

Riddhi Datta

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

425
citations

840776

11
h-index

794594

19
g-index

24
all docs

24
docs citations

24
times ranked

612
citing authors

#	ARTICLE	IF	CITATIONS
1	Glutathione regulates ACC synthase transcription via WRKY33 and ACC oxidase by modulating mRNA stability to induce ethylene synthesis during stress. <i>Plant Physiology</i> , 2015, 169, pp.01543.2015.	4.8	95
2	Multistep involvement of glutathione with salicylic acid and ethylene to combat environmental stress. <i>Journal of Plant Physiology</i> , 2014, 171, 940-950.	3.5	54
3	De novo transcriptome analysis using 454 pyrosequencing of the Himalayan Mayapple, <i>Podophyllum hexandrum</i> . <i>BMC Genomics</i> , 2013, 14, 748.	2.8	43
4	Transcriptome analysis of <i>Arabidopsis</i> mutants suggests a crosstalk between ABA, ethylene and GSH against combined cold and osmotic stress. <i>Scientific Reports</i> , 2016, 6, 36867.	3.3	32
5	Transcriptomic Profiling of <i>Arabidopsis thaliana</i> Mutant pad2.1 in Response to Combined Cold and Osmotic Stress. <i>PLoS ONE</i> , 2015, 10, e0122690.	2.5	25
6	Integrated transcriptomic and proteomic analysis of <i>Arabidopsis thaliana</i> exposed to glutathione unravels its role in plant defense. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 120, 975-988.	2.3	20
7	Rice lectin protein r40c1 imparts drought tolerance by modulating <i>S</i> -adenosylmethionine synthase 2, stress-associated protein 8 and chromatin-associated proteins. <i>Journal of Experimental Botany</i> , 2020, 71, 7331-7346.	4.8	20
8	Changes in leaf proteome profile of <i>Arabidopsis thaliana</i> in response to salicylic acid. <i>Journal of Biosciences</i> , 2013, 38, 317-328.	1.1	18
9	Transcriptome-wide identification and characterization of CAD isoforms specific for podophyllotoxin biosynthesis from <i>Podophyllum hexandrum</i> . <i>Plant Molecular Biology</i> , 2016, 92, 1-23.	3.9	18
10	Long non-coding RNAs: Fine-tuning the developmental responses in plants. <i>Journal of Biosciences</i> , 2019, 44, 1.	1.1	17
11	Leaf proteome profiling of transgenic mint infected with <i>Alternaria alternata</i> . <i>Journal of Proteomics</i> , 2013, 93, 117-132.	2.4	14
12	Proteomic profiling of β -ECS overexpressed transgenic <i>Nicotiana</i> in response to drought stress. <i>Plant Signaling and Behavior</i> , 2014, 9, e29246.	2.4	12
13	Plant microRNAs: master regulator of gene expression mechanism. <i>Cell Biology International</i> , 2015, 39, 1185-1190.	3.0	9
14	Changes in the proteome of pad2-1, a glutathione depleted <i>Arabidopsis</i> mutant, during <i>Pseudomonas syringae</i> infection. <i>Journal of Proteomics</i> , 2015, 126, 82-93.	2.4	9
15	Long non-coding RNAs: Fine-tuning the developmental responses in plants. <i>Journal of Biosciences</i> , 2019, 44, .	1.1	8
16	Glutathione regulates transcriptional activation of iron transporters via <i>S</i> -nitrosylation of bHLH factors to modulate subcellular iron homeostasis. <i>Plant, Cell and Environment</i> , 2022, 45, 2176-2190.	5.7	8
17	Jacalin domain-containing protein OsSalT interacts with OsDREB2A and OsNAC1 to impart drought stress tolerance in planta. <i>Environmental and Experimental Botany</i> , 2021, 183, 104362.	4.2	7
18	Exploitation of a new Schiff-base ligand for boric acid fluorescent sensing in aqueous medium with bio-imaging studies in a living plant system. <i>RSC Advances</i> , 2015, 5, 51875-51882.	3.6	6

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19	Membrane proteome profiling of <i>Mentha arvensis</i> leaves in response to <i>Alternaria alternata</i> infection identifies crucial candidates for defense response. <i>Plant Signaling and Behavior</i> , 2018, 13, e1178423.	2.4	5
20	Networking by Small Molecule Hormones during Drought Stress in Plants. , 2020, , 203-228.		3