

# Bhaskar Reddy

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6308961/publications.pdf>

Version: 2024-02-01

31  
papers

773  
citations

623188

14  
h-index

525886

27  
g-index

33  
all docs

33  
docs citations

33  
times ranked

899  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	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
18	Deciphering core phyllosphere microbiome assemblage on rice genotypes grown in contrasting agroclimatic zones: implications for phyllosphere microbiome engineering against blast disease. <i>Environmental Microbiomes</i> , 2022, 17, .	2.2	9

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Identification of Single Nucleotide Polymorphism from Indian &Bubalus bubalis through Targeted Sequence Capture. <i>Current Science</i> , 2017, 112, 1230.	0.4	7
22	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
23	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
24	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
25	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
26	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, 1071.	0.1	1
27	Identification of Genetic Variants in PDC, RHO, PDE6A and PDE6B in Dogs with Progressive Retinal Atrophy. <i>Current Science</i> , 2016, 111, 1640.	0.4	2
28	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
29	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
30	Advancements in Microbial Genome Sequencing and Microbial Community Characterization. , 2019, , 87-113.		1
31	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