

# Xian Zhang

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

35  
papers

840  
citations

16  
h-index

28  
g-index

37  
ext. papers

1,110  
ext. citations

4.9  
avg, IF

4.08  
L-index

#	Paper	IF	Citations
35	Current research scenario for biological effect of exogenous factors on microcystin synthesis.. <i>Environmental Science and Pollution Research</i> , <b>2022</b> , 1	5.1	1
34	Estimation of Avian Influenza Viruses in Water Environments of Live Poultry Markets in Changsha, China, 2014 to 2018.. <i>Food and Environmental Virology</i> , <b>2022</b> , 1	4	
33	A review on the effect of gut microbiota on metabolic diseases.. <i>Archives of Microbiology</i> , <b>2022</b> , 204, 192	3	0
32	Current knowledge on molecular mechanisms of microorganism-mediated bioremediation for arsenic contamination: A review.. <i>Microbiological Research</i> , <b>2022</b> , 258, 126990	5.3	4
31	A complete route for biodegradation of potentially carcinogenic cyanotoxin microcystin-LR in a novel indigenous bacterium. <i>Water Research</i> , <b>2020</b> , 174, 115638	12.5	50
30	Insights into ecological roles and potential evolution of Mlr-dependent microcystin-degrading bacteria. <i>Science of the Total Environment</i> , <b>2020</b> , 710, 136401	10.2	11
29	Functional role of bloom-forming cyanobacterium Planktothrix in ecologically shaping aquatic environments. <i>Science of the Total Environment</i> , <b>2020</b> , 710, 136314	10.2	10
28	Genome-Wide Analysis Reveals Genetic Potential for Aromatic Compounds Biodegradation of. <i>BioMed Research International</i> , <b>2020</b> , 2020, 5849123	3	6
27	Phylogeny, Divergent Evolution, and Speciation of Sulfur-Oxidizing Acidithiobacillus Populations. <i>BMC Genomics</i> , <b>2019</b> , 20, 438	4.5	12
26	The dissolution and passivation mechanism of chalcopyrite in bioleaching: An overview. <i>Minerals Engineering</i> , <b>2019</b> , 136, 140-154	4.9	81
25	MicroRNA expression profiling involved in MC-LR-induced hepatotoxicity using high-throughput sequencing analysis. <i>Journal of Toxicology and Environmental Health - Part A: Current Issues</i> , <b>2018</b> , 81, 89-97	3.2	38
24	Pan-Genome Analysis Links the Hereditary Variation of With Its Evolutionary Adaptation. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 577	5.7	12
23	Genome-Wide Analysis Reveals the Potential Links Between Core Genome of and Its Autotrophic Lifestyle. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 1255	5.7	12
22	Importance of bacterial biodegradation and detoxification processes of microcystins for environmental health. <i>Journal of Toxicology and Environmental Health - Part B: Critical Reviews</i> , <b>2018</b> , 21, 357-369	8.6	26
21	Adaptive Evolution of Extreme Acidophile <i>Sulfobacillus thermosulfidooxidans</i> Potentially Driven by Horizontal Gene Transfer and Gene Loss. <i>Applied and Environmental Microbiology</i> , <b>2017</b> , 83,	4.8	33
20	Effects of pyrite and sphalerite on population compositions, dynamics and copper extraction efficiency in chalcopyrite bioleaching process. <i>Archives of Microbiology</i> , <b>2017</b> , 199, 757-766	3	5
19	Responses of zinc recovery to temperature and mineral composition during sphalerite bioleaching process. <i>AMB Express</i> , <b>2017</b> , 7, 190	4.1	7

18	Draft Genome Sequence of LH-42, Isolated from Petroleum-Contaminated Soil. <i>Genome Announcements</i> , <b>2017</b> , 5,		1
17	Comparative Genomics Unravels the Functional Roles of Co-occurring Acidophilic Bacteria in Bioleaching Heaps. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 790	5.7	13
16	Insights into functional genes and taxonomical/phylogenetic diversity of microbial communities in biological heap leaching system and their correlation with functions. <i>Applied Microbiology and Biotechnology</i> , <b>2016</b> , 100, 9745-9756	5.7	14
15	Comparison of microbial taxonomic and functional shift pattern along contamination gradient. <i>BMC Microbiology</i> , <b>2016</b> , 16, 110	4.5	14
14	The shift of microbial communities and their roles in sulfur and iron cycling in a copper ore bioleaching system. <i>Scientific Reports</i> , <b>2016</b> , 6, 34744	4.9	14
13	Genomic Analysis Unravels Reduced Inorganic Sulfur Compound Oxidation of Heterotrophic Acidophilic <i>Acidithiobacillus</i> sp. Strain DX-1. <i>BioMed Research International</i> , <b>2016</b> , 2016, 8137012	3	2
12	Gene Turnover Contributes to the Evolutionary Adaptation of : Insights from Comparative Genomics. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 1960	5.7	20
11	Comparative Genomics of the Extreme Acidophile <i>Acidithiobacillus thiooxidans</i> Reveals Intraspecific Divergence and Niche Adaptation. <i>International Journal of Molecular Sciences</i> , <b>2016</b> , 17,	6.3	22
10	Metabolic diversity and adaptive mechanisms of iron- and/or sulfur-oxidizing autotrophic acidophiles in extremely acidic environments. <i>Environmental Microbiology Reports</i> , <b>2016</b> , 8, 738-751	3.7	33
9	Metagenome-scale analysis yields insights into the structure and function of microbial communities in a copper bioleaching heap. <i>BMC Genetics</i> , <b>2016</b> , 17, 21	2.6	63
8	Microbial communities from different subsystems in biological heap leaching system play different roles in iron and sulfur metabolisms. <i>Applied Microbiology and Biotechnology</i> , <b>2016</b> , 100, 6871-6880	5.7	23
7	Comparative genomics unravels metabolic differences at the species and/or strain level and extremely acidic environmental adaptation of ten bacteria belonging to the genus <i>Acidithiobacillus</i> . <i>Systematic and Applied Microbiology</i> , <b>2016</b> , 39, 493-502	4.2	20
6	The complicated substrates enhance the microbial diversity and zinc leaching efficiency in sphalerite bioleaching system. <i>Applied Microbiology and Biotechnology</i> , <b>2015</b> , 99, 10311-22	5.7	23
5	An integrated insight into the response of sedimentary microbial communities to heavy metal contamination. <i>Scientific Reports</i> , <b>2015</b> , 5, 14266	4.9	138
4	Theoretical Model of the Structure and the Reaction Mechanisms of Sulfur Oxygenase Reductase in <i>Acidithiobacillus thiooxidans</i> . <i>Advanced Materials Research</i> , <b>2015</b> , 1130, 67-70	0.5	8
3	Comparative genome analysis reveals metabolic versatility and environmental adaptations of <i>Sulfolobus</i> <i>thermosulfidooxidans</i> strain ST. <i>PLoS ONE</i> , <b>2014</b> , 9, e99417	3.7	34
2	Draft Genome Sequence of the Extremophile <i>Acidithiobacillus thiooxidans</i> A01, Isolated from the Wastewater of a Coal Dump. <i>Genome Announcements</i> , <b>2014</b> , 2,		19
1	Whole-genome sequencing reveals novel insights into sulfur oxidation in the extremophile <i>Acidithiobacillus thiooxidans</i> . <i>BMC Microbiology</i> , <b>2014</b> , 14, 179	4.5	69

