

Zongyun Li

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

1,464
citations

304743

22
h-index

377865

34
g-index

60
all docs

60
docs citations

60
times ranked

1321
citing authors

#	ARTICLE	IF	CITATIONS
1	Basic leucine zipper transcription factor SlbZIP1 mediates salt and drought stress tolerance in tomato. <i>BMC Plant Biology</i> , 2018, 18, 83.	3.6	119
2	Melatonin-Stimulated Triacylglycerol Breakdown and Energy Turnover under Salinity Stress Contributes to the Maintenance of Plasma Membrane H ⁺ -ATPase Activity and K ⁺ /Na ⁺ Homeostasis in Sweet Potato. <i>Frontiers in Plant Science</i> , 2018, 9, 256.	3.6	101
3	RNA-Seq and iTRAQ reveal multiple pathways involved in storage root formation and development in sweet potato (<i>Ipomoea batatas</i> L.). <i>BMC Plant Biology</i> , 2019, 19, 136.	3.6	78
4	NaCl-induced changes of ion homeostasis and nitrogen metabolism in two sweet potato (<i>Ipomoea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Experimental Botany, 2016, 129, 23-36.	4.2	70
5	Genome-wide identification, structural and gene expression analysis of the bZIP transcription factor family in sweet potato wild relative <i>Ipomoea trifida</i> . <i>BMC Genetics</i> , 2019, 20, 41.	2.7	63
6	Root-zone-specific sensitivity of K ⁺ -and Ca ²⁺ -permeable channels to H ₂ O ₂ determines ion homeostasis in salinized diploid and hexaploid <i>Ipomoea trifida</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 1389-1405.	4.8	48
7	High-throughput deep sequencing reveals the important role that microRNAs play in the salt response in sweet potato (<i>Ipomoea batatas</i> L.). <i>BMC Genomics</i> , 2020, 21, 164.	2.8	46
8	Research Progress of Betalain in Response to Adverse Stresses and Evolutionary Relationship Compared with Anthocyanin. <i>Molecules</i> , 2019, 24, 3078.	3.8	43
9	Genome-wide identification, characterisation and functional evaluation of WRKY genes in the sweet potato wild ancestor <i>Ipomoea trifida</i> (H.B.K.) G. Don. under abiotic stresses. <i>BMC Genetics</i> , 2019, 20, 90.	2.7	42
10	Genome-wide identification and expression analysis of glycine-rich RNA-binding protein family in sweet potato wild relative <i>Ipomoea trifida</i> . <i>Gene</i> , 2019, 686, 177-186.	2.2	42
11	Comparative Metabolomic and Transcriptome Analysis Reveal Distinct Flavonoid Biosynthesis Regulation Between Petals of White and Purple <i>Phalaenopsis amabilis</i> . <i>Journal of Plant Growth Regulation</i> , 2020, 39, 823-840.	5.1	42
12	Comparative Transcriptome and Proteome Analysis of Salt-Tolerant and Salt-Sensitive Sweet Potato and Overexpression of IbNAC7 Confers Salt Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 572540.	3.6	42
13	Genome-wide analysis of expression quantitative trait loci (eQTLs) reveals the regulatory architecture of gene expression variation in the storage roots of sweet potato. <i>Horticulture Research</i> , 2020, 7, 90.	6.3	38
14	Calcium-Mobilizing Properties of <i>Salvia miltiorrhiza</i> -Derived Carbon Dots Confer Enhanced Environmental Adaptability in Plants. <i>ACS Nano</i> , 2022, 16, 4357-4370.	14.6	35
15	A high-resolution cucumber cytogenetic map integrated with the genome assembly. <i>BMC Genomics</i> , 2013, 14, 461.	2.8	33
16	Isolation, Expression Analysis, and Function Evaluation of 12 Novel Stress-Responsive Genes of NAC Transcription Factors in Sweetpotato. <i>Crop Science</i> , 2018, 58, 1328-1341.	1.8	33
17	NaCl-elicited, vacuolar Ca ²⁺ release facilitates prolonged cytosolic Ca ²⁺ signaling in the salt response of <i>Populus euphratica</i> cells. <i>Cell Calcium</i> , 2015, 57, 348-365.	2.4	32
18	Targeting of SPCSVâ€œRNase3 via CRISPRâ€œCas13 confers resistance against sweet potato virus disease. <i>Molecular Plant Pathology</i> , 2022, 23, 104-117.	4.2	32

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19	Identification and expression analysis of GRAS transcription factors in the wild relative of sweet potato <i>Ipomoea trifida</i> . <i>BMC Genomics</i> , 2019, 20, 911.	2.8	31
20	Chilling and Heat Stress-Induced Physiological Changes and MicroRNA-Related Mechanism in Sweetpotato (<i>Ipomoea batatas</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 687.	3.6	30
21	Involvement of Phosphatidylserine and Triacylglycerol in the Response of Sweet Potato Leaves to Salt Stress. <i>Frontiers in Plant Science</i> , 2019, 10, 1086.	3.6	28
22	The Interaction Network and Signaling Specificity of Two-Component System in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4898.	4.1	25
23	High throughput sequencing identifies chilling responsive genes in sweetpotato (<i>Ipomoea batatas</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 2.9 24	2.9	24
24	Drought-Induced Responses of Nitrogen Metabolism in <i>Ipomoea batatas</i> . <i>Plants</i> , 2020, 9, 1341.	3.5	24
25	Characterization of a Novel Chitinase from Sweet Potato and Its Fungicidal Effect against <i>Ceratocystis fimbriata</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 7591-7600.	5.2	23
26	A Single Nucleotide Deletion in <i>Gibberellin20-oxidase1</i> Causes Alpine Dwarfism in Arabidopsis. <i>Plant Physiology</i> , 2015, 168, 930-937.	4.8	22
27	Overexpression of phosphatidylserine synthase IbPSS1 affords cellular Na ⁺ homeostasis and salt tolerance by activating plasma membrane Na ⁺ /H ⁺ antiport activity in sweet potato roots. <i>Horticulture Research</i> , 2020, 7, 131.	6.3	21
28	High throughput deep sequencing reveals the important roles of microRNAs during sweetpotato storage at chilling temperature. <i>Scientific Reports</i> , 2017, 7, 16578.	3.3	20
29	<i>SISTE1</i> promotes abscisic acid-dependent salt stress-responsive pathways via improving ion homeostasis and reactive oxygen species scavenging in tomato. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 1942-1966.	8.5	19
30	Genome-wide in silico identification and expression analysis of beta-galactosidase family members in sweetpotato [<i>Ipomoea batatas</i> (L.) Lam]. <i>BMC Genomics</i> , 2021, 22, 140.	2.8	18
31	Identification of candidate miRNAs related in storage root development of sweet potato by high throughput sequencing. <i>Journal of Plant Physiology</i> , 2020, 251, 153224.	3.5	17
32	Identification, expression analysis, and function evaluation of 42 tomato DEAD-box RNA helicase genes in growth development and stress response. <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	2.1	16
33	Improving CRISPR-Cas-mediated RNA targeting and gene editing using SPLCV replicon-based expression vectors in <i>Nicotiana benthamiana</i> . <i>Plant Biotechnology Journal</i> , 2020, 18, 1993-1995.	8.3	15
34	Functional characteristic analysis of three odorant-binding proteins from the sweet potato weevil (<i>Sitona</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Science, 2021, 77, 300-312.	3.4	14
35	Comparative Transcriptome Analysis Reveals Key Genes and Pathways Involved in Prickle Development in Eggplant. <i>Genes</i> , 2021, 12, 341.	2.4	14
36	Molecular characterization of nine sweet potato (<i>Ipomoea batatas</i> Lam.) MADS-box transcription factors during storage root development and following abiotic stress. <i>Plant Breeding</i> , 2018, 137, 790-804.	1.9	13

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37	A bacterial Fâ€œbox effector suppresses SAR immunity through mediating the proteasomal degradation of OsTrxh2 in rice. <i>Plant Journal</i> , 2020, 104, 1054-1072.	5.7	12
38	Potassium Fertilization Stimulates Sucrose-to-Starch Conversion and Root Formation in Sweet Potato (<i>Ipomoea batatas</i> (L.) Lam.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 4826.	4.1	12
39	Molecular Characterization and Target Prediction of Candidate miRNAs Related to Abiotic Stress Responses and/or Storage Root Development in Sweet Potato. <i>Genes</i> , 2022, 13, 110.	2.4	12
40	High Soil Available Phosphorus Favors Carbon Metabolism in Cotton Leaves in Pot Trials. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 974-985.	5.1	11
41	Three chemosensory proteins from the sweet potato weevil, <sc><i>Cylas formicarius</i></sc>, are involved in the perception of host plant volatiles. <i>Pest Management Science</i> , 2021, 77, 4497-4509.	3.4	11
42	Expression of IbVPE1 from sweet potato in <i>Arabidopsis</i> affects leaf development, flowering time and chlorophyll catabolism. <i>BMC Plant Biology</i> , 2019, 19, 184.	3.6	10
43	A systematic comparison of eight new plastome sequences from <i>Ipomoea</i> L. <i>PeerJ</i> , 2019, 7, e6563.	2.0	10
44	Comparative Chromosomal Localization of 45S and 5S rDNA Sites in 76 Purple-Fleshed Sweet Potato Cultivars. <i>Plants</i> , 2020, 9, 865.	3.5	9
45	Identification, expression analysis, and functional characterization of salt stressâ€œresponsive genes of AP2/ERF transcription factors in sweetpotato. <i>Crop Science</i> , 2020, 60, 3247-3260.	1.8	9
46	Selection of stable reference genes for gene expression analysis in sweet potato (<i>Ipomoea batatas</i> L.). <i>Molecular and Cellular Probes</i> , 2020, 53, 101610.	2.1	9
47	Karyotypic stability of <i>Fragaria</i> (strawberry) species revealed by cross-species chromosome painting. <i>Chromosome Research</i> , 2021, , 1.	2.2	8
48	Differential response of physiology and metabolic response to drought stress in different sweetpotato cultivars. <i>PLoS ONE</i> , 2022, 17, e0264847.	2.5	8
49	Heat shock responses in <i>Populus euphratica</i> cell cultures: important role of crosstalk among hydrogen peroxide, calcium and potassium. <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 125, 215-230.	2.3	6
50	Comparative karyotype analysis among six species of <i>Ipomoea</i> based on two newly identified repetitive sequences. <i>Genome</i> , 2019, 62, 243-252.	2.0	6
51	Comparative Analysis of the Complete Mitochondrial Genomes for Development Application. <i>Frontiers in Genetics</i> , 2019, 9, 651.	2.3	4
52	High-Density Single Nucleotide Polymorphisms Genetic Map Construction and Quantitative Trait Locus Mapping of Color-Related Traits of Purple Sweet Potato [<i>Ipomoea batatas</i> (L.) Lam.]. <i>Frontiers in Plant Science</i> , 2021, 12, 797041.	3.6	4
53	Blocking IbmiR319a Impacts Plant Architecture and Reduces Drought Tolerance in Sweet Potato. <i>Genes</i> , 2022, 13, 404.	2.4	4
54	Comparative Analysis of Anthocyanin Compositions and Starch Physiochemical Properties of Purple-Fleshed Sweetpotato â€œXuzhishu8â€œ in Desert Regions of China. <i>Frontiers in Plant Science</i> , 2022, 13, 841969.	3.6	3

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55	The sweetpotato GIGANTEA gene promoter is co-regulated by phytohormones and abiotic stresses in <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 168, 143-154.	5.8	2
56	1-Butanol triggers programmed cell death in <i>Populus euphratica</i> cell cultures. <i>Plant Growth Regulation</i> , 2014, 74, 33-45.	3.4	1
57	The complete mitochondrial genome of the <i>Placidochromis longimanus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 340-341.	0.7	0