

Bhaskar Reddy

List of Publications by Year in descending order

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31
papers

773
citations

623574

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docs citations

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering core phyllosphere microbiome assemblage on rice genotypes grown in contrasting agroclimatic zones: implications for phyllosphere engineering against blast disease. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	9
2	Structured Framework and Genome Analysis of <i>Magnaporthe grisea</i> Inciting Pearl Millet Blast Disease Reveals Versatile Metabolic Pathways, Protein Families, and Virulence Factors. <i>Journal of Fungi (Basel)</i> , 2021, 7, 1010.	0.1	0
3	Methods of Assessments of Microbial Diversity and Their Functional Role in Soil Fertility and Crop Productivity. <i>Rhizosphere Biology</i> , 2021, , 293-314.	0.4	1
4	Exploring the allochthonous pollution influence on bacterial community and co-occurrence dynamics of River Ganga water through 16S rRNA-tagged amplicon metagenome. <i>Environmental Science and Pollution Research</i> , 2021, 28, 26990-27005.	2.7	8
5	Potential Environmental and Human Health Risks Caused by Antibiotic-Resistant Bacteria (ARB), Antibiotic Resistance Genes (ARGs) and Emerging Contaminants (ECs) from Municipal Solid Waste (MSW) Landfill. <i>Antibiotics</i> , 2021, 10, 374.	1.5	80
6	Deciphering core-microbiome of rice leaf endosphere: Revelation by metagenomic and microbiological analysis of aromatic and non-aromatic genotypes grown in three geographical zones. <i>Microbiological Research</i> , 2021, 246, 126704.	2.5	27
7	Integrated Metabarcoding and Culturomic-Based Microbiome Profiling of Rice Phyllosphere Reveal Diverse and Functional Bacterial Communities for Blast Disease Suppression. <i>Frontiers in Microbiology</i> , 2021, 12, 780458.	1.5	10
8	Hybrid de novo genome-reassembly reveals new insights on pathways and pathogenicity determinants in rice blast pathogen <i>Magnaporthe oryzae</i> RMg_Dl. <i>Scientific Reports</i> , 2021, 11, 22922.	1.6	8
9	De novo genome assembly and comparative annotation reveals metabolic versatility in cellulolytic bacteria from cropland and forest soils. <i>Functional and Integrative Genomics</i> , 2020, 20, 89-101.	1.4	4
10	Temporal shift in methanotrophic community and methane oxidation potential in forest soils of dry tropics: high-throughput metagenomic approach. <i>Biology and Fertility of Soils</i> , 2020, 56, 859-867.	2.3	9
11	Assessment of environmental gene tags linked with carbohydrate metabolism and chemolithotrophy associated microbial community in River Ganga. <i>Gene</i> , 2019, 704, 31-41.	1.0	23
12	River Ganges water as reservoir of microbes with antibiotic and metal ion resistance genes: High throughput metagenomic approach. <i>Environmental Pollution</i> , 2019, 246, 443-451.	3.7	105
13	Advancements in Microbial Genome Sequencing and Microbial Community Characterization. , 2019, , 87-113.		1
14	Identification of Single Nucleotide Polymorphism from Indian <i>Bubalus bubalis</i> through Targeted Sequence Capture. <i>Current Science</i> , 2017, 112, 1230.	0.4	7
15	Transcriptomic comparison of primary bovine horn core carcinoma culture and parental tissue at early stage. <i>Veterinary World</i> , 2017, 10, 38-55.	0.7	1
16	Influence of Aerobic and Nitrogen Flush Packaging Methods and Frozen Storage on Quality Characteristics of Prune Puree Incorporated Ready-to-Eat Mutton Kheema. <i>Journal of Pure and Applied Microbiology</i> , 2017, 11, 249-258.	0.3	2
17	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
18	Identification of Genetic Variants in <i>PDC</i> , <i>RHO</i> , <i>PDE6A</i> and <i>PDE6B</i> in Dogs with Progressive Retinal Atrophy. <i>Current Science</i> , 2016, 111, 1640.	0.4	2

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19	De Novo Assembly and Transcriptome Characterization of Canine Retina Using High-Throughput Sequencing. <i>Genetics Research International</i> , 2015, 2015, 1-11.	2.0	3
20	Effect of roughage on rumen microbiota composition in the efficient feed converter and sturdy Indian Jaffrabadi buffalo (<i>Bubalus bubalis</i>). <i>BMC Genomics</i> , 2015, 16, 1116.	1.2	45
21	Potential functional gene diversity involved in methanogenesis and methanogenic community structure in Indian buffalo (<i>Bubalus bubalis</i>) rumen. <i>Journal of Applied Genetics</i> , 2015, 56, 411-426.	1.0	15
22	Identification of putative SNPs in progressive retinal atrophy affected <i>Canis lupus familiaris</i> using exome sequencing. <i>Mammalian Genome</i> , 2015, 26, 638-649.	1.0	3
23	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
24	Microbial profiles of liquid and solid fraction associated biomaterial in buffalo rumen fed green and dry roughage diets by tagged 16S rRNA gene pyrosequencing. <i>Molecular Biology Reports</i> , 2015, 42, 95-103.	1.0	34
25	High Potential Source for Biomass Degradation Enzyme Discovery and Environmental Aspects Revealed through Metagenomics of Indian Buffalo Rumen. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	35
26	Characterization of the rumen microbiome of Indian Kankrej cattle (<i>Bos indicus</i>) adapted to different forage diet. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9749-9761.	1.7	40
27	Taxonomic and gene-centric metagenomics of the fecal microbiome of low and high feed conversion ratio (FCR) broilers. <i>Journal of Applied Genetics</i> , 2014, 55, 145-154.	1.0	74
28	Bacterial diversity associated with feeding dry forage at different dietary concentrations in the rumen contents of Mehshana buffalo (<i>Bubalus bubalis</i>) using 16S pyrotags. <i>Anaerobe</i> , 2014, 25, 31-41.	1.0	84
29	Insights into resistome and stress responses genes in <i>Bubalus bubalis</i> rumen through metagenomic analysis. <i>Molecular Biology Reports</i> , 2014, 41, 6405-6417.	1.0	14
30	Metagenomic analysis of buffalo rumen microbiome: Effect of roughage diet on Dormancy and Sporulation genes. <i>Meta Gene</i> , 2014, 2, 252-268.	0.3	33
31	Bacterial Diversity Dynamics Associated with Different Diets and Different Primer Pairs in the Rumen of Kankrej Cattle. <i>PLoS ONE</i> , 2014, 9, e111710.	1.1	71