

# Huaqun Yin

## List of Publications by Year in descending order

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98  
papers

4,396  
citations

81743

39  
h-index

123241

61  
g-index

99  
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99  
docs citations

99  
times ranked

3996  
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.9	10
2	Interactions and Stability of Gut Microbiota in Zebrafish Increase with Host Development. <i>Microbiology Spectrum</i> , 2022, 10, e0169621.	1.2	11
3	Life cycle assessment and cost analysis for copper hydrometallurgy industry in China. <i>Journal of Environmental Management</i> , 2022, 309, 114689.	3.8	19
4	Current knowledge on molecular mechanisms of microorganism-mediated bioremediation for arsenic contamination: A review. <i>Microbiological Research</i> , 2022, 258, 126990.	2.5	26
5	The Self-Organization of Marine Microbial Networks under Evolutionary and Ecological Processes: Observations and Modeling. <i>Biology</i> , 2022, 11, 592.	1.3	0
6	Influence of Association Network Properties and Ecological Assembly of the Foliar Fungal Community on Crop Quality. <i>Frontiers in Microbiology</i> , 2022, 13, 783923.	1.5	4
7	Insights into the Interactions Between Root Phenotypic Traits and the Rhizosphere Bacterial Community. <i>Current Microbiology</i> , 2022, 79, 176.	1.0	3
8	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.	2.9	26
9	An integrated insight into bioleaching performance of chalcopyrite mediated by microbial factors: Functional types and biodiversity. <i>Bioresource Technology</i> , 2021, 319, 124219.	4.8	19
10	Production and functionality of exopolysaccharides in bacteria exposed to a toxic metal environment. <i>Ecotoxicology and Environmental Safety</i> , 2021, 208, 111567.	2.9	51
11	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.	2.4	18
12	Microbiological Sulfide Removal From Microorganism Isolation to Treatment of Industrial Effluent. <i>Microorganisms</i> , 2021, 9, 611.	1.6	12
13	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.	1.8	12
14	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.	1.3	9
15	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.	1.3	6
16	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.	1.7	12
17	Decomposition of Microbial Necromass Is Divergent at the Individual Taxonomic Level in Soil. <i>Frontiers in Microbiology</i> , 2021, 12, 679793.	1.5	6
18	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.	2.9	5

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19	Comparative Genomics Provides Insights into the Genetic Diversity and Evolution of the DPANN Superphylum. <i>MSystems</i> , 2021, 6, e0060221.	1.7	9
20	Soil potentials to resist continuous cropping obstacle: Three field cases. <i>Environmental Research</i> , 2021, 200, 111319.	3.7	71
21	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.	3.7	10
22	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.	4.2	9
23	Host development overwhelms environmental dispersal in governing the ecological succession of zebrafish gut microbiota. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 5.	2.9	64
24	Bacterial adaptive strategies to cope with metal toxicity in the contaminated environment – A review. <i>Ecotoxicology and Environmental Safety</i> , 2021, 226, 112863.	2.9	77
25	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.	2.9	11
26	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.	1.5	8
27	Progressive Microbial Community Networks with Incremental Organic Loading Rates Underlie Higher Anaerobic Digestion Performance. <i>MSystems</i> , 2020, 5, .	1.7	15
28	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.	2.9	51
29	Bioremediation of cadmium-contaminated paddy soil using an autotrophic and heterotrophic mixture. <i>RSC Advances</i> , 2020, 10, 26090-26101.	1.7	32
30	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.	1.2	17
31	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.	2.9	19
32	Effects of graphene oxide on PCR amplification for microbial community survey. <i>BMC Microbiology</i> , 2020, 20, 278.	1.3	4
33	Insights into the Metabolism and Evolution of the Genus <i>Acidiphilium</i> , a Typical Acidophile in Acid Mine Drainage. <i>MSystems</i> , 2020, 5, .	1.7	31
34	Bio-Oxidation of a Double Refractory Gold Ore and Investigation of Preg-Robbing of Gold from Thiourea Solution. <i>Metals</i> , 2020, 10, 1216.	1.0	10
35	Florfenicol restructured the microbial interaction network for wastewater treatment by microbial electrolysis cells. <i>Environmental Research</i> , 2020, 183, 109145.	3.7	14
36	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.	3.7	54

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37	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.	1.2	10
38	Soil microbiome mediated nutrients decline during forest degradation process. <i>Soil Ecology Letters</i> , 2019, 1, 59-71.	2.4	29
39	Flavonoid Biosynthesis Is Likely More Susceptible to Elevation and Tree Age Than Other Branch Pathways Involved in Phenylpropanoid Biosynthesis in Ginkgo Leaves. <i>Frontiers in Plant Science</i> , 2019, 10, 983.	1.7	31
40	Responses of phyllosphere microbiota and plant health to application of two different biocontrol agents. <i>AMB Express</i> , 2019, 9, 42.	1.4	44
41	Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. <i>MSystems</i> , 2019, 4, .	1.7	54
42	Responses of <i>Acidithiobacillus thiooxidans</i> A01 to Individual and Joint Nickel (Ni <sup>2+</sup> ) and Ferric (Fe <sup>3+</sup> ). <i>Minerals (Basel, Switzerland)</i> , 2019, 9, 82.	0.8	4
43	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, .	1.4	35
44	Mixotrophic acidophiles increase cadmium soluble fraction and phytoextraction efficiency from cadmium contaminated soils. <i>Science of the Total Environment</i> , 2019, 655, 347-355.	3.9	30
45	Deterministic Assembly and Diversity Gradient Altered the Biofilm Community Performances of Bioreactors. <i>Environmental Science &amp; Technology</i> , 2019, 53, 1315-1324.	4.6	109
46	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.	2.9	76
47	Effects of redox potential on soil cadmium solubility: Insight into microbial community. <i>Journal of Environmental Sciences</i> , 2019, 75, 224-232.	3.2	87
48	Stochastic and deterministic drivers of seasonal variation of fungal community in tobacco field soil. <i>PeerJ</i> , 2019, 7, e6962.	0.9	1
49	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.	3.9	79
50	Responses of bacterial community to dibutyl phthalate pollution in a soil-vegetable ecosystem. <i>Journal of Hazardous Materials</i> , 2018, 353, 142-150.	6.5	104
51	Warming differentially altered multidimensional soil legacy induced by past land use history. <i>Scientific Reports</i> , 2018, 8, 1546.	1.6	5
52	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.	1.7	47
53	Integrated network analysis reveals the importance of microbial interactions for maize growth. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 3805-3818.	1.7	94
54	Traits of Exogenous Species and Indigenous Community Contribute to the Species Colonization and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 3087.	1.5	9

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55	Chalcopyrite bioleaching of an <i>in situ</i> leaching system by introducing different functional oxidizers. RSC Advances, 2018, 8, 37040-37049.	1.7	12
56	Habitat environments impacted the gut microbiome of long-distance migratory swan geese but central species conserved. Scientific Reports, 2018, 8, 13314.	1.6	54
57	Environmental factors shaping the diversity of bacterial communities that promote rice production. BMC Microbiology, 2018, 18, 51.	1.3	50
58	Carbon Material with High Specific Surface Area Improves Complex Copper Ores'™ Bioleaching Efficiency by Mixed Moderate Thermophiles. Minerals (Basel, Switzerland), 2018, 8, 301.	0.8	11
59	Exploring abundance, diversity and variation of a widespread antibiotic resistance gene in wastewater treatment plants. Environment International, 2018, 117, 186-195.	4.8	40
60	Adaptive Evolution of Extreme Acidophile Sulfolobus thermosulfidooxidans Potentially Driven by Horizontal Gene Transfer and Gene Loss. Applied and Environmental Microbiology, 2017, 83, .	1.4	48
61	Effects of pyrite and sphalerite on population compositions, dynamics and copper extraction efficiency in chalcopyrite bioleaching process. Archives of Microbiology, 2017, 199, 757-766.	1.0	6
62	Large-scale seaweed cultivation diverges water and sediment microbial communities in the coast of Nan'ao Island, South China Sea. Science of the Total Environment, 2017, 598, 97-108.	3.9	49
63	The microbially mediated soil organic carbon loss under degenerative succession in an alpine meadow. Molecular Ecology, 2017, 26, 3676-3686.	2.0	22
64	Response of soil microbial communities and microbial interactions to long-term heavy metal contamination. Environmental Pollution, 2017, 231, 908-917.	3.7	320
65	Biodiversity and species competition regulate the resilience of microbial biofilm community. Molecular Ecology, 2017, 26, 6170-6182.	2.0	299
66	Soil bacterial quantification approaches coupling with relative abundances reflecting the changes of taxa. Scientific Reports, 2017, 7, 4837.	1.6	131
67	Maize growth responses to soil microbes and soil properties after fertilization with different green manures. Applied Microbiology and Biotechnology, 2017, 101, 1289-1299.	1.7	83
68	Co-culture microorganisms with different initial proportions reveal the mechanism of chalcopyrite bioleaching coupling with microbial community succession. Bioresource Technology, 2017, 223, 121-130.	4.8	64
69	Significant relationship between soil bacterial community structure and incidence of bacterial wilt disease under continuous cropping system. Archives of Microbiology, 2017, 199, 267-275.	1.0	111
70	Insight into the effects of different cropping systems on soil bacterial community and tobacco bacterial wilt rate. Journal of Basic Microbiology, 2017, 57, 3-11.	1.8	69
71	An Integrated Insight into the Relationship between Soil Microbial Community and Tobacco Bacterial Wilt Disease. Frontiers in Microbiology, 2017, 8, 2179.	1.5	108
72	Responses of zinc recovery to temperature and mineral composition during sphalerite bioleaching process. AMB Express, 2017, 7, 190.	1.4	9

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73	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.	1.8	39
74	The succession pattern of soil microbial communities and its relationship with tobacco bacterial wilt. <i>BMC Microbiology</i> , 2016, 16, 233.	1.3	50
75	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.	1.0	45
76	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
77	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.	1.7	29
78	Microbial functional genes enriched in the Xiangjiang River sediments with heavy metal contamination. <i>BMC Microbiology</i> , 2016, 16, 179.	1.3	50
79	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.	1.2	36
80	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.	1.4	11
81	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.	1.7	18
82	Comparison of microbial taxonomic and functional shift pattern along contamination gradient. <i>BMC Microbiology</i> , 2016, 16, 110.	1.3	16
83	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.	1.6	18
84	An integrated insight into the response of sedimentary microbial communities to heavy metal contamination. <i>Scientific Reports</i> , 2015, 5, 14266.	1.6	235
85	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.	0.9	22
86	Analyses of soil microbial community compositions and functional genes reveal potential consequences of natural forest succession. <i>Scientific Reports</i> , 2015, 5, 10007.	1.6	162
87	Comparative metagenomics reveals microbial community differentiation in a biological heap leaching system. <i>Research in Microbiology</i> , 2015, 166, 525-534.	1.0	21
88	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.	1.7	26
89	Comparative Genome Analysis Reveals Metabolic Versatility and Environmental Adaptations of <i>Sulfobacillus thermosulfidooxidans</i> Strain ST. <i>PLoS ONE</i> , 2014, 9, e99417.	1.1	45
90	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

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91	Whole-genome sequencing reveals novel insights into sulfur oxidation in the extremophile <i>Acidithiobacillus thiooxidans</i> . <i>BMC Microbiology</i> , 2014, 14, 179.	1.3	102
92	Identification of Nitrogen-Fixing Genes and Gene Clusters from Metagenomic Library of Acid Mine Drainage. <i>PLoS ONE</i> , 2014, 9, e87976.	1.1	43
93	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.	0.8	4
94	The co-culture of <i>Acidithiobacillus ferrooxidans</i> and <i>Acidiphilium acidophilum</i> enhances the growth, iron oxidation, and CO <sub>2</sub> fixation. <i>Archives of Microbiology</i> , 2011, 193, 857-866.	1.0	59
95	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.	0.6	33
96	Molecular diversity of 16S rRNA and <i>gyrB</i> genes in copper mines. <i>Archives of Microbiology</i> , 2008, 189, 101-110.	1.0	37
97	Bacterial diversity based on 16S rRNA and <i>gyrB</i> genes at Yinshan mine, China. <i>Systematic and Applied Microbiology</i> , 2008, 31, 302-311.	1.2	40
98	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.	0.7	62