

Ashwani Pareek

List of Publications by Year in descending order

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Version: 2024-02-01

175
papers

7,626
citations

50276

46
h-index

64796

79
g-index

186
all docs

186
docs citations

186
times ranked

7119
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription Factors and Plants Response to Drought Stress: Current Understanding and Future Directions. <i>Frontiers in Plant Science</i> , 2016, 7, 1029.	3.6	611
2	Abiotic Stress Responses and Microbe-Mediated Mitigation in Plants: The Omics Strategies. <i>Frontiers in Plant Science</i> , 2017, 8, 172.	3.6	574
3	Transgenic Tobacco Overexpressing Glyoxalase Pathway Enzymes Grow and Set Viable Seeds in Zinc-Spiked Soils. <i>Plant Physiology</i> , 2006, 140, 613-623.	4.8	237
4	Engineering abiotic stress tolerance via CRISPR/ Cas-mediated genome editing. <i>Journal of Experimental Botany</i> , 2020, 71, 470-479.	4.8	184
5	Enhancing salt tolerance in a crop plant by overexpression of glyoxalase II. <i>Transgenic Research</i> , 2008, 17, 171-180.	2.4	168
6	Genome-wide analysis of rice and Arabidopsis identifies two glyoxalase genes that are highly expressed in abiotic stresses. <i>Functional and Integrative Genomics</i> , 2011, 11, 293-305.	3.5	146
7	Transcriptome map for seedling stage specific salinity stress response indicates a specific set of genes as candidate for saline tolerance in <i>Oryza sativa</i> L. <i>Functional and Integrative Genomics</i> , 2009, 9, 109-123.	3.5	140
8	An improved protocol for efficient transformation and regeneration of diverse indica rice cultivars. <i>Plant Methods</i> , 2011, 7, 49.	4.3	136
9	Clustered metallothionein genes are co-regulated in rice and ectopic expression of OsMT1e-Pconfers multiple abiotic stress tolerance in tobacco via ROS scavenging. <i>BMC Plant Biology</i> , 2012, 12, 107.	3.6	131
10	Whole-Genome Analysis of <i>Oryza sativa</i> Reveals Similar Architecture of Two-Component Signaling Machinery with Arabidopsis. <i>Plant Physiology</i> , 2006, 142, 380-397.	4.8	130
11	Knockdown of an inflorescence meristem-specific cytokinin oxidase " OsCKX2 in rice reduces yield penalty under salinity stress condition. <i>Plant, Cell and Environment</i> , 2018, 41, 936-946.	5.7	122
12	Physiological responses among Brassica species under salinity stress show strong correlation with transcript abundance for SOS pathway-related genes. <i>Journal of Plant Physiology</i> , 2009, 166, 507-520.	3.5	120
13	Mitigating the impact of climate change on plant productivity and ecosystem sustainability. <i>Journal of Experimental Botany</i> , 2020, 71, 451-456.	4.8	120
14	Immunological evidence for accumulation of two high-molecular-weight (104 and 90 kDa) HSPs in response to different stresses in rice and in response to high temperature stress in diverse plant genera. <i>Plant Molecular Biology</i> , 1995, 29, 293-301.	3.9	117
15	Cyclophilins: Proteins in search of function. <i>Plant Signaling and Behavior</i> , 2013, 8, e22734.	2.4	113
16	A unique N ² -dependent and methylglyoxal-inducible rice glyoxalase I possesses a single active site and functions in abiotic stress response. <i>Plant Journal</i> , 2014, 78, 951-963.	5.7	113
17	Genome wide expression analysis of CBS domain containing proteins in Arabidopsis thaliana (L.) Heynh and <i>Oryza sativa</i> L. reveals their developmental and stress regulation. <i>BMC Genomics</i> , 2009, 10, 200.	2.8	105
18	A glutathione responsive rice glyoxalase II, OsGLYII ² , functions in salinity adaptation by maintaining better photosynthesis efficiency and anti-oxidant pool. <i>Plant Journal</i> , 2014, 80, 93-105.	5.7	102

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19	Presence of unique glyoxalase III proteins in plants indicates the existence of shorter route for methylglyoxal detoxification. <i>Scientific Reports</i> , 2016, 6, 18358.	3.3	100
20	Glyoxalases and stress tolerance in plants. <i>Biochemical Society Transactions</i> , 2014, 42, 485-490.	3.4	97
21	Manipulation of glyoxalase pathway confers tolerance to multiple stresses in rice. <i>Plant, Cell and Environment</i> , 2018, 41, 1186-1200.	5.7	95
22	Molecular mechanisms of salinity tolerance in rice. <i>Crop Journal</i> , 2021, 9, 506-520.	5.2	91
23	Overexpression of Rice CBS Domain Containing Protein Improves Salinity, Oxidative, and Heavy Metal Tolerance in Transgenic Tobacco. <i>Molecular Biotechnology</i> , 2012, 52, 205-216.	2.4	90
24	Histidine kinases in plants. <i>Plant Signaling and Behavior</i> , 2012, 7, 1230-1237.	2.4	87
25	Understanding salinity responses and adopting omics-based approaches to generate salinity tolerant cultivars of rice. <i>Frontiers in Plant Science</i> , 2015, 6, 712.	3.6	86
26	Abiotic Stresses Cause Differential Regulation of Alternative Splice Forms of GATA Transcription Factor in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 1944.	3.6	86
27	Enhancing trehalose biosynthesis improves yield potential in marker-free transgenic rice under drought, saline, and sodic conditions. <i>Journal of Experimental Botany</i> , 2020, 71, 653-668.	4.8	82
28	Towards salinity tolerance in Brassica: an overview. <i>Physiology and Molecular Biology of Plants</i> , 2008, 14, 39-49.	3.1	81
29	What determines a leaf's shape?. <i>EvoDevo</i> , 2014, 5, 47.	3.2	74
30	Nomenclature for Two-Component Signaling Elements of Rice. <i>Plant Physiology</i> , 2007, 143, 555-557.	4.8	72
31	Ectopic expression of Pokkali phosphoglycerate kinase-2 (OsPGK2-P) improves yield in tobacco plants under salinity stress. <i>Plant Cell Reports</i> , 2016, 35, 27-41.	5.6	72
32	A suite of new genes defining salinity stress tolerance in seedlings of contrasting rice genotypes. <i>Functional and Integrative Genomics</i> , 2013, 13, 351-365.	3.5	71
33	Oxidative environment and redox homeostasis in plants: dissecting out significant contribution of major cellular organelles. <i>Frontiers in Environmental Science</i> , 2015, 2, .	3.3	71
34	Molecular breeding in Brassica for salt tolerance: importance of microsatellite (SSR) markers for molecular breeding in Brassica. <i>Frontiers in Plant Science</i> , 2015, 6, 688.	3.6	70
35	A nuclear-localized histone-gene binding protein from rice (OsHBP1b) functions in salinity and drought stress tolerance by maintaining chlorophyll content and improving the antioxidant machinery. <i>Journal of Plant Physiology</i> , 2015, 176, 36-46.	3.5	70
36	Analysis of global gene expression profile of rice in response to methylglyoxal indicates its possible role as a stress signal molecule. <i>Frontiers in Plant Science</i> , 2015, 6, 682.	3.6	68

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37	Halophytes As Bioenergy Crops. <i>Frontiers in Plant Science</i> , 2016, 7, 1372.	3.6	68
38	Membrane dynamics during individual and combined abiotic stresses in plants and tools to study the same. <i>Physiologia Plantarum</i> , 2021, 171, 653-676.	5.2	68
39	Genomics Approaches For Improving Salinity Stress Tolerance in Crop Plants. <i>Current Genomics</i> , 2016, 17, 343-357.	1.6	66
40	Photosynthesis and salinity: are these mutually exclusive?. <i>Photosynthetica</i> , 2018, 56, 366-381.	1.7	61
41	Deciphering the Role of Trehalose in Tripartite Symbiosis Among Rhizobia, Arbuscular Mycorrhizal Fungi, and Legumes for Enhancing Abiotic Stress Tolerance in Crop Plants. <i>Frontiers in Microbiology</i> , 2020, 11, 509919.	3.5	55
42	Heterologous Expression of a Salinity and Developmentally Regulated Rice Cyclophilin Gene (OsCyp2) in <i>E. coli</i> and <i>S. cerevisiae</i> Confers Tolerance Towards Multiple Abiotic Stresses. <i>Molecular Biotechnology</i> , 2009, 42, 195-204.	2.4	53
43	Transcriptome profiling of <i>Camelina sativa</i> to identify genes involved in triacylglycerol biosynthesis and accumulation in the developing seeds. <i>Biotechnology for Biofuels</i> , 2016, 9, 136.	6.2	53
44	Proteomics of contrasting rice genotypes: Identification of potential targets for raising crops for saline environment. <i>Plant, Cell and Environment</i> , 2018, 41, 947-969.	5.7	51
45	Silicon-mediated abiotic and biotic stress mitigation in plants: Underlying mechanisms and potential for stress resilient agriculture. <i>Plant Physiology and Biochemistry</i> , 2021, 163, 15-25.	5.8	51
46	Histidine kinase and response regulator genes as they relate to salinity tolerance in rice. <i>Functional and Integrative Genomics</i> , 2009, 9, 411-417.	3.5	50
47	A unique bZIP transcription factor imparting multiple stress tolerance in Rice. <i>Rice</i> , 2019, 12, 58.	4.0	50
48	Rice intermediate filament, OsIF, stabilizes photosynthetic machinery and yield under salinity and heat stress. <i>Scientific Reports</i> , 2018, 8, 4072.	3.3	49
49	Functional screening of cDNA library from a salt tolerant rice genotype Pokkali identifies mannose-1-phosphate guanyl transferase gene (OsMPG1) as a key member of salinity stress response. <i>Plant Molecular Biology</i> , 2012, 79, 555-568.	3.9	47
50	Narrowing down the targets for yield improvement in rice under normal and abiotic stress conditions via expression profiling of yield-related genes. <i>Rice</i> , 2012, 5, 37.	4.0	45
51	De Novo Assembly and Characterization of Stress Transcriptome in a Salinity-Tolerant Variety CS52 of <i>Brassica juncea</i> . <i>PLoS ONE</i> , 2015, 10, e0126783.	2.5	45
52	Histone chaperones in <i>Arabidopsis</i> and rice: genome-wide identification, phylogeny, architecture and transcriptional regulation. <i>BMC Plant Biology</i> , 2015, 15, 42.	3.6	44
53	A NAP-Family Histone Chaperone Functions in Abiotic Stress Response and Adaptation. <i>Plant Physiology</i> , 2016, 171, 2854-2868.	4.8	44
54	Engineering abiotic stress response in plants for biomass production. <i>Journal of Biological Chemistry</i> , 2018, 293, 5035-5043.	3.4	43

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55	Ion transporters and their regulatory signal transduction mechanisms for salinity tolerance in plants. <i>Physiologia Plantarum</i> , 2022, 174, e13702.	5.2	43
56	Tissue specific and abiotic stress regulated transcription of histidine kinases in plants is also influenced by diurnal rhythm. <i>Frontiers in Plant Science</i> , 2015, 6, 711.	3.6	42
57	Genome-wide investigation and expression analysis of Sodium/Calcium exchanger gene family in rice and Arabidopsis. <i>Rice</i> , 2015, 8, 54.	4.0	41
58	Expression of a cyclophilin OsCyp2-P isolated from a salt-tolerant landrace of rice in tobacco alleviates stress via ion homeostasis and limiting ROS accumulation. <i>Functional and Integrative Genomics</i> , 2015, 15, 395-412.	3.5	41
59	Mapping the "Two-component system"™ network in rice. <i>Scientific Reports</i> , 2017, 7, 9287.	3.3	41
60	Raising salinity tolerant rice: recent progress and future perspectives. <i>Physiology and Molecular Biology of Plants</i> , 2008, 14, 137-154.	3.1	40
61	Integrating the dynamics of yield traits in rice in response to environmental changes. <i>Journal of Experimental Botany</i> , 2020, 71, 490-506.	4.8	39
62	Drought and High Temperature Stress in Sorghum: Physiological, Genetic, and Molecular Insights and Breeding Approaches. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9826.	4.1	39
63	Shaping the root system architecture in plants for adaptation to drought stress. <i>Physiologia Plantarum</i> , 2022, 174, e13651.	5.2	39
64	The Saltol QTL-localized transcription factor OsGATA8 plays an important role in stress tolerance and seed development in Arabidopsis and rice. <i>Journal of Experimental Botany</i> , 2020, 71, 684-698.	4.8	37
65	Mapping the "early salinity response"™ triggered proteome adaptation in contrasting rice genotypes using iTRAQ approach. <i>Rice</i> , 2019, 12, 3.	4.0	37
66	The quest for osmosensors in plants. <i>Journal of Experimental Botany</i> , 2020, 71, 595-607.	4.8	37
67	Elucidating the Response of Crop Plants towards Individual, Combined and Sequentially Occurring Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6119.	4.1	37
68	A nuclear-localized rice glyoxalase I enzyme, OsGLYI ⁸ , functions in the detoxification of methylglyoxal in the nucleus. <i>Plant Journal</i> , 2017, 89, 565-576.	5.7	36
69	Characterization and functional validation of glyoxalase II from rice. <i>Protein Expression and Purification</i> , 2007, 51, 126-132.	1.3	35
70	Evidence for nuclear interaction of a cytoskeleton protein (OsIFL) with metallothionein and its role in salinity stress tolerance. <i>Scientific Reports</i> , 2016, 6, 34762.	3.3	35
71	Reassessing plant glyoxalases: large family and expanding functions. <i>New Phytologist</i> , 2020, 227, 714-721.	7.3	35
72	Gaining Acceptance of Novel Plant Breeding Technologies. <i>Trends in Plant Science</i> , 2021, 26, 575-587.	8.8	34

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73	MATH-Domain Family Shows Response toward Abiotic Stress in Arabidopsis and Rice. <i>Frontiers in Plant Science</i> , 2016, 7, 923.	3.6	33
74	Metabolic shift in sugars and amino acids regulates sprouting in Saffron corm. <i>Scientific Reports</i> , 2017, 7, 11904.	3.3	32
75	How do rice seedlings of landrace Pokkali survive in saline fields after transplantation? <i>Physiology, biochemistry, and photosynthesis. Photosynthesis Research</i> , 2021, 150, 117-135.	2.9	32
76	Transcription dynamics of Saltol QTL localized genes encoding transcription factors, reveals their differential regulation in contrasting genotypes of rice. <i>Functional and Integrative Genomics</i> , 2017, 17, 69-83.	3.5	31
77	Distribution patterns of 104 kDa stress-associated protein in rice. <i>Plant Molecular Biology</i> , 1998, 37, 911-919.	3.9	29
78	Salt Overly Sensitive pathway members are influenced by diurnal rhythm in rice. <i>Plant Signaling and Behavior</i> , 2013, 8, e24738.	2.4	28
79	Characterization of Peptidyl-Prolyl Cis-Trans Isomerase- and Calmodulin-Binding Activity of a Cytosolic Arabidopsis thaliana Cyclophilin AtCyp19-3. <i>PLoS ONE</i> , 2015, 10, e0136692.	2.5	28
80	Forward and reverse genetics approaches for combined stress tolerance in rice. <i>Indian Journal of Plant Physiology</i> , 2018, 23, 630-646.	0.8	27
81	CO ₂ uptake and chlorophyll a fluorescence of Suaeda fruticosa grown under diurnal rhythm and after transfer to continuous dark. <i>Photosynthesis Research</i> , 2019, 142, 211-227.	2.9	27
82	Growth and secretome analysis of possible synergistic interaction between green algae and cyanobacteria. <i>Journal of Bioscience and Bioengineering</i> , 2019, 127, 213-221.	2.2	27
83	Stacking for future: Pyramiding genes to improve drought and salinity tolerance in rice. <i>Physiologia Plantarum</i> , 2021, 172, 1352-1362.	5.2	27
84	Characteristic Variations and Similarities in Biochemical, Molecular, and Functional Properties of Glyoxalases across Prokaryotes and Eukaryotes. <i>International Journal of Molecular Sciences</i> , 2017, 18, 250.	4.1	25
85	Silicon nutrition stimulates Salt-Overly Sensitive (SOS) pathway to enhance salinity stress tolerance and yield in rice. <i>Plant Physiology and Biochemistry</i> , 2021, 166, 593-604.	5.8	24
86	The chloride channels: Silently serving the plants. <i>Physiologia Plantarum</i> , 2021, 171, 688-702.	5.2	23
87	Rewilding staple crops for the lost halophytism: Toward sustainability and profitability of agricultural production systems. <i>Molecular Plant</i> , 2022, 15, 45-64.	8.3	23
88	Unraveling the contribution of <i>OsSOS2</i> in conferring salinity and drought tolerance in a high yielding rice. <i>Physiologia Plantarum</i> , 2022, 174, e13638.	5.2	23
89	Biochemical composition of green alga <i>Chlorella minutissima</i> in mixotrophic cultures under the effect of different carbon sources. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 624-627.	2.2	22
90	Molecular cloning and characterization of salt overly sensitive gene promoter from Brassica juncea (<i>BjSOS2</i>). <i>Molecular Biology Reports</i> , 2015, 42, 1139-1148.	2.3	22

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91	Yeast HSP104 homologue rice HSP110 is developmentally- and stress-regulated. <i>Plant Science</i> , 1997, 125, 211-219.	3.6	21
92	Distribution patterns of HSP 90 protein in rice. <i>Plant Science</i> , 1997, 125, 221-230.	3.6	20
93	<i>DPS1</i> regulates cuticle development and leaf senescence in rice. <i>Food and Energy Security</i> , 2021, 10, e273.	4.3	20
94	Increased Cuticle Waxes by Overexpression of WSD1 Improves Osmotic Stress Tolerance in <i>Arabidopsis thaliana</i> and <i>Camelina sativa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 5173.	4.1	19
95	Structural and biochemical characterization of the cytosolic wheat cyclophilin TaCypA-1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 555-563.	2.5	18
96	Analysis of a salinity induced BjsOS3 protein from Brassica indicate it to be structurally and functionally related to its ortholog from Arabidopsis. <i>Plant Physiology and Biochemistry</i> , 2011, 49, 996-1004.	5.8	17
97	A Salt Overly Sensitive Pathway Member from Brassica juncea BjsOS3 Can Functionally Complement <i>At</i> Ats3 in Arabidopsis. <i>Current Genomics</i> , 2017, 19, 60-69.	1.6	17
98	Evidence for the possible involvement of calmodulin in regulation of steady state levels of Hsp90 family members (Hsp87 and Hsp85) in response to heat shock in sorghum. <i>Plant Signaling and Behavior</i> , 2011, 6, 393-399.	2.4	16
99	Physiological characterization of gamma-ray induced mutant population of rice to facilitate biomass and yield improvement under salinity stress. <i>Indian Journal of Plant Physiology</i> , 2016, 21, 545-555.	0.8	16
100	The peptidyl-prolyl cis-trans isomerase activity of the wheat cyclophilin, TaCypA-1, is essential for inducing thermotolerance in <i>Escherichia coli</i> . <i>Biochimie Open</i> , 2016, 2, 9-15.	3.2	16
101	Overview of Methods for Assessing Salinity and Drought Tolerance of Transgenic Wheat Lines. <i>Methods in Molecular Biology</i> , 2017, 1679, 83-95.	0.9	16
102	Maintenance of stress related transcripts in tolerant cultivar at a level higher than sensitive one appears to be a conserved salinity response among plants. <i>Plant Signaling and Behavior</i> , 2009, 4, 431-434.	2.4	15
103	Plant Hsp100 family with special reference to rice. <i>Journal of Biosciences</i> , 1998, 23, 337-345.	1.1	14
104	Putative osmosensor <i>OshK3b</i> a histidine kinase protein from rice shows high structural conservation with its ortholog <i>AtHK1</i> from <i>Arabidopsis</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1318-1332.	3.5	14
105	Simple and efficient way to detect small polymorphic bands in plants. <i>Genomics Data</i> , 2015, 5, 218-222.	1.3	14
106	Exploiting Microalgae and Macroalgae for Production of Biofuels and Biosequestration of Carbon Dioxide—A Review. <i>International Journal of Green Energy</i> , 2015, 12, 1122-1143.	3.8	14
107	Towards Understanding Abiotic Stress Signaling in Plants: Convergence of Genomic, Transcriptomic, Proteomic, and Metabolomic Approaches. , 2015, , 3-40.		13
108	Designing Climate-Smart Future Crops Employing Signal Transduction Components. , 2015, , 393-413.		13

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109	The Journey from Two-Step to Multi-Step Phosphorelay Signaling Systems. <i>Current Genomics</i> , 2021, 22, 59-74.	1.6	13
110	Plant Hsp90 family with special reference to rice. <i>Journal of Biosciences</i> , 1998, 23, 361-367.	1.1	12
111	UPLC-MS analysis of <i>Chlamydomonas reinhardtii</i> and <i>Scenedesmus obliquus</i> lipid extracts and their possible metabolic roles. <i>Journal of Applied Phycology</i> , 2015, 27, 1149-1159.	2.8	12
112	Comparative transcriptome and metabolome analysis suggests bottlenecks that limit seed and oil yields in transgenic <i>Camelina sativa</i> expressing diacylglycerol acyltransferase 1 and glycerol-3-phosphate dehydrogenase. <i>Biotechnology for Biofuels</i> , 2018, 11, 335.	6.2	12
113	Pre-Field Screening Protocols for Heat-Tolerant Mutants in Rice. , 2018, , .		12
114	Carbon dioxide responsiveness mitigates rice yield loss under high night temperature. <i>Plant Physiology</i> , 2022, 188, 285-300.	4.8	12
115	Genetic Conservation of CBS Domain Containing Protein Family in <i>Oryza</i> Species and Their Association with Abiotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1687.	4.1	12
116	Physiological and molecular signatures reveal differential response of rice genotypes to drought and drought combination with heat and salinity stress. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 899-910.	3.1	12
117	Developmental changes in storage proteins and peptidyl prolyl cis-trans isomerase activity in grains of different wheat cultivars. <i>Food Chemistry</i> , 2011, 128, 450-457.	8.2	11
118	OsCBSCBSPB4 is a Two Cystathionine-Î ² -Synthase Domain-containing Protein from Rice that Functions in Abiotic Stress Tolerance. <i>Current Genomics</i> , 2017, 19, 50-59.	1.6	11
119	Evidence for accumulation of a 55 kDa stress-related protein in rice and several other plant genera. <i>Plant Science</i> , 1998, 134, 191-197.	3.6	10
120	ASYMMETRIC LEAVES1 and REVOLUTA are the key regulatory genes associated with pitcher development in <i>Nepenthes khasiana</i> . <i>Scientific Reports</i> , 2019, 9, 6318.	3.3	10
121	Tracing the Evolution of Plant Glyoxalase III Enzymes for Structural and Functional Divergence. <i>Antioxidants</i> , 2021, 10, 648.	5.1	10
122	Dissecting Out the Crosstalk Between Salinity and Hormones in Roots of <i>Arabidopsis</i> . <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 913-924.	2.0	9
123	Biodiesel production from camelina oil: Present status and future perspectives. <i>Food and Energy Security</i> , 2023, 12, e340.	4.3	9
124	Biomass production and salinity response in plants: role of MicroRNAs. <i>Indian Journal of Plant Physiology</i> , 2017, 22, 448-457.	0.8	8
125	Molecular Mechanism and Signaling Response of Heavy Metal Stress Tolerance in Plants. , 2019, , 29-47.		8
126	Role of Cysteine Residues in Regulation of Peptidyl-prolyl cis-trans Isomerase Activity of Wheat Cyclophilin TaCYP1. <i>Protein and Peptide Letters</i> , 2017, 24, 551-560.	0.9	8

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127	Regulation of Leaf Senescence: Role of Reactive Oxygen Species. <i>Advances in Photosynthesis and Respiration</i> , 2013, , 393-416.	1.0	7
128	A temperature-responsive gene in sorghum encodes a glycine-rich protein that interacts with calmodulin. <i>Biochimie</i> , 2017, 137, 115-123.	2.6	7
129	Gene Expression Dynamics in Rice Peduncles at the Heading Stage. <i>Frontiers in Genetics</i> , 2020, 11, 584678.	2.3	7
130	Raising Climate-Resilient Crops: Journey From the Conventional Breeding to New Breeding Approaches. <i>Current Genomics</i> , 2021, 22, 450-467.	1.6	7
131	Signaling cross talk between biotic and abiotic stress responses in soybean. , 2016, , 27-52.		6
132	Sensing and signalling in plant stress responses: ensuring sustainable food security in an era of climate change. <i>New Phytologist</i> , 2020, 228, 823-827.	7.3	6
133	Two-component signaling system in plants: interaction network and specificity in response to stress and hormones. <i>Plant Cell Reports</i> , 2021, 40, 2037-2046.	5.6	6
134	How to survive in a salty desert: An adventure study with <i>Suaeda fruticosa</i> . <i>The Journal of Plant Science Research</i> , 2019, 35, 257-261.	0.1	6
135	Genetic diversity reveals synergistic interaction between yield components could improve the sink size and yield in rice. <i>Food and Energy Security</i> , 2022, 11, .	4.3	6
136	<i>OsCyp2</i> , an auxin-responsive cyclophilin, regulates Ca ²⁺ calmodulin interaction for an ion-mediated stress response in rice. <i>Physiologia Plantarum</i> , 2022, 174, e13631.	5.2	6
137	Seedling-stage salinity tolerance in rice: Decoding the role of transcription factors. <i>Physiologia Plantarum</i> , 2022, 174, e13685.	5.2	6
138	Glyoxalase III enhances salinity tolerance through reactive oxygen species scavenging and reduced glycation. <i>Physiologia Plantarum</i> , 2022, 174, e13693.	5.2	6
139	Pitchers of <i>Nepenthes khasiana</i> express several digestive-enzyme encoding genes, harbor mostly fungi and probably evolved through changes in the expression of leaf polarity genes. <i>BMC Plant Biology</i> , 2020, 20, 524.	3.6	5
140	TUNEL Assay to Assess Extent of DNA Fragmentation and Programmed Cell Death in Root Cells under Various Stress Conditions. <i>Bio-protocol</i> , 2017, 7, e2502.	0.4	5
141	Abiotic Stress Responses: Complexities in Gene Expression. , 2009, , 177-198.		4
142	Glyoxalase Pathway and Drought Stress Tolerance in Plants. , 2016, , 379-399.		4
143	Comparison and utilization of potential green algal and cyanobacterial species for power generation through algal microbial fuel cell. <i>Energy Sources, Part A: Recovery, Utilization and Environmental Effects</i> , 2017, 39, 451-457.	2.3	4
144	Expression dynamics of glyoxalase genes under high temperature stress in plants. <i>Plant Physiology Reports</i> , 2020, 25, 533-548.	1.5	4

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145	Innovative plant breeding could deliver crop revolution. <i>Nature</i> , 2020, 577, 622-622.	27.8	4
146	Microbial methylglyoxal metabolism contributes towards growth promotion and stress tolerance in plants. <i>Environmental Microbiology</i> , 2022, 24, 2817-2836.	3.8	4
147	The Two-Component System: Transducing Environmental and Hormonal Signals. , 2019, , 247-278.		4
148	<sc>DTH8</sc> overexpression induces early flowering, boosts yield, and improves stress recovery in rice cv <sc>IR64</sc>. <i>Physiologia Plantarum</i> , 2022, 174, e13691.	5.2	4
149	Raising crops for dry and saline lands: Challenges and the way forward. <i>Physiologia Plantarum</i> , 2022, 174, .	5.2	4
150	Analysis of Salt Stress-Related Transcriptome Fingerprints from Diverse Plant Species. , 2007, , 267-287.		3
151	Functional Genomics Approach Towards Dissecting Out Abiotic Stress Tolerance Trait in Plants. <i>Sustainable Development and Biodiversity</i> , 2019, , 1-24.	1.7	3
152	Molecular Chaperones: Key Players of Abiotic Stress Response in Plants. <i>Sustainable Development and Biodiversity</i> , 2019, , 125-165.	1.7	3
153	Recent Advancements in Developing Salinity Tolerant Rice. , 2019, , 87-112.		3
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