2.5	120
69	Metagenomic insights into chlorination effects on microbial antibiotic resistance in drinking water. Water Research, 2013, 47, 111-120.	11.3	423
70	Characterization of tetracycline resistant bacterial community in saline activated sludge using batch stress incubation with high-throughput sequencing analysis. Water Research, 2013, 47, 4207-4216.	11.3	175
71	Promotion of Melanoma Cell Invasion and Tumor Metastasis by Microcystin-LR via Phosphatidylinositol 3-Kinase/AKT Pathway. Environmental Science & Technology, 2013, 47, 130712144451004.	10.0	19
72	Hepatic gene expression analysis of mice exposed to raw water from Meiliang Bay, Lake Taihu, China. Journal of Applied Toxicology, 2013, 33, 1416-1423.	2.8	2

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73	Metagenomic analysis reveals significant changes of microbial compositions and protective functions during drinking water treatment. <i>Scientific Reports</i> , 2013, 3, 3550.	3.3	116
74	Metagenomic Profiling of Antibiotic Resistance Genes and Mobile Genetic Elements in a Tannery Wastewater Treatment Plant. <i>PLoS ONE</i> , 2013, 8, e76079.	2.5	93
75	Metagenomic analysis of cadmium and copper resistance genes in activated sludge of a tannery wastewater treatment plant. <i>Journal of Environmental Biology</i> , 2013, 34, 375-80.	0.5	14
76	Microcystin-LR Promotes Melanoma Cell Invasion and Enhances Matrix Metalloproteinase-2/-9 Expression Mediated by NF- κ B Activation. <i>Environmental Science & Technology</i> , 2012, 46, 11319-11326.	10.0	45
77	Evaluating the Transcriptomic and Metabolic Profile of Mice Exposed to Source Drinking Water. <i>Environmental Science & Technology</i> , 2012, 46, 78-83.	10.0	27
78	Effects of microcystin-LR exposure on matrix metalloproteinase-2/-9 expression and cancer cell migration. <i>Ecotoxicology and Environmental Safety</i> , 2012, 77, 88-93.	6.0	17
79	Cyanobacteria-blooming water samples from Lake Taihu induce endoplasmic reticulum stress in liver and kidney of mice. <i>Ecotoxicology</i> , 2012, 21, 1495-1503.	2.4	6
80	Chronic exposure to contaminated drinking water stimulates PPAR expression in mice livers. <i>Chemosphere</i> , 2012, 88, 407-412.	8.2	5
81	Occurrence, Abundance, and Diversity of Tetracycline Resistance Genes in 15 Sewage Treatment Plants across China and Other Global Locations. <i>Environmental Science & Technology</i> , 2011, 45, 2598-2604.	10.0	246
82	Assessing the toxicity of ingested Taihu Lake water on mice via hepatic histopathology and matrix metalloproteinase expression. <i>Ecotoxicology</i> , 2011, 20, 1047-1056.	2.4	6
83	NMR-based metabolic profiling for serum of mouse exposed to source water. <i>Ecotoxicology</i> , 2011, 20, 1065-1070.	2.4	3
84	Genome-wide screening of indicator genes for assessing the potential carcinogenic risk of Nanjing city drinking water. <i>Ecotoxicology</i> , 2011, 20, 1033-1040.	2.4	5
85	Occurrence, abundance and elimination of class 1 integrons in one municipal sewage treatment plant. <i>Ecotoxicology</i> , 2011, 20, 968-973.	2.4	39
86	Preliminary evaluation of gene expression profiles in liver of mice exposed to Taihu Lake drinking water for 90 days. <i>Ecotoxicology</i> , 2011, 20, 1071-1077.	2.4	4
87	Integration of gene chip and topological network techniques to screen a candidate biomarker gene (CBG) for predication of the source water carcinogenesis risks on mouse <i>Mus musculus</i> . <i>Ecotoxicology</i> , 2011, 20, 1026-1032.	2.4	2
88	Seasonal microbial community shift in a saline sewage treatment plant. <i>Frontiers of Environmental Science and Engineering in China</i> , 2011, 5, 40-47.	0.8	2
89	Plasmid Metagenome Reveals High Levels of Antibiotic Resistance Genes and Mobile Genetic Elements in Activated Sludge. <i>PLoS ONE</i> , 2011, 6, e26041.	2.5	272
90	Toxicity of purified terephthalic acid manufacturing wastewater on reproductive system of male mice (<i>Mus musculus</i>). <i>Journal of Hazardous Materials</i> , 2010, 176, 300-305.	12.4	35

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91	Genomic expression profiles in liver of mice exposed to purified terephthalic acid manufacturing wastewater. <i>Journal of Hazardous Materials</i> , 2010, 181, 1121-1126.	12.4	15
92	Enhanced degradation of 4-nitrophenol by microwave assisted Fe/EDTA process. <i>Journal of Hazardous Materials</i> , 2010, 176, 213-219.	12.4	20
93	Influences of hydraulic loading rate on SVOC removal and microbial community structure in drinking water treatment biofilters. <i>Journal of Hazardous Materials</i> , 2010, 178, 652-657.	12.4	25
94	Effects of Yangtze River source water on genomic polymorphisms of male mice detected by RAPD. <i>Human and Experimental Toxicology</i> , 2010, 29, 113-120.	2.2	3
95	Endoplasmic reticulum stress in murine liver and kidney exposed to microcystin-LR. <i>Toxicol</i> , 2010, 56, 1334-1341.	1.6	46
96	Stimulation effect of microcystin-LR on matrix metalloproteinase-2/-9 expression in mouse liver. <i>Toxicology Letters</i> , 2010, 199, 377-382.	0.8	16
97	Gene expression profiles in liver of mouse after chronic exposure to drinking water. <i>Journal of Applied Toxicology</i> , 2009, 29, 569-577.	2.8	16
98	Semi-volatile organic compounds and trace elements in the Yangtze River source of drinking water. <i>Ecotoxicology</i> , 2009, 18, 707-714.	2.4	42
99	Class 1 integronase gene and tetracycline resistance genes tetA and tetC in different water environments of Jiangsu Province, China. <i>Ecotoxicology</i> , 2009, 18, 652-660.	2.4	83
100	Toxicity of the Yangtze River source of drinking water on reproductive system of male mice (Mus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.4	14
101	Effects of the Yangtze River source of drinking water on metabolites of <i>Mus musculus</i> . <i>Ecotoxicology</i> , 2009, 18, 722-728.	2.4	8
102	Transcriptional toxicity of the Yangtze River source water on mouse (<i>Mus musculus</i>) detected by cDNA microarray. <i>Ecotoxicology</i> , 2009, 18, 715-721.	2.4	12
103	Antibiotic resistance genes in water environment. <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 397-414.	3.6	801
104	Characterization and quantification of class 1 integrons and associated gene cassettes in sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2009, 82, 1169-1177.	3.6	120
105	Genetic analysis of protoplast fusant Xhhh constructed for pharmaceutical wastewater treatment. <i>Bioresource Technology</i> , 2009, 100, 1910-1914.	9.6	16
106	Tetracycline Resistance Genes and Tetracycline Resistant Lactose-Fermenting <i>Enterobacteriaceae</i> in Activated Sludge of Sewage Treatment Plants. <i>Environmental Science & Technology</i> , 2009, 43, 3455-3460.	10.0	196
107	A Comparative Analysis of Environmental Quality Assessment Methods for Heavy Metal-Contaminated Soils. <i>Pedosphere</i> , 2008, 18, 344-352.	4.0	51