

Renesh Bedre

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

459
citations

840119

11
h-index

794141

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27
all docs

27
docs citations

27
times ranked

556
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome analysis of smooth cordgrass (<i>Spartina alterniflora</i> Loisel), a monocot halophyte, reveals candidate genes involved in its adaptation to salinity. <i>BMC Genomics</i> , 2016, 17, 657.	1.2	55
2	Genetic Mapping of Quantitative Trait Loci for Grain Yield under Drought in Rice under Controlled Greenhouse Conditions. <i>Frontiers in Chemistry</i> , 2017, 5, 129.	1.8	43
3	Identification of cold-responsive genes in energycane for their use in genetic diversity analysis and future functional marker development. <i>Plant Science</i> , 2013, 211, 122-131.	1.7	42
4	Salt Adaptation Mechanisms of Halophytes: Improvement of Salt Tolerance in Crop Plants. , 2015, , 243-279.		36
5	Plant hairy roots enable high throughput identification of antimicrobials against <i>Candidatus Liberibacter</i> spp.. <i>Nature Communications</i> , 2020, 11, 5802.	5.8	36
6	Global Awakening of Cryptic Biosynthetic Gene Clusters in <i>Burkholderia thailandensis</i> . <i>ACS Chemical Biology</i> , 2017, 12, 3012-3021.	1.6	35
7	Genome-Wide Transcriptome Analysis of Cotton (<i>Gossypium hirsutum</i> L.) Identifies Candidate Gene Signatures in Response to Aflatoxin Producing Fungus <i>Aspergillus flavus</i> . <i>PLoS ONE</i> , 2015, 10, e0138025.	1.1	30
8	An actin-depolymerizing factor from the halophyte smooth cordgrass, <i>Spartina alterniflora</i> (<i>Scp2</i>), is superior to its rice homolog (<i>OsADF2</i>) in conferring drought and salt tolerance when constitutively overexpressed in rice. <i>Plant Biotechnology Journal</i> , 2019, 17, 188-205.	4.1	25
9	Genome-wide alternative splicing landscapes modulated by biotrophic sugarcane smut pathogen. <i>Scientific Reports</i> , 2019, 9, 8876.	1.6	24
10	Sequencing and expression analysis of salt-responsive miRNAs and target genes in the halophyte smooth cordgrass (<i>Spartina alternifolia</i> Loisel). <i>Molecular Biology Reports</i> , 2015, 42, 1341-1350.	1.0	19
11	GenFam: A web application and database for gene family-based classification and functional enrichment analysis. <i>Plant Direct</i> , 2019, 3, e00191.	0.8	16
12	<i>Brachypodium</i> Phenylalanine Ammonia Lyase (PAL) Promotes Antiviral Defenses against <i>Panicum mosaic virus</i> and Its Satellites. <i>MBio</i> , 2021, 12, .	1.8	16
13	Developing Growth-Associated Molecular Markers Via High-Throughput Phenotyping in Spinach. <i>Plant Genome</i> , 2019, 12, 190027.	1.6	15
14	Single-marker and haplotype-based association analysis of anthracnose (<i>Colletotrichum</i>) in rice (<i>Oryza sativa</i>). <i>Plant Disease</i> , 2017, 99, 1000-1007.	1.0	11
15	Identifying cotton (<i>Gossypium hirsutum</i> L.) genes induced in response to <i>Aspergillus flavus</i> infection. <i>Physiological and Molecular Plant Pathology</i> , 2012, 80, 35-40.	1.3	9
16	New Era in Plant Alternative Splicing Analysis Enabled by Advances in High-Throughput Sequencing (HTS) Technologies. <i>Frontiers in Plant Science</i> , 2019, 10, 740.	1.7	9
17	Genetic Diversity and Population Structure of Tomato (<i>Solanum) in the Americas. <i>American Journal of Plant Sciences</i> , 2019, 10, 1154-1180.	0.3	8
18	Antiviral therapy with nucleotide/nucleoside analogues in chronic hepatitis B: A meta-analysis of prospective randomized trials. <i>Indian Journal of Gastroenterology</i> , 2016, 35, 75-82.	0.7	6

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19	Minor alleles are associated with white rust (<i>Albugo occidentalis</i>) susceptibility in spinach (<i>Spinacia</i>) Tj ETQq1 1 0.784314 rgBT /Over	2.9	14
20	Genomic Approaches to Analyze Alternative Splicing, A Key Regulator of Transcriptome and Proteome Diversity in <i>Brachypodium distachyon</i> . <i>Methods in Molecular Biology</i> , 2018, 1667, 73-85.	0.4	4
21	Phenotypic Diversity and Association Mapping of Ascorbic Acid Content in Spinach. <i>Frontiers in Genetics</i> , 2021, 12, 752313.	1.1	4
22	Identification of candidate resistance genes of cotton against <i>Aspergillus flavus</i> infection using a comparative transcriptomics approach. <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 513-519.	1.4	3
23	HTSQualC is a flexible and one-step quality control software for high-throughput sequencing data analysis. <i>Scientific Reports</i> , 2021, 11, 18725.	1.6	3
24	Efficacy of Sucralfate in Reflux Disease in comparison to H2 â€“ Receptor Antagonist: A Meta-Analysis of Randomized Trials. <i>Biology Engineering Medicine and Science Reports</i> , 2016, 2, 18-22.	0.5	0