

Yan-Ping Mao

List of Publications by Year in descending order

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papers

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docs citations

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#	ARTICLE	IF	CITATIONS
1	Enhanced Bioremediation Potential of <i>Shewanella decolorationis</i> RNA Polymerase Mutants and Evidence for Novel Azo Dye Biodegradation Pathways. <i>Frontiers in Microbiology</i> , 2022, 13, 843807.	3.5	0
2	Isolation of Anaerobic Bromate-Reducing Bacteria Using Different Carbon Sources and Transcriptomic Insights From <i>Klebsiella variicola</i> Glu3. <i>Frontiers in Microbiology</i> , 2022, 13, 851844.	3.5	2
3	Transcriptome analysis provides new insights into the tolerance and aerobic reduction of <i>Shewanella decolorationis</i> Ni1-3 to bromate. <i>Applied Microbiology and Biotechnology</i> , 2022, 106, 4749-4761.	3.6	2
4	Noble metal-free NiCo ₂ S ₄ /CN sheet-on-sheet heterostructure for highly efficient visible-light-driven photocatalytic hydrogen evolution. <i>Journal of Alloys and Compounds</i> , 2021, 853, 157284.	5.5	26
5	Seasonal Prevalence of Ammonia-Oxidizing Archaea in a Full-Scale Municipal Wastewater Treatment Plant Treating Saline Wastewater Revealed by a 6-Year Time-Series Analysis. <i>Environmental Science & Technology</i> , 2021, 55, 2662-2673.	10.0	11
6	The first complete genome sequence of species <i>Shewanella decolorationis</i> , from a bioremediation competent strain Ni1-3. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	2
7	Phylogenetically divergent bacteria consortium from neutral activated sludge showed heightened potential on bioleaching spent lithium-ion batteries. <i>Ecotoxicology and Environmental Safety</i> , 2021, 223, 112592.	6.0	11
8	Characterizing community dynamics and exploring bacterial assemblages in two activated sludge systems. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 1795-1808.	3.6	11
9	Facile one-pot synthesis of mesoporous g-C ₃ N ₄ nanosheets with simultaneous iodine doping and N-vacancies for efficient visible-light-driven H ₂ evolution performance. <i>Catalysis Science and Technology</i> , 2020, 10, 549-559.	4.1	39
10	Diversity of gut microbiomes in marine fishes is shaped by host-related factors. <i>Molecular Ecology</i> , 2020, 29, 5019-5034.	3.9	57
11	A comprehensive review of anaerobic digestion of organic solid wastes in relation to microbial community and enhancement process. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 507-516.	3.5	24
12	Multiple-cycle operation of sulphur-cycle-enhanced biological phosphorus removal to maintain stable performance at high temperatures. <i>Bioresource Technology</i> , 2019, 289, 121736.	9.6	9
13	Microbial reduction of bromate: current status and prospects. <i>Biodegradation</i> , 2019, 30, 365-374.	3.0	8
14	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , 2019, 10, 4574.	12.8	90
15	Investigation on polyphosphate accumulation in the sulfur transformation-centric EBPR (SEBPR) process for treatment of high-temperature saline wastewater. <i>Water Research</i> , 2019, 167, 115138.	11.3	8
16	Synthesis of Sea Urchin-Like NiCo ₂ O ₄ via Charge-Driven Self-Assembly Strategy for High-Performance Lithium-Ion Batteries. <i>Nanoscale Research Letters</i> , 2019, 14, 6.	5.7	10
17	Phylogenetic characterization of bromate-reducing microbial community enriched anaerobically from activated sludge. <i>Ecotoxicology and Environmental Safety</i> , 2019, 184, 109630.	6.0	6
18	Microbial characterization of heavy metal resistant bacterial strains isolated from an electroplating wastewater treatment plant. <i>Ecotoxicology and Environmental Safety</i> , 2019, 181, 472-480.	6.0	49

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19	Mining traits for the enrichment and isolation of not-yet-cultured populations. <i>Microbiome</i> , 2019, 7, 96.	11.1	8
20	Genome-centric metagenomics resolves microbial diversity and prevalent truncated denitrification pathways in a denitrifying PAO-enriched bioprocess. <i>Water Research</i> , 2019, 155, 275-287.	11.3	77
21	Gaseous bubble-assisted in-situ construction of worm-like porous g-C ₃ N ₄ with superior visible light photocatalytic performance. <i>Applied Catalysis A: General</i> , 2019, 573, 13-21.	4.3	24
22	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
23	Free-living bacteria and potential bacterial pathogens in sewage treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2455-2464.	3.6	47
24	Partnership of <i>Arthrobacter</i> and <i>Pimelobacter</i> in Aerobic Degradation of Sulfadiazine Revealed by Metagenomics Analysis and Isolation. <i>Environmental Science & Technology</i> , 2018, 52, 2963-2972.	10.0	26
25	Controllable synthesis of graphitic carbon nitride nanomaterials for solar energy conversion and environmental remediation: the road travelled and the way forward. <i>Catalysis Science and Technology</i> , 2018, 8, 4576-4599.	4.1	99
26	Thermodynamic and physiological study of caproate and 1,3-propanediol co-production through glycerol fermentation and fatty acids chain elongation. <i>Water Research</i> , 2017, 114, 200-209.	11.3	62
27	Comammox in drinking water systems. <i>Water Research</i> , 2017, 116, 332-341.	11.3	163
28	Exploring the Shift in Structure and Function of Microbial Communities Performing Biological Phosphorus Removal. <i>PLoS ONE</i> , 2016, 11, e0161506.	2.5	9
29	Development of Quantitative Real-time PCR Assays for Different Clades of <i>Candidatus Accumulibacter</i> . <i>Scientific Reports</i> , 2016, 6, 23993.	3.3	32
30	Aerobic Degradation of Sulfadiazine by <i>Arthrobacter</i> spp.: Kinetics, Pathways, and Genomic Characterization. <i>Environmental Science & Technology</i> , 2016, 50, 9566-9575.	10.0	134
31	Novel nitrifiers and comammox in a full-scale hybrid biofilm and activated sludge reactor revealed by metagenomic approach. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8225-8237.	3.6	90
32	Dominant and novel clades of <i>Candidatus Accumulibacter phosphatis</i> in 18 globally distributed full-scale wastewater treatment plants. <i>Scientific Reports</i> , 2015, 5, 11857.	3.3	64
33	Diversity and functions of bacterial community in drinking water biofilms revealed by high-throughput sequencing. <i>Scientific Reports</i> , 2015, 5, 10044.	3.3	71
34	Reconstructing a <i>Thauera</i> genome from a hydrogenotrophic-denitrifying consortium using metagenomic sequence data. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 6885-6895.	3.6	38
35	Genome Reconstruction and Gene Expression of <i>Candidatus Accumulibacter phosphatis</i> Clade IB Performing Biological Phosphorus Removal. <i>Environmental Science & Technology</i> , 2014, 48, 10363-10371.	10.0	64
36	Characterization of <i>Thauera</i> -dominated hydrogen-oxidizing autotrophic denitrifying microbial communities by using high-throughput sequencing. <i>Bioresource Technology</i> , 2013, 128, 703-710.	9.6	144