Neelam Mishra

List of Publications by Year
in descending order

17 papers	543 citations	759233 12 h-index	888059 17 g-index
18 all docs	18 docs citations	18 times ranked	701 citing authors

#	Article	IF	Citations
1	Water-Deficit Inducible Expression of a Cytokinin Biosynthetic Gene IPT Improves Drought Tolerance in Cotton. PLoS ONE, 2013, 8, e64190.	2.5	104
2	Overexpression of the Rice SUMO E3 Ligase Gene OsSIZ1 in Cotton Enhances Drought and Heat Tolerance, and Substantially Improves Fiber Yields in the Field under Reduced Irrigation and Rainfed Conditions. Plant and Cell Physiology, 2017, 58, 735-746.	3.1	86
3	Co-overexpressing a Plasma Membrane and a Vacuolar Membrane Sodium/Proton Antiporter Significantly Improves Salt Tolerance in Transgenic Arabidopsis Plants. Plant and Cell Physiology, 2016, 57, 1069-1084.	3.1	78
4	Expression of the Arabidopsis vacuolar H+-pyrophosphatase gene AVP1 in peanut to improve drought and salt tolerance. Plant Biotechnology Reports, 2013, 7, 345-355.	1.5	61
5	Overexpression of the rice gene OsSIZ1 in Arabidopsis improves drought-, heat-, and salt-tolerance simultaneously. PLoS ONE, 2018, 13, e0201716.	2.5	41
6	The yield difference between wild-type cotton and transgenic cotton that expresses IPT depends on when water-deficit stress is applied. Scientific Reports, 2018, 8, 2538.	3.3	32
7	Towards doubling fibre yield for cotton in the semiarid agricultural area by increasing tolerance to drought, heat and salinity simultaneously. Plant Biotechnology Journal, 2021, 19, 462-476.	8.3	29
8	Improving drought-, salinity-, and heat-tolerance in transgenic plants by co-overexpressing Arabidopsis vacuolar pyrophosphatase gene AVP1 and Larrea Rubisco activase gene RCA. Plant Science, 2020, 296, 110499.	3.6	25
9	AKR2A interacts with KCS1 to improve VLCFAs contents and chilling tolerance of <i>Arabidopsis thaliana</i>. Plant Journal, 2020, 103, 1575-1589.	5.7	21
10	Co-overexpression of AVP1 and PP2A-C5 in Arabidopsis makes plants tolerant to multiple abiotic stresses. Plant Science, 2018, 274, 271-283.	3.6	17
11	MAPK cascade gene family in Camellia sinensis: In-silico identification, expression profiles and regulatory network analysis. BMC Genomics, 2020, 21, 613.	2.8	15
12	Identification and Functional Analysis of microRNAs Involved in the Anther Development in Cotton Genic Male Sterile Line Yu98-8A. International Journal of Molecular Sciences, 2016, 17, 1677.	4.1	14
13	NHX Gene Family in Camellia sinensis: In-silico Genome-Wide Identification, Expression Profiles, and Regulatory Network Analysis. Frontiers in Plant Science, 2021, 12, 777884.	3.6	8
14	Flavanones: A potential natural inhibitor of the ATP binding site of PknG of<i>Mycobacterium tuberculosis</i>. Journal of Biomolecular Structure and Dynamics, 2022, 40, 11885-11899.	3.5	4
15	In-silico genome wide analysis of Mitogen activated protein kinase kinase kinase gene family in C. sinensis. PLoS ONE, 2021, 16, e0258657.	2.5	4
16	Defensive manoeuvres of NHX1 and SOS1 co/overexpression in plant salt tolerance. Turkish Journal of Botany, 2020, 44, 367-376.	1.2	3
17	Thermodynamics of ferredoxin binding to cyanobacterial nitrate reductase. Photosynthesis Research, 2020, 144, 73-84.	2.9	1