## H B Mahesh

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1355605/publications.pdf Version: 2024-02-01



H R MAHESH

#	Article	IF	CITATIONS
1	Genome and Transcriptome sequence of Finger millet (Eleusine coracana (L.) Gaertn.) provides insights into drought tolerance and nutraceutical properties. BMC Genomics, 2017, 18, 465.	2.8	165
2	Indica rice genome assembly, annotation and mining of blast disease resistance genes. BMC Genomics, 2016, 17, 242.	2.8	51
3	Multi-Omics Driven Assembly and Annotation of the Sandalwood ( <i>Santalum album</i> ) Genome. Plant Physiology, 2018, 176, 2772-2788.	4.8	45
4	Genome-Wide Comparison of Magnaporthe Species Reveals a Host-Specific Pattern of Secretory Proteins and Transposable Elements. PLoS ONE, 2016, 11, e0162458.	2.5	43
5	Comprehensive analyses of genomes, transcriptomes and metabolites of neem tree. PeerJ, 2015, 3, e1066.	2.0	35
6	Genome analysis of rice-blast fungus Magnaporthe oryzae field isolates from southern India. Genomics Data, 2015, 5, 284-291.	1.3	35
7	De novo genome assembly and annotation of rice sheath rot fungus Sarocladium oryzae reveals genes involved in Helvolic acid and Cerulenin biosynthesis pathways. BMC Genomics, 2016, 17, 271.	2.8	33
8	LAMP-based foldable microdevice platform for the rapid detection of Magnaporthe oryzae and Sarocladium oryzae in rice seed. Scientific Reports, 2021, 11, 178.	3.3	17
9	Bio-priming of rice seeds with novel bacterial strains, for management of seedborne Magnaporthe oryzae L Plant Physiology Reports, 2019, 24, 507-520.	1.5	14
10	Biostimulants derived from red seaweed stimulate the plant defence mechanism in rice against Magnaporthe oryzae. Journal of Applied Phycology, 2022, 34, 659-665.	2.8	12
11	Metagenome sequencing of fingermillet-associated microbial consortia provides insights into structural and functional diversity of endophytes. 3 Biotech, 2020, 10, 15.	2.2	11
12	Comparative genomics of rice false smut fungi Ustilaginoidea virens Uv-Gvt strain from India reveals genetic diversity and phylogenetic divergence. 3 Biotech, 2020, 10, 342.	2.2	10
13	Loop-mediated isothermal amplification assay for pre-symptomatic stage detection of Xanthomonas axonopodis pv. punicae infection in pomegranate. Australasian Plant Pathology, 2020, 49, 467-473.	1.0	9
14	First report of bacterial soft rot of carrot caused by <i>Klebsiella variicola</i> in India. New Disease Reports, 2018, 37, 21-21.	0.8	9
15	Rapid genotyping of bacterial leaf blight resistant genes of rice using loop-mediated isothermal amplification assay. Molecular Biology Reports, 2021, 48, 467-474.	2.3	7
16	Genome, Transcriptome, and Germplasm Sequencing Uncovers Functional Variation in the Warm-Season Grain Legume Horsegram Macrotyloma uniflorum (Lam.) Verdc Frontiers in Plant Science, 2021, 12, 758119.	3.6	7
17	Diversity and biopotential of Bacillus velezensis strains A6 and P42 against rice blast and bacterial blight of pomegranate. Archives of Microbiology, 2021, 203, 4189-4199.	2.2	6
18	In planta transcriptome analysis reveals tissue-specific expression of pathogenicity genes and microRNAs during rice-Magnaporthe interactions. Genomics, 2021, 113, 265-275.	2.9	5

H B Mahesh

#	Article	IF	CITATIONS
19	Comparative metagenomic analysis of rice soil samples revealed the diverse microbial population and biocontrol organisms against plant pathogenic fungus Magnaporthe oryzae. 3 Biotech, 2021, 11, 245.	2.2	5
20	Rice Blast Disease in India: Present Status and Future Challenges. , 0, , .		5
21	Antibiotic Resilience in <l>Xanthomonas axonopodis</l> Pv. <l>punicae</l> Causing Bacterial Blight Of Pomegranate. Current Science, 2021, 119, 1564.	0.8	5
22	Comparative analysis of secondary metabolite gene clusters in different strains of <i>Magnaporthe oryzae</i> . FEMS Microbiology Letters, 2021, 368, .	1.8	3
23	Host range and virulence diversity of <i>Pectobacterium carotovorum</i> subsp. <i>brasiliense</i> strain <scp>RDKLR</scp> infecting radish in India, and development of a <scp>LAMP</scp> â€based diagnostics. Journal of Applied Microbiology, 2022, , .	3.1	3
24	Mining of SSRs and SNPs in Sandalwood Genome. Compendium of Plant Genomes, 2022, , 57-64.	0.5	0
25	Whole Genome Sequence of Sandalwood and Its Comparative Study. Compendium of Plant Genomes, 2022, , 47-55.	0.5	Ο