

Neelam M Nathani

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

354
citations

1307594

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888059

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21
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docs citations

21
times ranked

612
citing authors

#	ARTICLE	IF	CITATIONS
1	Sediment Plasmidome of the Gulfs of Kathiawar Peninsula and Arabian Sea: Insights Gained from Metagenomics Data. <i>Microbial Ecology</i> , 2021, 81, 540-548.	2.8	4
2	In-Silico analysis reveals lower transcription efficiency of C241T variant of SARS-CoV-2 with host replication factors MADP1 and hnRNP-1. <i>Informatics in Medicine Unlocked</i> , 2021, 25, 100670.	3.4	16
3	Fungi with high ability to crunch multiple Polycyclic Aromatic Hydrocarbons (PAHs) from the pelagic sediments of Gulfs of Gujarat. <i>Marine Pollution Bulletin</i> , 2021, 167, 112293.	5.0	6
4	309 metagenome assembled microbial genomes from deep sediment samples in the Gulfs of Kathiawar Peninsula. <i>Scientific Data</i> , 2021, 8, 194.	5.3	6
5	Viral footprints across Gulfs of Kathiawar Peninsula and Arabian Sea: Unraveled from pelagic sediment metagenomic data. <i>Virus Research</i> , 2021, 302, 198485.	2.2	4
6	Bacterial line of defense in <i>Dirinaria</i> lichen from two different ecosystems: First genomic insights of its mycobiont <i>Dirinaria</i> sp. GBRC AP01. <i>Microbiological Research</i> , 2020, 233, 126407.	5.3	3
7	Living soil of fifty-year-old saw mill: Dawn bioresource with differential hydrolytic potentials. <i>Ecological Genetics and Genomics</i> , 2020, 16, 100061.	0.5	0
8	Antibiotic Resistome Biomarkers associated to the Pelagic Sediments of the Gulfs of Kathiawar Peninsula and Arabian Sea. <i>Scientific Reports</i> , 2019, 9, 17281.	3.3	12
9	Antibiotic resistance genes allied to the pelagic sediment microbiome in the Gulf of Khambhat and Arabian Sea. <i>Science of the Total Environment</i> , 2019, 653, 446-454.	8.0	29
10	Functional gene profiling through metaRNAseq approach reveals diet-dependent variation in rumen microbiota of buffalo (<i>Bubalus bubalis</i>). <i>Anaerobe</i> , 2017, 44, 106-116.	2.1	13
11	Assessment of bacterial community composition in response to uranium levels in sediment samples of sacred Cauvery River. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 831-841.	3.6	37
12	Haplotype variation and phylogenetic analyses of three commercially important morphological variants of genus <i>Turbinella</i> from the southeast coast of India based on the 16S rRNA gene. <i>Bulletin of Marine Science</i> , 2017, 93, 931-941.	0.8	0
13	Genetic architecture of three <i>Turbinella pyrum</i> varieties (Linnaeus, 1758) from the southeast coast of India. <i>Marine Ecology</i> , 2016, 37, 588-598.	1.1	1
14	Draft Genome Sequence of Commercial Textile Dye-Decolorizing and -Degrading <i>Bacillus subtilis</i> Strain C3 Isolated in India. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
15	Correlation between genomic analyses with metatranscriptomic study reveals various functional pathways of <i>Clostridium sartagoforme</i> AAU1, a buffalo rumen isolate. <i>Journal of Applied Animal Research</i> , 2016, 44, 498-507.	1.2	6
16	Isolation of chitinolytic <i>Clostridium</i> sp. NCR from Mehsani buffalo rumen, its genomic analysis and potential role in rumen. <i>Genomics Data</i> , 2015, 5, 109-111.	1.3	6
17	Exploring genetic polymorphism in innate immune genes in Indian cattle (<i>Bos indicus</i>) and buffalo (<i>Bubalus bubalis</i>) using next generation sequencing technology. <i>Meta Gene</i> , 2015, 3, 50-58.	0.6	7
18	In silico analysis of consequences of non-synonymous SNPs of <i>Slc11a2</i> gene in Indian bovines. <i>Genomics Data</i> , 2015, 5, 72-79.	1.3	19

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19	Method to quantify live and dead cells in multi-species oral biofilm by real-time PCR with propidium monoazide. <i>AMB Express</i> , 2013, 3, 1.	3.0	181