

Mahendra Modi

List of Publications by Year in descending order

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papers

559
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687363

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docs citations

47
times ranked

859
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of promising inhibitors for Plasmodium haemoglobinase Falcipain-2, using virtual screening, molecular docking, and MD Simulation. Journal of Molecular Structure, 2022, 1248, 131427.	3.6	10
2	Understanding the thermal response of rice eukaryotic transcription factor eIF4A1 towards dynamic temperature stress: insights from expression profiling and molecular dynamics simulation. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2575-2584.	3.5	8
3	Genetic Diversity and DNA Barcoding of Wild Mushrooms from Northeast India. Iranian Journal of Science and Technology, Transaction A: Science, 2021, 45, 469-479.	1.5	5
4	Genome-wide association studies for agronomical traits in winter rice accessions of Assam. Genomics, 2021, 113, 1037-1047.	2.9	16
5	Niche differentiation of belowground microorganisms and their functional signatures in Assam type tea (Camellia sinensis var. assamica). Archives of Microbiology, 2021, 203, 5661-5674.	2.2	2
6	Combined CADD and Virtual Screening to Identify Novel Nonpeptidic Falcipain-2 Inhibitors. Current Computer-Aided Drug Design, 2021, 17, 579-588.	1.2	3
7	Identification and characterization of drought responsive miRNAs from a drought tolerant rice genotype of Assam. Plant Gene, 2020, 21, 100213.	2.3	20
8	Mechanism of interaction of an endofungal bacterium Serratia marcescens D1 with its host and non-host fungi. PLoS ONE, 2020, 15, e0224051.	2.5	22
9	Title is missing!. , 2020, 15, e0224051.		0
10	Title is missing!. , 2020, 15, e0224051.		0
11	Title is missing!. , 2020, 15, e0224051.		0
12	Title is missing!. , 2020, 15, e0224051.		0
13	Mechanism Underlying Heat Stability of the Rice Endosperm Cytosolic ADP-Glucose Pyrophosphorylase. Frontiers in Plant Science, 2019, 10, 70.	3.6	8
14	Insights into the mode of flavin mononucleotide binding and catalytic mechanism of bacterial chromate reductases: A molecular dynamics simulation study. Journal of Cellular Biochemistry, 2019, 120, 16990-17005.	2.6	1
15	Revealing shared differential co-expression profiles in rice infected by virus from reoviridae and sequiviridae group. Gene, 2019, 698, 82-91.	2.2	5
16	Molecular characterization and sequence analyses of Banana bunchy top virus infecting banana cultivar Jahaji (Dwarf Cavendish) in Assam, India. 3 Biotech, 2019, 9, 110.	2.2	3
17	Identification and validation of plant miRNA from NGS data—an experimental approach. Briefings in Functional Genomics, 2019, 18, 13-22.	2.7	7
18	RNAi mediated silencing of 3-hydroxy-3-methylglutaryl-CoA reductases (HMGR) in Centella asiatica. Gene Reports, 2018, 11, 52-57.	0.8	7

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19	Bacillus megaterium adapts to acid stress condition through a network of genes: Insight from a genome-wide transcriptome analysis. Scientific Reports, 2018, 8, 16105.	3.3	30
20	Phenotypic Screening and Evaluation of Sub1 Introgressed Lines in Popular Rice Varieties Ranjit and Bahadur of Assam. International Journal of Current Microbiology and Applied Sciences, 2018, 7, 1744-1755.	0.1	1
21	An Insight Into Structure, Function, and Expression Analysis of 3-Hydroxy-3-Methylglutaryl-CoA Reductase of <i>Cymbopogon winterianus</i> . Bioinformatics and Biology Insights, 2017, 11, 117793221770173.	2.0	6
22	Molecular Modeling and Dynamics Simulation Analysis of KATNAL1 for Identification of Novel Inhibitor of Sperm Maturation. Combinatorial Chemistry and High Throughput Screening, 2017, 20, 82-92.	1.1	7
23	In vitro Regeneration of Banana and Assessment of Genetic Fidelity in the Regenerated Plantlets through RAPD. Annual Research & Review in Biology, 2017, 17, 1-11.	0.4	2
24	Development of advanced breeding lines for high grain yield under drought stress in elite rice genetic background. Research on Crops, 2017, 18, 705.	0.1	3
25	Mapping of QTLs for Grain Yield and its Component Traits under Drought Stress in Elite Rice Variety of Assam. International Journal of Current Microbiology and Applied Sciences, 2017, 6, 1443-1455.	0.1	5
26	Genome wide transcriptome profiling reveals differential gene expression in secondary metabolite pathway of <i>Cymbopogon winterianus</i> . Scientific Reports, 2016, 6, 21026.	3.3	27
27	In Silico Identification of Natural Lead Molecules from the Genus of Phyllanthus Against Hepatitis B Virus Reverse Transcriptase. Natural Products Journal, 2016, 6, 292-304.	0.3	2
28	Molecular recognition of avirulence protein (avrxa5) by eukaryotic transcription factor xa5 of rice (<i>Oryza sativa</i> L.): Insights from molecular dynamics simulations. Journal of Molecular Graphics and Modelling, 2015, 57, 49-61.	2.4	8
29	E-Microsatellite Markers for <i>Centella asiatica</i> (Gotu Kola) Genome: Validation and Cross-Transferability in Apiaceae Family for Plant Omics Research and Development. OMICS A Journal of Integrative Biology, 2015, 19, 52-65.	2.0	9
30	Novel insights into structure–function mechanism and tissue–specific expression profiling of full-length <i>dxr</i> gene from <i>Cymbopogon winterianus</i> . FEBS Open Bio, 2015, 5, 325-334.	2.3	10
31	Molecular cloning, characterization and expression analysis of 3-hydroxy-3-methylglutaryl coenzyme A reductase gene from <i>Centella asiatica</i> L.. Molecular Biology Reports, 2015, 42, 1431-1439.	2.3	21
32	Computational identification and characterization of conserved miRNAs and their target genes in garlic (<i>Allium sativum</i> L.) expressed sequence tags. Gene, 2014, 537, 333-342.	2.2	43
33	Rediscovering Medicinal Plants' Potential with OMICS: Microsatellite Survey in Expressed Sequence Tags of Eleven Traditional Plants with Potent Antidiabetic Properties. OMICS A Journal of Integrative Biology, 2014, 18, 298-309.	2.0	20
34	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. PLoS ONE, 2014, 9, e97852.	2.5	28
35	Insights into the structure–function relationship of disease resistance protein HCTR in maize (<i>Zea</i>) Tj ETQq1 1 0.784314 rgBT /Over 2013, 45, 50-64.	2.4	9
36	Molecular Phylogeny, Homology Modeling, and Molecular Dynamics Simulation of Race-Specific Bacterial Blight Disease Resistance Protein (xa5) of Rice: A Comparative Agriproteomics Approach. OMICS A Journal of Integrative Biology, 2013, 17, 423-438.	2.0	9

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37	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
38	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
39	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
40	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
41	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
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	Towards an efficient computational mining approach to identify EST-SSR markers. <i>Bioinformatics</i> , 2012, 8, 201-202.	0.5	6
44	ESMP: A high-throughput computational pipeline for mining SSR markers from ESTs. <i>Bioinformatics</i> , 2012, 8, 206-208.	0.5	7
45	Mining for SSRs and FDMs from expressed sequence tags of <i>Camellia sinensis</i> . <i>Bioinformatics</i> , 2012, 8, 260-266.	0.5	19
46	The cytoplasmic-localized, cytoskeletal-associated RNA binding protein <i>OsTudor</i> : evidence for an essential role in storage protein RNA transport and localization. <i>Plant Journal</i> , 2008, 55, 443-454.	5.7	48
47	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