

Muhammad Farhan Ul Haque

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

797
citations

471371
17
h-index

526166
27
g-index

31
all docs

31
docs citations

31
times ranked

989
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Genome Sequences of Six Strains of the Genus <i>Methylobacterium</i> . <i>Journal of Bacteriology</i> , 2012, 194, 4746-4748.	1.0	99
2	Cerium Regulates Expression of Alternative Methanol Dehydrogenases in <i>Methylosinus trichosporium</i> OB3b. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7546-7552.	1.4	78
3	Methylmercury uptake and degradation by methanotrophs. <i>Science Advances</i> , 2017, 3, e1700041.	4.7	78
4	Detection and isolation of chloromethane-degrading bacteria from the <i>Arabidopsis thaliana</i> phyllosphere, and characterization of chloromethane utilization genes. <i>FEMS Microbiology Ecology</i> , 2011, 77, 438-448.	1.3	45
5	A TonB-Dependent Transporter Is Responsible for Methanobactin Uptake by <i>Methylosinus trichosporium</i> OB3b. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1917-1923.	1.4	43
6	Uptake and effect of rare earth elements on gene expression in <i>Methylosinus trichosporium</i> OB3b. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw129.	0.7	40
7	Novel coronavirus disease (COVID-19) pandemic: A recent mini review. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 612-623.	1.9	35
8	Complete Genome Sequence of the Chloromethane-Degrading <i>Hyphomicrobium</i> sp. Strain MC1. <i>Journal of Bacteriology</i> , 2011, 193, 5035-5036.	1.0	31
9	Facultative methanotrophs – diversity, genetics, molecular ecology and biotechnological potential: a mini-review. <i>Microbiology (United Kingdom)</i> , 2020, 166, 894-908.	0.7	30
10	Facultative methanotrophs are abundant at terrestrial natural gas seeps. <i>Microbiome</i> , 2018, 6, 118.	4.9	26
11	Methanobactin from <i>Methylocystis</i> sp. Strain SB2 Affects Gene Expression and Methane Monooxygenase Activity in <i>Methylosinus trichosporium</i> OB3b. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2466-2473.	1.4	25
12	Gene probing reveals the widespread distribution, diversity and abundance of isoprene-degrading bacteria in the environment. <i>Microbiome</i> , 2018, 6, 219.	4.9	25
13	Competition between Metals for Binding to Methanobactin Enables Expression of Soluble Methane Monooxygenase in the Presence of Copper. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1024-1031.	1.4	24
14	Marker Exchange Mutagenesis of <i>mxoA</i> , Encoding the Large Subunit of the Mxa Methanol Dehydrogenase, in <i>Methylosinus trichosporium</i> OB3b. <i>Applied and Environmental Microbiology</i> , 2016, 82, 1549-1555.	1.4	24
15	Methanethiol and Dimethylsulfide Cycling in Stiffkey Saltmarsh. <i>Frontiers in Microbiology</i> , 2019, 10, 1040.	1.5	23
16	Herbicide degradation and copper complexation by bacterial mixed cultures from a vineyard stormwater basin. <i>Journal of Soils and Sediments</i> , 2011, 11, 860-873.	1.5	19
17	Novel facultative <i>Methylocella</i> strains are active methane consumers at terrestrial natural gas seeps. <i>Microbiome</i> , 2019, 7, 134.	4.9	19
18	Fluorescence-Based Bacterial Bioreporter for Specific Detection of Methyl Halide Emissions in the Environment. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6561-6567.	1.4	18

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19	A unique bacteriohopanetetrol stereoisomer of marine anammox. <i>Organic Geochemistry</i> , 2020, 143, 103994.	0.9	18
20	Carbon source regulation of gene expression in <i>Methylosinus trichosporium</i> OB3b. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3871-3879.	1.7	16
21	Isoprene Oxidation by the Gram-Negative Model bacterium <i>Variovorax</i> sp. WS11. <i>Microorganisms</i> , 2020, 8, 349.	1.6	16
22	Characterization of the role of copCD in copper uptake and the "copper-switch"™ in <i>Methylosinus trichosporium</i> OB3b. <i>FEMS Microbiology Letters</i> , 2017, 364, .	0.7	11
23	Correlated production and consumption of chloromethane in the <i>Arabidopsis thaliana</i> phyllosphere. <i>Scientific Reports</i> , 2017, 7, 17589.	1.6	11
24	Genome Sequence of the Dichloromethane-Degrading Bacterium <i>Hyphomicrobium</i> sp. Strain GJ21. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
25	Revealing the community and metabolic potential of active methanotrophs by targeted metagenomics in the Zoige wetland of the Tibetan Plateau. <i>Environmental Microbiology</i> , 2021, 23, 6520-6535.	1.8	8
26	Identification of active gaseous-alkane degraders at natural gas seeps. <i>ISME Journal</i> , 2022, 16, 1705-1716.	4.4	7
27	Draft Genome Sequence of <i>Methylocella silvestris</i> TVC, a Facultative Methanotroph Isolated from Permafrost. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
28	Complete Genome Sequence of the Aerobic Facultative Methanotroph <i>Methylocella tundrae</i> Strain T4. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
29	Human BK and JC polyomaviruses: Molecular insights and prevalence in Asia. <i>Virus Research</i> , 2020, 278, 197860.	1.1	5
30	Metagenomic approach for the isolation of novel extremophiles. , 2022, , 55-66.		3
31	Analysis of student sentiment during video class with multi-layer deep learning approach. <i>International Journal of Electrical and Computer Engineering</i> , 2022, 12, 3981.	0.5	0