Minggen Cheng

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The Two-Component Monooxygenase MeaXY Initiates the Downstream Pathway of Chloroacetanilide Herbicide Catabolism in Sphingomonads. Applied and Environmental Microbiology, 2017, 83, .	3.1	23
2	Lysinibacillus fluoroglycofenilyticus sp. nov., a bacterium isolated from fluoroglycofen contaminated soil. Antonie Van Leeuwenhoek, 2015, 107, 157-164.	1.7	20
3	Flavobacterium suzhouense sp. nov., isolated from farmland river sludge. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 370-374.	1.7	20
4	Pseudomonas zeshuii sp. nov., isolated from herbicide-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 2608-2612.	1.7	17
5	Pedobacter nanyangensis sp. nov., isolated from herbicide-contaminated soil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3517-3521.	1.7	15
6	PbaR, an IclR Family Transcriptional Activator for the Regulation of the 3-Phenoxybenzoate 1′,2′-Dioxygenase Gene Cluster in Sphingobium wenxiniae JZ-1 ^T . Applied and Environmental Microbiology, 2015, 81, 8084-8092.	3.1	14
7	McbG, a LysR Family Transcriptional Regulator, Activates the <i>mcbBCDEF</i> Gene Cluster Involved in the Upstream Pathway of Carbaryl Degradation in <i>Pseudomonas</i> sp. Strain XWY-1. Applied and Environmental Microbiology, 2021, 87, .	3.1	13
8	Oxygenases as Powerful Weapons in the Microbial Degradation of Pesticides. Annual Review of Microbiology, 2022, 76, 325-348.	7.3	13
9	Mangrovibacter yixingensis sp. nov., isolated from farmland soil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 2447-2452.	1.7	11
10	Comparative genome analysis reveals the evolution of chloroacetanilide herbicide mineralization in Sphingomonas wittichii DC-6. Archives of Microbiology, 2019, 201, 907-918.	2.2	10
11	pheSAG Based Rapid and Efficient Markerless Mutagenesis in Methylotuvimicrobium. Frontiers in Microbiology, 2020, 11, 441.	3.5	9
12	Cloning, expression and mutation of a triazophos hydrolase gene from <i>Burkholderia</i> sp. SZL-1. FEMS Microbiology Letters, 2016, 363, fnw108.	1.8	7
13	The Operon Encoding Hydrolytic Dehalogenation of 4-Chlorobenzoate Is Transcriptionally Regulated by the TetR-Type Repressor FcbR and Its Ligand 4-Chlorobenzoyl Coenzyme A. Applied and Environmental Microbiology, 2021, 87, .	3.1	6
14	Biodegradation of diphenyl ether herbicide lactofen by Bacillus sp. YS-1 and characterization of two initial degrading esterases. Science of the Total Environment, 2022, 806, 151357.	8.0	6
15	PicR as a MarR Family Transcriptional Repressor Multiply Controls the Transcription of Picolinic Acid Degradation Gene Cluster <i>pic</i> in Alcaligenes faecalis JQ135. Applied and Environmental Microbiology, 2022, 88, .	3.1	6
16	Methylomonas rhizoryzae sp. nov., a type I methanotroph isolated from the rhizosphere soil of rice. Antonie Van Leeuwenhoek, 2020, 113, 2167-2176.	1.7	4
17	Complete Genome Sequence of Sphingobium baderi DE-13, an Alkyl-Substituted Aniline-Mineralizing Bacterium. Current Microbiology, 2018, 75, 27-31.	2.2	4
18	A plasmid-based genomic screening system for transcriptional regulators of non-adjacent xenobiotic catabolism genes. Applied Microbiology and Biotechnology, 2020, 104, 1163-1174.	3.6	3

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19	Random Mutagenesis by Insertion of Error-Prone PCR Products to the Chromosome of Bacillus subtilis. Frontiers in Microbiology, 2020, 11, 570280.	3.5	2
20	The lowâ€nanomolar 4â€nitrobenzoateâ€responsive repressor <scp>PnbX</scp> negatively regulates the actinomyceteâ€derived 4â€nitrobenzoateâ€degrading <i>pnb</i> locus. Environmental Microbiology, 2021, 23, 7028-7041.	3.8	2
21	Characterization of the 2,6-Dimethylphenol Monooxygenase MpdAB and Evaluation of Its Potential in Vitamin E Precursor Synthesis. Applied and Environmental Microbiology, 2022, 88, e0011022.	3.1	2
22	The Novel Monooxygenase Gene <i>dipD</i> in the <i>dip</i> Gene Cluster of <i>Alcaligenes faecalis</i> JQ135 Is Essential for the Initial Catabolism of Dipicolinic Acid. Applied and Environmental Microbiology, 2022, 88, .	3.1	2