

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	Metagenomic approach for the isolation of novel extremophiles. , 2022, , 55-66.		3
2	Identification of active gaseous-alkane degraders at natural gas seeps. ISME Journal, 2022, 16, 1705-1716.	4.4	7
3	Analysis of student sentiment during video class with multi-layer deep learning approach. International Journal of Electrical and Computer Engineering, 2022, 12, 3981.	0.5	0
4	Revealing the community and metabolic potential of active methanotrophs by targeted metagenomics in the Zoige wetland of the Tibetan Plateau. Environmental Microbiology, 2021, 23, 6520-6535.	1.8	8
5	Novel coronavirus disease (COVID-19) pandemic: A recent mini review. Computational and Structural Biotechnology Journal, 2021, 19, 612-623.	1.9	35
6	Human BK and JC polyomaviruses: Molecular insights and prevalence in Asia. Virus Research, 2020, 278, 197860.	1.1	5
7	Isoprene Oxidation by the Gram-Negative Model bacterium <i>Variovorax</i> sp. WS11. Microorganisms, 2020, 8, 349.	1.6	16
8	A unique bacteriohopanetetrol stereoisomer of marine anammox. Organic Geochemistry, 2020, 143, 103994.	0.9	18
9	Facultative methanotrophs – diversity, genetics, molecular ecology and biotechnological potential: a mini-review. Microbiology (United Kingdom), 2020, 166, 894-908.	0.7	30
10	Novel facultative <i>Methylocella</i> strains are active methane consumers at terrestrial natural gas seeps. Microbiome, 2019, 7, 134.	4.9	19
11	Complete Genome Sequence of the Aerobic Facultative Methanotroph <i>Methylocella tundrae</i> Strain T4. Microbiology Resource Announcements, 2019, 8, .	0.3	5
12	Methanethiol and Dimethylsulfide Cycling in Stiffkey Saltmarsh. Frontiers in Microbiology, 2019, 10, 1040.	1.5	23
13	Draft Genome Sequence of <i>Methylocella silvestris</i> TVC, a Facultative Methanotroph Isolated from Permafrost. Genome Announcements, 2018, 6, .	0.8	6
14	Gene probing reveals the widespread distribution, diversity and abundance of isoprene-degrading bacteria in the environment. Microbiome, 2018, 6, 219.	4.9	25
15	Facultative methanotrophs are abundant at terrestrial natural gas seeps. Microbiome, 2018, 6, 118.	4.9	26
16	Carbon source regulation of gene expression in <i>Methylosinus trichosporium</i> OB3b. Applied Microbiology and Biotechnology, 2017, 101, 3871-3879.	1.7	16
17	Methylmercury uptake and degradation by methanotrophs. Science Advances, 2017, 3, e1700041.	4.7	78
18	Characterization of the role of copCD in copper uptake and the –copper-switch™ in <i>Methylosinus trichosporium</i> OB3b. FEMS Microbiology Letters, 2017, 364, .	0.7	11

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19	Correlated production and consumption of chloromethane in the Arabidopsis thaliana phyllosphere. Scientific Reports, 2017, 7, 17589.	1.6	11
20	Genome Sequence of the Dichloromethane-Degrading Bacterium Hyphomicrobium sp. Strain GJ21. Genome Announcements, 2017, 5, .	0.8	9
21	Uptake and effect of rare earth elements on gene expression in Methylosinus trichosporium OB3b. FEMS Microbiology Letters, 2016, 363, fnw129.	0.7	40
22	A TonB-Dependent Transporter Is Responsible for Methanobactin Uptake by Methylosinus trichosporium OB3b. Applied and Environmental Microbiology, 2016, 82, 1917-1923.	1.4	43
23	Marker Exchange Mutagenesis of <i>mxoA</i> , Encoding the Large Subunit of the Mxa Methanol Dehydrogenase, in Methylosinus trichosporium OB3b. Applied and Environmental Microbiology, 2016, 82, 1549-1555.	1.4	24
24	Methanobactin from Methylocystis sp. Strain SB2 Affects Gene Expression and Methane Monooxygenase Activity in Methylosinus trichosporium OB3b. Applied and Environmental Microbiology, 2015, 81, 2466-2473.	1.4	25
25	Competition between Metals for Binding to Methanobactin Enables Expression of Soluble Methane Monooxygenase in the Presence of Copper. Applied and Environmental Microbiology, 2015, 81, 1024-1031.	1.4	24
26	Cerium Regulates Expression of Alternative Methanol Dehydrogenases in Methylosinus trichosporium OB3b. Applied and Environmental Microbiology, 2015, 81, 7546-7552.	1.4	78
27	Fluorescence-Based Bacterial Bioreporter for Specific Detection of Methyl Halide Emissions in the Environment. Applied and Environmental Microbiology, 2013, 79, 6561-6567.	1.4	18
28	Complete Genome Sequences of Six Strains of the Genus Methylobacterium. Journal of Bacteriology, 2012, 194, 4746-4748.	1.0	99
29	Detection and isolation of chloromethane-degrading bacteria from the Arabidopsis thaliana phyllosphere, and characterization of chloromethane utilization genes. FEMS Microbiology Ecology, 2011, 77, 438-448.	1.3	45
30	Herbicide degradation and copper complexation by bacterial mixed cultures from a vineyard stormwater basin. Journal of Soils and Sediments, 2011, 11, 860-873.	1.5	19
31	Complete Genome Sequence of the Chloromethane-Degrading Hyphomicrobium sp. Strain MC1. Journal of Bacteriology, 2011, 193, 5035-5036.	1.0	31