Chengjian Jiang

List of Publications by Year
in descending order

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37	537	759233 12	713466 21
papers	citations	h-index	g-index

40	40	40	641
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integration of Microbial Transformation Mechanism of Polyphosphate Accumulation and Sulfur Cycle in Subtropical Marine Mangrove Ecosystems with Spartina alterniflora Invasion. Microbial Ecology, 2023, 85, 478-494.	2.8	9
2	Whole-Genome and Transcriptome Sequencing-Based Characterization of Bacillus Cereus NR1 From Subtropical Marine Mangrove and Its Potential Role in Sulfur Metabolism. Frontiers in Microbiology, 2022, 13, 856092.	3.5	8
3	MicrobioSee: A Web-Based Visualization Toolkit for Multi-Omics of Microbiology. Frontiers in Genetics, 2022, 13, 853612.	2.3	2
4	Effects of Spartina alterniflora Invasion on Nitrogen Fixation and Phosphorus Solubilization in a Subtropical Marine Mangrove Ecosystem. Microbiology Spectrum, 2022, 10, .	3.0	9
5	Characterization of <scp>NMCR</scp>â€2, a new <scp>nonâ€mobile</scp> colistin resistance enzyme: implications for an <scp>MCR</scp>â€8 ancestor. Environmental Microbiology, 2021, 23, 844-860.	3.8	12
6	Whole genome sequencing and metabolomics analyses reveal the biosynthesis of nerol in a multi-stress-tolerant Meyerozyma guilliermondii GXDK6. Microbial Cell Factories, 2021, 20, 4.	4.0	14
7	Desulfobacterales stimulates nitrate reduction in the mangrove ecosystem of a subtropical gulf. Science of the Total Environment, 2021, 769, 144562.	8.0	33
8	L-Cysteine Synthase Enhanced Sulfide Biotransformation in Subtropical Marine Mangrove Sediments as Revealed by Metagenomics Analysis. Water (Switzerland), 2021, 13, 3053.	2.7	2
9	Copper Tolerance Mechanism of the Novel Marine Multi-Stress Tolerant Yeast Meyerozyma guilliermondii GXDK6 as Revealed by Integrated Omics Analysis. Frontiers in Microbiology, 2021, 12, 771878.	3.5	4
10	Multi-Omics Analysis of Lipid Metabolism for a Marine Probiotic Meyerozyma guilliermondii GXDK6 Under High NaCl Stress. Frontiers in Genetics, 2021, 12, 798535.	2.3	2
11	Harnessing efficient multiplex PCR methods to detect the expanding Tet(X) family of tigecycline resistance genes. Virulence, 2020, 11, 49-56.	4.4	29
12	Assessment of Multiple Anaerobic Co-Digestions and Related Microbial Community of Molasses with Rice-Alcohol Wastewater. Energies, 2020, 13, 4866.	3.1	5
13	V^V Reduction by Polaromonas spp. in Vanadium Mine Tailings. Environmental Science & Technology, 2020, 54, 14442-14454.	10.0	47
14	Patterns and drivers of Vibrio isolates phylogenetic diversity in the Beibu Gulf, China. Journal of Microbiology, 2020, 58, 998-1009.	2.8	2
15	Isolation and biochemical characterization of a metagenome-derived 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase gene from subtropical marine mangrove wetland sediments. AMB Express, 2019, 9, 19.	3.0	7
16	Prevalence and proliferation of antibiotic resistance genes in the subtropical mangrove wetland ecosystem of South China Sea. MicrobiologyOpen, 2019, 8, e871.	3.0	27
17	Carbohydrate metabolism genes dominant in a subtropical marine mangrove ecosystem revealed by metagenomics analysis. Journal of Microbiology, 2019, 57, 575-586.	2.8	18
18	Identification and molecular characterization of a psychrophilic GH1 Î²-glucosidase from the subtropical soil microorganism Exiguobacterium sp. GXG2. AMB Express, 2019, 9, 159.	3.0	6

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19	Simultaneous Enhancement of Thermostability and Catalytic Activity of a Metagenome-Derived Î²-Glucosidase Using Directed Evolution for the Biosynthesis of Butyl Glucoside. International Journal of Molecular Sciences, 2019, 20, 6224.	4.1	7
20	Molecular Characterization and Directed Evolution of a Metagenome-Derived L-Cysteine Sulfinate Decarboxylase. Food Technology and Biotechnology, 2018, 56, 117-123.	2.1	0
21	Characterization of a metagenome-derived protease from contaminated agricultural soil microorganisms and its random mutagenesis. Folia Microbiologica, 2017, 62, 499-508.	2.3	12
22	Identification and molecular characterization of a metagenome-derived L-lysine decarboxylase gene from subtropical soil microorganisms. PLoS ONE, 2017, 12, e0185060.	2.5	11
23	A novel d-amino acid oxidase from a contaminated agricultural soil metagenome and its characterization. Antonie Van Leeuwenhoek, 2015, 107, 1615-1623.	1.7	8
24	Isolation and characterization of a gene associated with sulfate assimilation in Sinorhizobium fredii WGF03. World Journal of Microbiology and Biotechnology, 2014, 30, 3027-3035.	3.6	0
25	Screening of Burkholderia sp. WGB31 producing anisic acid from anethole and optimization of fermentation conditions. Journal of Basic Microbiology, 2014, 54, 1251-1257.	3.3	5
26	Expression of a metagenome-derived fumarate reductase from marine microorganisms and its characterization. Folia Microbiologica, 2013, 58, 663-671.	2.3	2
27	Changes in microbial community structure in two anaerobic systems to treat bagasse spraying wastewater with and without addition of molasses alcohol wastewater. Bioresource Technology, 2013, 131, 333-340.	9.6	40
28	Identification of a metagenome-derived prephenate dehydrogenase gene from an alkaline-polluted soil microorganism. Antonie Van Leeuwenhoek, 2013, 103, 1209-1219.	1.7	7
29	Characterization of a Novel Serine Protease Inhibitor Gene from a Marine Metagenome. Marine Drugs, 2011, 9, 1487-1501.	4.6	12
30	Biochemical characterization of two novel Î²-glucosidase genes by metagenome expression cloning. Bioresource Technology, 2011, 102, 3272-3278.	9.6	50
31	A novel Î²-glucosidase with lipolytic activity from a soil metagenome. Folia Microbiologica, 2011, 56, 563-570.	2.3	11
32	Enhancing Production of l-Serine by Increasing the glyA Gene Expression in Methylobacterium sp. MB200. Applied Biochemistry and Biotechnology, 2010, 160, 740-750.	2.9	14
33	Identification of a metagenome-derived Î²-glucosidase from bioreactor contents. Journal of Molecular Catalysis B: Enzymatic, 2010, 63, 11-16.	1.8	18
34	Identification and characterization of a novel fumarase gene by metagenome expression cloning from marine microorganisms. Microbial Cell Factories, 2010, 9, 91.	4.0	29
35	Characterization of a novel Î²-glucosidase-like activity from a soil metagenome. Journal of Microbiology, 2009, 47, 542-548.	2.8	40
36	Biochemical characterization of a metagenome-derived decarboxylase. Enzyme and Microbial Technology, 2009, 45, 58-63.	3.2	8

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37	Molecular cloning and functional characterization of a novel decarboxylase from uncultured microorganisms. Biochemical and Biophysical Research Communications, 2007, 357, 421-426.	2.1	21