

Huaqun Yin

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

4,396
citations

81900
39
h-index

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docs citations

99
times ranked

3996
citing authors

#	ARTICLE	IF	CITATIONS
1	Response of soil microbial communities and microbial interactions to long-term heavy metal contamination. <i>Environmental Pollution</i> , 2017, 231, 908-917.	7.5	320
2	Biodiversity and species competition regulate the resilience of microbial biofilm community. <i>Molecular Ecology</i> , 2017, 26, 6170-6182.	3.9	299
3	An integrated insight into the response of sedimentary microbial communities to heavy metal contamination. <i>Scientific Reports</i> , 2015, 5, 14266.	3.3	235
4	Analyses of soil microbial community compositions and functional genes reveal potential consequences of natural forest succession. <i>Scientific Reports</i> , 2015, 5, 10007.	3.3	162
5	Soil bacterial quantification approaches coupling with relative abundances reflecting the changes of taxa. <i>Scientific Reports</i> , 2017, 7, 4837.	3.3	131
6	Significant relationship between soil bacterial community structure and incidence of bacterial wilt disease under continuous cropping system. <i>Archives of Microbiology</i> , 2017, 199, 267-275.	2.2	111
7	Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. <i>Environmental Science & Technology</i> , 2019, 53, 1315-1324.	10.0	109
8	An Integrated Insight into the Relationship between Soil Microbial Community and Tobacco Bacterial Wilt Disease. <i>Frontiers in Microbiology</i> , 2017, 8, 2179.	3.5	108
9	Responses of bacterial community to dibutyl phthalate pollution in a soil-vegetable ecosystem. <i>Journal of Hazardous Materials</i> , 2018, 353, 142-150.	12.4	104
10	Whole-genome sequencing reveals novel insights into sulfur oxidation in the extremophile <i>Acidithiobacillus thiooxidans</i> . <i>BMC Microbiology</i> , 2014, 14, 179.	3.3	102
11	Integrated network analysis reveals the importance of microbial interactions for maize growth. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3805-3818.	3.6	94
12	Effects of redox potential on soil cadmium solubility: Insight into microbial community. <i>Journal of Environmental Sciences</i> , 2019, 75, 224-232.	6.1	87
13	Maize growth responses to soil microbes and soil properties after fertilization with different green manures. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1289-1299.	3.6	83
14	Metagenome-scale analysis yields insights into the structure and function of microbial communities in a copper bioleaching heap. <i>BMC Genetics</i> , 2016, 17, 21.	2.7	82
15	The divergence between fungal and bacterial communities in seasonal and spatial variations of wastewater treatment plants. <i>Science of the Total Environment</i> , 2018, 628-629, 969-978.	8.0	79
16	Bacterial adaptive strategies to cope with metal toxicity in the contaminated environment – A review. <i>Ecotoxicology and Environmental Safety</i> , 2021, 226, 112863.	6.0	77
17	Spatial distribution and risk assessment of heavy metals in contaminated paddy fields – A case study in Xiangtan City, southern China. <i>Ecotoxicology and Environmental Safety</i> , 2019, 171, 281-289.	6.0	76
18	Soil potentials to resist continuous cropping obstacle: Three field cases. <i>Environmental Research</i> , 2021, 200, 111319.	7.5	71

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19	Insight into the effects of different cropping systems on soil bacterial community and tobacco bacterial wilt rate. <i>Journal of Basic Microbiology</i> , 2017, 57, 3-11.	3.3	69
20	Co-culture microorganisms with different initial proportions reveal the mechanism of chalcophyrite bioleaching coupling with microbial community succession. <i>Bioresource Technology</i> , 2017, 223, 121-130.	9.6	64
21	Host development overwhelms environmental dispersal in governing the ecological succession of zebrafish gut microbiota. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 5.	6.4	64
22	Development and evaluation of 50-mer oligonucleotide arrays for detecting microbial populations in Acid Mine Drainages and bioleaching systems. <i>Journal of Microbiological Methods</i> , 2007, 70, 165-178.	1.6	62
23	The co-culture of <i>Acidithiobacillus ferrooxidans</i> and <i>Acidiphilium acidophilum</i> enhances the growth, iron oxidation, and CO ₂ fixation. <i>Archives of Microbiology</i> , 2011, 193, 857-866.	2.2	59
24	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. <i>Scientific Reports</i> , 2018, 8, 13314.	3.3	54
25	Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. <i>MSystems</i> , 2019, 4, .	3.8	54
26	Isolation, characterization and inoculation of Cd tolerant rice endophytes and their impacts on rice under Cd contaminated environment. <i>Environmental Pollution</i> , 2020, 260, 113990.	7.5	54
27	The utilization of biomineralization technique based on microbial induced phosphate precipitation in remediation of potentially toxic ions contaminated soil: A mini review. <i>Ecotoxicology and Environmental Safety</i> , 2020, 191, 110009.	6.0	51
28	Production and functionality of exopolysaccharides in bacteria exposed to a toxic metal environment. <i>Ecotoxicology and Environmental Safety</i> , 2021, 208, 111567.	6.0	51
29	The succession pattern of soil microbial communities and its relationship with tobacco bacterial wilt. <i>BMC Microbiology</i> , 2016, 16, 233.	3.3	50
30	Microbial functional genes enriched in the Xiangjiang River sediments with heavy metal contamination. <i>BMC Microbiology</i> , 2016, 16, 179.	3.3	50
31	Environmental factors shaping the diversity of bacterial communities that promote rice production. <i>BMC Microbiology</i> , 2018, 18, 51.	3.3	50
32	Large-scale seaweed cultivation diverges water and sediment microbial communities in the coast of Nan'ao Island, South China Sea. <i>Science of the Total Environment</i> , 2017, 598, 97-108.	8.0	49
33	Adaptive Evolution of Extreme Acidophile <i>Sulfobacillus thermosulfidooxidans</i> Potentially Driven by Horizontal Gene Transfer and Gene Loss. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	48
34	The role of soil bacterial community during winter fallow period in the incidence of tobacco bacterial wilt disease. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2399-2412.	3.6	47
35	Comparative Genome Analysis Reveals Metabolic Versatility and Environmental Adaptations of <i>Sulfobacillus thermosulfidooxidans</i> Strain ST. <i>PLoS ONE</i> , 2014, 9, e99417.	2.5	45
36	Metabolic diversity and adaptive mechanisms of iron and/or sulfur oxidizing autotrophic acidophiles in extremely acidic environments. <i>Environmental Microbiology Reports</i> , 2016, 8, 738-751.	2.4	45

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37	Responses of phyllosphere microbiota and plant health to application of two different biocontrol agents. <i>AMB Express</i> , 2019, 9, 42.	3.0	44
38	Identification of Nitrogen-Fixing Genes and Gene Clusters from Metagenomic Library of Acid Mine Drainage. <i>PLoS ONE</i> , 2014, 9, e87976.	2.5	43
39	Bacterial diversity based on 16S rRNA and gyrB genes at Yinshan mine, China. <i>Systematic and Applied Microbiology</i> , 2008, 31, 302-311.	2.8	40
40	Exploring abundance, diversity and variation of a widespread antibiotic resistance gene in wastewater treatment plants. <i>Environment International</i> , 2018, 117, 186-195.	10.0	40
41	Comparative Genomics of the Extreme Acidophile <i>Acidithiobacillus thiooxidans</i> Reveals Intraspecific Divergence and Niche Adaptation. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1355.	4.1	39
42	Molecular diversity of 16S rRNA and gyrB genes in copper mines. <i>Archives of Microbiology</i> , 2008, 189, 101-110.	2.2	37
43	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> , 2016, 39, 493-502.	2.8	36
44	Comparative Genomic Analysis Reveals the Distribution, Organization, and Evolution of Metal Resistance Genes in the Genus <i>Acidithiobacillus</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	35
45	Development and application of SCAR markers for sex identification in the dioecious species <i>Ginkgo biloba</i> L. <i>Euphytica</i> , 2009, 169, 49-55.	1.2	33
46	Bioremediation of cadmium-contaminated paddy soil using an autotrophic and heterotrophic mixture. <i>RSC Advances</i> , 2020, 10, 26090-26101.	3.6	32
47	Flavonoid Biosynthesis Is Likely More Susceptible to Elevation and Tree Age Than Other Branch Pathways Involved in Phenylpropanoid Biosynthesis in <i>Ginkgo</i> Leaves. <i>Frontiers in Plant Science</i> , 2019, 10, 983.	3.6	31
48	Insights into the Metabolism and Evolution of the Genus <i>Acidiphilium</i> , a Typical Acidophile in Acid Mine Drainage. <i>MSystems</i> , 2020, 5, .	3.8	31
49	Mixotrophic acidophiles increase cadmium soluble fraction and phytoextraction efficiency from cadmium contaminated soils. <i>Science of the Total Environment</i> , 2019, 655, 347-355.	8.0	30
50	Microbial communities from different subsystems in biological heap leaching system play different roles in iron and sulfur metabolisms. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 6871-6880.	3.6	29
51	Soil microbiome mediated nutrients decline during forest degradation process. <i>Soil Ecology Letters</i> , 2019, 1, 59-71.	4.5	29
52	The complicated substrates enhance the microbial diversity and zinc leaching efficiency in sphalerite bioleaching system. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10311-10322.	3.6	26
53	Current knowledge on molecular mechanisms of microorganism-mediated bioremediation for arsenic contamination: A review. <i>Microbiological Research</i> , 2022, 258, 126990.	5.3	26
54	Cadmium, lead and arsenic contamination in an abandoned nonferrous metal smelting site in southern China: Chemical speciation and mobility. <i>Ecotoxicology and Environmental Safety</i> , 2022, 239, 113617.	6.0	26

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55	Effects of Arsenite Resistance on the Growth and Functional Gene Expression of <i>Leptospirillum ferriphilum</i> and <i>Acidithiobacillus thiooxidans</i> in Pure Culture and Coculture. <i>BioMed Research International</i> , 2015, 2015, 1-13.	1.9	22
56	The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. <i>Molecular Ecology</i> , 2017, 26, 3676-3686.	3.9	22
57	Draft Genome Sequence of the Extremophile <i>Acidithiobacillus thiooxidans</i> A01, Isolated from the Wastewater of a Coal Dump. <i>Genome Announcements</i> , 2014, 2, .	0.8	21
58	Comparative metagenomics reveals microbial community differentiation in a biological heap leaching system. <i>Research in Microbiology</i> , 2015, 166, 525-534.	2.1	21
59	Reduction mechanism of Cd accumulation in rice grain by Chinese milk vetch residue: Insight into microbial community. <i>Ecotoxicology and Environmental Safety</i> , 2020, 202, 110908.	6.0	19
60	An integrated insight into bioleaching performance of chalcopyrite mediated by microbial factors: Functional types and biodiversity. <i>Bioresource Technology</i> , 2021, 319, 124219.	9.6	19
61	Life cycle assessment and cost analysis for copper hydrometallurgy industry in China. <i>Journal of Environmental Management</i> , 2022, 309, 114689.	7.8	19
62	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> , 2016, 100, 9745-9756.	3.6	18
63	The shift of microbial communities and their roles in sulfur and iron cycling in a copper ore bioleaching system. <i>Scientific Reports</i> , 2016, 6, 34744.	3.3	18
64	Characterization and Biotechnological Functional Activities of Exopolysaccharides Produced by <i>Lysinibacillus fusiformis</i> KMNTT-10. <i>Journal of Polymers and the Environment</i> , 2021, 29, 1742-1751.	5.0	18
65	Spatial Distribution of Toxic Metal(loid)s and Microbial Community Analysis in Soil Vertical Profile at an Abandoned Nonferrous Metal Smelting Site. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 7101.	2.6	17
66	Comparison of microbial taxonomic and functional shift pattern along contamination gradient. <i>BMC Microbiology</i> , 2016, 16, 110.	3.3	16
67	Progressive Microbial Community Networks with Incremental Organic Loading Rates Underlie Higher Anaerobic Digestion Performance. <i>MSystems</i> , 2020, 5, .	3.8	15
68	Florfenicol restructured the microbial interaction network for wastewater treatment by microbial electrolysis cells. <i>Environmental Research</i> , 2020, 183, 109145.	7.5	14
69	Chalcopyrite bioleaching of an <i>in situ</i> leaching system by introducing different functional oxidizers. <i>RSC Advances</i> , 2018, 8, 37040-37049.	3.6	12
70	Microbiological Sulfide Removal—From Microorganism Isolation to Treatment of Industrial Effluent. <i>Microorganisms</i> , 2021, 9, 611.	3.6	12
71	Mobile genetic elements mediate the mixotrophic evolution of novel <i>Alicyclobacillus</i> species for acid mine drainage adaptation. <i>Environmental Microbiology</i> , 2021, 23, 3896-3912.	3.8	12
72	Root Endophytes and <i>Ginkgo biloba</i> Are Likely to Share and Compensate Secondary Metabolic Processes, and Potentially Exchange Genetic Information by LTR-RTs. <i>Frontiers in Plant Science</i> , 2021, 12, 704985.	3.6	12

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73	Insights into the fluoride-resistant regulation mechanism of <i>Acidithiobacillus ferrooxidans</i> ATCC 23270 based on whole genome microarrays. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2016, 43, 1441-1453.	3.0	11
74	Carbon Material with High Specific Surface Area Improves Complex Copper Ores' Bioleaching Efficiency by Mixed Moderate Thermophiles. <i>Minerals (Basel, Switzerland)</i> , 2018, 8, 301.	2.0	11
75	Vertical distribution of the toxic metal(loid)s chemical fraction and microbial community in waste heap at a nonferrous metal mining site. <i>Ecotoxicology and Environmental Safety</i> , 2021, 228, 113037.	6.0	11
76	Interactions and Stability of Gut Microbiota in Zebrafish Increase with Host Development. <i>Microbiology Spectrum</i> , 2022, 10, e0169621.	3.0	11
77	Bio-Oxidation of a Double Refractory Gold Ore and Investigation of Preg-Robbing of Gold from Thiourea Solution. <i>Metals</i> , 2020, 10, 1216.	2.3	10
78	Assessing Chromium Contamination in Red Soil: Monitoring the Migration of Fractions and the Change of Related Microorganisms. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 2835.	2.6	10
79	Distribution of the potential pathogenic <i>Alternaria</i> on plant leaves determines foliar fungal communities around the disease spot. <i>Environmental Research</i> , 2021, 200, 111715.	7.5	10
80	Ecological responses of bacterial assembly and functions to steep Cd gradient in a typical Cd-contaminated farmland ecosystem. <i>Ecotoxicology and Environmental Safety</i> , 2022, 229, 113067.	6.0	10
81	Responses of zinc recovery to temperature and mineral composition during sphalerite bioleaching process. <i>AMB Express</i> , 2017, 7, 190.	3.0	9
82	Traits of Exogenous Species and Indigenous Community Contribute to the Species Colonization and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 3087.	3.5	9
83	Ecological strategies of biological and chemical control agents on wildfire disease of tobacco (<i>Nicotiana tabacum</i> L.). <i>BMC Microbiology</i> , 2021, 21, 184.	3.3	9
84	Comparative Genomics Provides Insights into the Genetic Diversity and Evolution of the DPANN Superphylum. <i>MSystems</i> , 2021, 6, e0060221.	3.8	9
85	Biostimulation of sulfate-reducing bacteria used for treatment of hydrometallurgical waste by secondary metabolites of urea decomposition by <i>Ochrobactrum</i> sp. POC9: From genome to microbiome analysis. <i>Chemosphere</i> , 2021, 282, 131064.	8.2	9
86	Mechanism of Intermittent Deep Tillage and Different Depths Improving Crop Growth From the Perspective of Rhizosphere Soil Nutrients, Root System Architectures, Bacterial Communities, and Functional Profiles. <i>Frontiers in Microbiology</i> , 2021, 12, 759374.	3.5	8
87	Effects of pyrite and sphalerite on population compositions, dynamics and copper extraction efficiency in chalcopyrite bioleaching process. <i>Archives of Microbiology</i> , 2017, 199, 757-766.	2.2	6
88	Synergic Effect of Adsorption and Biodegradation by Microsphere Immobilizing <i>Bacillus velezensis</i> for Enhanced Removal Organics in Slaughter Wastewater. <i>Processes</i> , 2021, 9, 1145.	2.8	6
89	Decomposition of Microbial Necromass Is Divergent at the Individual Taxonomic Level in Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 679793.	3.5	6
90	Warming differentially altered multidimensional soil legacy induced by past land use history. <i>Scientific Reports</i> , 2018, 8, 1546.	3.3	5

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91	Development of the yeast and lactic acid bacteria co-culture agent for atmospheric ammonia removing: Genomic features and on-site applications. <i>Ecotoxicology and Environmental Safety</i> , 2021, 218, 112287.	6.0	5
92	Distinctive heat-shock response of bioleaching microorganism <i>Acidithiobacillus ferrooxidans</i> observed using genome-wide microarray. <i>Canadian Journal of Microbiology</i> , 2012, 58, 628-636.	1.7	4
93	Responses of <i>Acidithiobacillus thiooxidans</i> A01 to Individual and Joint Nickel (Ni ²⁺) and Ferric (Fe ³⁺). <i>Minerals (Basel, Switzerland)</i> , 2019, 9, 82.	2.0	4
94	Effects of graphene oxide on PCR amplification for microbial community survey. <i>BMC Microbiology</i> , 2020, 20, 278.	3.3	4
95	Influence of Association Network Properties and Ecological Assembly of the Foliar Fungal Community on Crop Quality. <i>Frontiers in Microbiology</i> , 2022, 13, 783923.	3.5	4
96	Insights into the Interactions Between Root Phenotypic Traits and the Rhizosphere Bacterial Community. <i>Current Microbiology</i> , 2022, 79, 176.	2.2	3
97	Stochastic and deterministic drivers of seasonal variation of fungal community in tobacco field soil. <i>PeerJ</i> , 2019, 7, e6962.	2.0	1
98	The Self-Organization of Marine Microbial Networks under Evolutionary and Ecological Processes: Observations and Modeling. <i>Biology</i> , 2022, 11, 592.	2.8	0