

Mahendra Modi

List of Publications by Year in descending order

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47
papers

559
citations

687363

13
h-index

713466

21
g-index

47
all docs

47
docs citations

47
times ranked

859
citing authors

#	ARTICLE	IF	CITATIONS
1	The cytoplasmic-localized, cytoskeletal-associated RNA binding protein <i>OstTudor5N</i> : evidence for an essential role in storage protein RNA transport and localization. <i>Plant Journal</i> , 2008, 55, 443-454.	5.7	48
2	In silico identification and characterization of conserved miRNAs and their target genes in sweet potato (<i>Ipomoea batatas</i> L.) Expressed Sequence Tags (ESTs). <i>Plant Signaling and Behavior</i> , 2013, 8, e26543.	2.4	45
3	Computational identification and characterization of conserved miRNAs and their target genes in garlic (<i>Allium sativum</i> L.) expressed sequence tags. <i>Gene</i> , 2014, 537, 333-342.	2.2	43
4	In silico analyses of superoxide dismutases (SODs) of rice (<i>Oryza sativa</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2013, 22, 150-156.	1.7	30
5	<i>Bacillus megaterium</i> adapts to acid stress condition through a network of genes: Insight from a genome-wide transcriptome analysis. <i>Scientific Reports</i> , 2018, 8, 16105.	3.3	30
6	Structure-Based Computational Study of Two Disease Resistance Gene Homologues (Hm1 and Hm2) in Maize (<i>Zea mays</i> L.) with Implications in Plant-Pathogen Interactions. <i>PLoS ONE</i> , 2014, 9, e97852.	2.5	28
7	Genome wide transcriptome profiling reveals differential gene expression in secondary metabolite pathway of <i>Cymbopogon winterianus</i> . <i>Scientific Reports</i> , 2016, 6, 21026.	3.3	27
8	Mechanism of interaction of an endofungal bacterium <i>Serratia marcescens</i> D1 with its host and non-host fungi. <i>PLoS ONE</i> , 2020, 15, e0224051.	2.5	22
9	Molecular cloning, characterization and expression analysis of 3-hydroxy-3-methylglutaryl coenzyme A reductase gene from <i>Centella asiatica</i> L.. <i>Molecular Biology Reports</i> , 2015, 42, 1431-1439.	2.3	21
10	Rediscovering Medicinal Plants' Potential with OMICS: Microsatellite Survey in Expressed Sequence Tags of Eleven Traditional Plants with Potent Antidiabetic Properties. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 298-309.	2.0	20
11	Identification and characterization of drought responsive miRNAs from a drought tolerant rice genotype of Assam. <i>Plant Gene</i> , 2020, 21, 100213.	2.3	20
12	Mining for SSRs and FDMs from expressed sequence tags of <i>Camellia sinensis</i> . <i>Bioinformatics</i> , 2012, 8, 260-266.	0.5	19
13	Genome-wide association studies for agronomical traits in winter rice accessions of Assam. <i>Genomics</i> , 2021, 113, 1037-1047.	2.9	16
14	Isolation and characterization of cDNA clones encoding ADP-glucose pyrophosphorylase (AGPase) large and small subunits from chickpea (<i>Cicer arietinum</i> L.). <i>Phytochemistry</i> , 2002, 59, 261-268.	2.9	13
15	Construction of cDNA library and preliminary analysis of expressed sequence tags from tea plant [<i>Camellia sinensis</i> (L) O. Kuntze]. <i>Gene</i> , 2012, 506, 202-206.	2.2	12
16	Structural analysis and molecular dynamics simulations of novel Î-endotoxin Cry1Id from <i>Bacillus thuringiensis</i> to pave the way for development of novel fusion proteins against insect pests of crops. <i>Journal of Molecular Modeling</i> , 2013, 19, 5301-5316.	1.8	12
17	Novel insights into structure-function mechanism and tissue-specific expression profiling of full-length <i>dxr</i> gene from <i>Cymbopogon winterianus</i> . <i>FEBS Open Bio</i> , 2015, 5, 325-334.	2.3	10
18	Identification of promising inhibitors for <i>Plasmodium</i> haemoglobinase Falcipain-2, using virtual screening, molecular docking, and MD Simulation. <i>Journal of Molecular Structure</i> , 2022, 1248, 131427.	3.6	10

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19	A comparative proteomic approach to analyse structure, function and evolution of rice chitinases: a step towards increasing plant fungal resistance. <i>Journal of Molecular Modeling</i> , 2012, 18, 4761-4780.	1.8	9
20	Insights into the structure–function relationship of disease resistance protein HCTR in maize (<i>Zea mays</i>) using X-ray crystallography and molecular dynamics simulation. <i>Journal of Molecular Modeling</i> , 2013, 19, 50-64.	2.4	9
21	Molecular Phylogeny, Homology Modeling, and Molecular Dynamics Simulation of Race-Specific Bacterial Blight Disease Resistance Protein (xa5) of Rice: A Comparative Agriproteomics Approach. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 423-438.	2.0	9
22	E-Microsatellite Markers for <i>Centella asiatica</i> (Gotu Kola) Genome: Validation and Cross-Transferability in Apiaceae Family for Plant Omics Research and Development. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 52-65.	2.0	9
23	Molecular recognition of avirulence protein (avrxa5) by eukaryotic transcription factor xa5 of rice (<i>Oryza sativa</i> L.): Insights from molecular dynamics simulations. <i>Journal of Molecular Graphics and Modelling</i> , 2015, 57, 49-61.	2.4	8
24	Mechanism Underlying Heat Stability of the Rice Endosperm Cytosolic ADP-Glucose Pyrophosphorylase. <i>Frontiers in Plant Science</i> , 2019, 10, 70.	3.6	8
25	Understanding the thermal response of rice eukaryotic transcription factor eIF4A1 towards dynamic temperature stress: insights from expression profiling and molecular dynamics simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 2575-2584.	3.5	8
26	RNAi mediated silencing of 3-hydroxy-3-methylglutaryl-CoA reductases (HMGR) in <i>Centella asiatica</i> . <i>Gene Reports</i> , 2018, 11, 52-57.	0.8	7
27	Identification and validation of plant miRNA from NGS data—an experimental approach. <i>Briefings in Functional Genomics</i> , 2019, 18, 13-22.	2.7	7
28	Molecular Modeling and Dynamics Simulation Analysis of KATNAL1 for Identification of Novel Inhibitor of Sperm Maturation. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 82-92.	1.1	7
29	ESMP: A high-throughput computational pipeline for mining SSR markers from ESTs. <i>Bioinformatics</i> , 2012, 8, 206-208.	0.5	7
30	An Insight Into Structure, Function, and Expression Analysis of 3-Hydroxy-3-Methylglutaryl-CoA Reductase of <i>Cymbopogon winterianus</i> . <i>Bioinformatics and Biology Insights</i> , 2017, 11, 117793221770173.	2.0	6
31	Towards an efficient computational mining approach to identify EST-SSR markers. <i>Bioinformatics</i> , 2012, 8, 201-202.	0.5	6
32	Revealing shared differential co-expression profiles in rice infected by virus from reoviridae and sequiviridae group. <i>Gene</i> , 2019, 698, 82-91.	2.2	5
33	Genetic Diversity and DNA Barcoding of Wild Mushrooms from Northeast India. <i>Iranian Journal of Science and Technology, Transaction A: Science</i> , 2021, 45, 469-479.	1.5	5
34	Mapping of QTLs for Grain Yield and its Component Traits under Drought Stress in Elite Rice Variety of Assam. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2017, 6, 1443-1455.	0.1	5
35	Molecular characterization and sequence analyses of Banana bunchy top virus infecting banana cultivar Jahaji (Dwarf Cavendish) in Assam, India. <i>3 Biotech</i> , 2019, 9, 110.	2.2	3
36	Combined CADD and Virtual Screening to Identify Novel Nonpeptidic Falcipain-2 Inhibitors. <i>Current Computer-Aided Drug Design</i> , 2021, 17, 579-588.	1.2	3

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37	Development of advanced breeding lines for high grain yield under drought stress in elite rice genetic background. <i>Research on Crops</i> , 2017, 18, 705.	0.1	3
38	Niche differentiation of belowground microorganisms and their functional signatures in Assam type tea (<i>Camellia sinensis</i> var. <i>assamica</i>). <i>Archives of Microbiology</i> , 2021, 203, 5661-5674.	2.2	2
39	In Silico Identification of Natural Lead Molecules from the Genus of <i>Phyllanthus</i> Against Hepatitis B Virus Reverse Transcriptase. <i>Natural Products Journal</i> , 2016, 6, 292-304.	0.3	2
40	In vitro Regeneration of Banana and Assessment of Genetic Fidelity in the Regenerated Plantlets through RAPD. <i>Annual Research & Review in Biology</i> , 2017, 17, 1-11.	0.4	2
41	Insights into the mode of flavin mononucleotide binding and catalytic mechanism of bacterial chromate reductases: A molecular dynamics simulation study. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 16990-17005.	2.6	1
42	An approach to delineate primers for a group of poorly conserved sequences incorporating the common motif region. <i>Bioinformatics</i> , 2012, 8, 181-184.	0.5	1
43	Phenotypic Screening and Evaluation of Sub1 Introgressed Lines in Popular Rice Varieties Ranjit and Bahadur of Assam. <i>International Journal of Current Microbiology and Applied Sciences</i> , 2018, 7, 1744-1755.	0.1	1
44	Title is missing!. , 2020, 15, e0224051.		0
45	Title is missing!. , 2020, 15, e0224051.		0
46	Title is missing!. , 2020, 15, e0224051.		0
47	Title is missing!. , 2020, 15, e0224051.		0