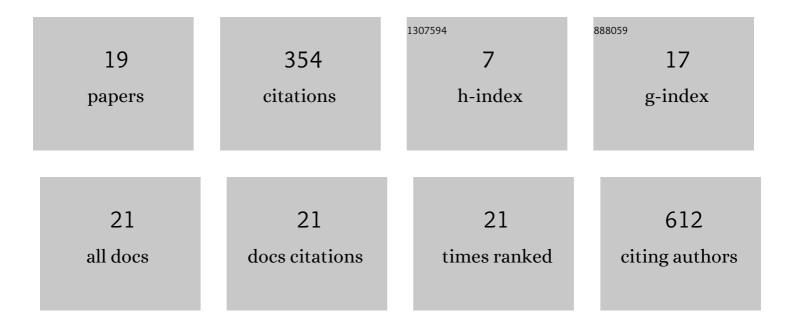
## Neelam M Nathani

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5182458/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Method to quantify live and dead cells in multi-species oral biofilm by real-time PCR with propidium monoazide. AMB Express, 2013, 3, 1.	3.0	181
2	Assessment of bacterial community composition in response to uranium levels in sediment samples of sacred Cauvery River. Applied Microbiology and Biotechnology, 2017, 101, 831-841.	3.6	37
3	Antibiotic resistance genes allied to the pelagic sediment microbiome in the Gulf of Khambhat and Arabian Sea. Science of the Total Environment, 2019, 653, 446-454.	8.0	29
4	In silico analysis of consequences of non-synonymous SNPs of Slc11a2 gene in Indian bovines. Genomics Data, 2015, 5, 72-79.	1.3	19
5	In-Silico analysis reveals lower transcription efficiency of C241T variant of SARS-CoV-2 with host replication factors MADP1 and hnRNP-1. Informatics in Medicine Unlocked, 2021, 25, 100670.	3.4	16
6	Functional gene profiling through metaRNAseq approach reveals diet-dependent variation in rumen microbiota of buffalo (Bubalus bubalis). Anaerobe, 2017, 44, 106-116.	2.1	13
7	Antibiotic Resistome Biomarkers associated to the Pelagic Sediments of the Gulfs of Kathiawar Peninsula and Arabian Sea. Scientific Reports, 2019, 9, 17281.	3.3	12
8	Exploring genetic polymorphism in innate immune genes in Indian cattle (Bos indicus) and buffalo (Bubalus bubalis) using next generation sequencing technology. Meta Gene, 2015, 3, 50-58.	0.6	7
9	Isolation of chitinolytic Clostridium sp. NCR from Mehsani buffalo rumen, its genomic analysis and potential role in rumen. Genomics Data, 2015, 5, 109-111.	1.3	6
10	Correlation between genomic analyses with metatranscriptomic study reveals various functional pathways ofClostridium sartagoformeAAU1, a buffalo rumen isolate. Journal of Applied Animal Research, 2016, 44, 498-507.	1.2	6
11	Fungi with high ability to crunch multiple Polycyclic Aromatic Hydrocarbons (PAHs) from the pelagic sediments of Gulfs of Gujarat. Marine Pollution Bulletin, 2021, 167, 112293.	5.0	6
12	309 metagenome assembled microbial genomes from deep sediment samples in the Gulfs of Kathiawar Peninsula. Scientific Data, 2021, 8, 194.	5.3	6
13	Sediment Plasmidome of the Gulfs of Kathiawar Peninsula and Arabian Sea: Insights Gained from Metagenomics Data. Microbial Ecology, 2021, 81, 540-548.	2.8	4
14	Viral footprints across Gulfs of Kathiawar Peninsula and Arabian Sea: Unraveled from pelagic sediment metagenomic data. Virus Research, 2021, 302, 198485.	2.2	4
15	Draft Genome Sequence of Commercial Textile Dye-Decolorizing and -Degrading Bacillus subtilis Strain C3 Isolated in India. Genome Announcements, 2016, 4, .	0.8	3
16	Bacterial line of defense in Dirinaria lichen from two different ecosystems: First genomic insights of its mycobiont Dirinaria sp. GBRC AP01. Microbiological Research, 2020, 233, 126407.	5.3	3
17	Genetic architecture of three <i>Turbinella pyrum</i> varieties (Linnaeus, 1758) from the southeast coast of India. Marine Ecology, 2016, 37, 588-598.	1.1	1
18	Haplotype variation and phylogenetic analyses of three commercially important morphological variants of genus Turbinella from the southeast coast of India based on the 16S rRNA gene. Bulletin of Marine Science, 2017, 93, 931-941.	0.8	0

#	Article	IF	CITATIONS
19	Living soil of fifty-year-old saw mill: Dawn bioresource with differential hydrolytic potentials. Ecological Genetics and Genomics, 2020, 16, 100061.	0.5	0