

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	Targeting of SPCS3 via CRISPR-Cas13 confers resistance against sweet potato virus disease. <i>Molecular Plant Pathology</i> , 2022, 23, 104-117.	4.2	32
2	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
3	Blocking lamiR319a Impacts Plant Architecture and Reduces Drought Tolerance in Sweet Potato. <i>Genes</i> , 2022, 13, 404.	2.4	4
4	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
5	Differential response of physiology and metabolic response to drought stress in different sweetpotato cultivars. <i>PLoS ONE</i> , 2022, 17, e0264847.	2.5	8
6	Comparative Analysis of Anthocyanin Compositions and Starch Physiochemical Properties of Purple-Fleshed Sweetpotato 'Xuzishu' in Desert Regions of China. <i>Frontiers in Plant Science</i> , 2022, 13, 841969.	3.6	3
7	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
8	Functional characteristic analysis of three odorant-binding proteins from the sweet potato weevil (<i>Colletotrichum gloeosporioides</i>) Tj ETQq000rgBT /Overlock 10 T. <i>Science</i> , 2021, 77, 300-312.	3.4	14
9	Comparative Transcriptome Analysis Reveals Key Genes and Pathways Involved in Prickle Development in Eggplant. <i>Genes</i> , 2021, 12, 341.	2.4	14
10	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
11	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
12	Karyotypic stability of <i>Fragaria</i> (strawberry) species revealed by cross-species chromosome painting. <i>Chromosome Research</i> , 2021, , 1.	2.2	8
13	Three chemosensory proteins from the sweet potato weevil, <i>Cylas formicarius</i> , are involved in the perception of host plant volatiles. <i>Pest Management Science</i> , 2021, 77, 4497-4509.	3.4	11
14	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
15	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
16	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
17	Drought-Induced Responses of Nitrogen Metabolism in <i>Ipomoea batatas</i> . <i>Plants</i> , 2020, 9, 1341.	3.5	24
18	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

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19	The Interaction Network and Signaling Specificity of Two-Component System in Arabidopsis. International Journal of Molecular Sciences, 2020, 21, 4898.	4.1	25
20	Identification, expression analysis, and functional characterization of salt stress-responsive genes of AP2/ERF transcription factors in sweetpotato. Crop Science, 2020, 60, 3247-3260.	1.8	9
21	Overexpression of phosphatidylserine synthase IbPSS1 affords cellular Na ⁺ homeostasis and salt tolerance by activating plasma membrane Na ⁺ /H ⁺ antiport activity in sweet potato roots. Horticulture Research, 2020, 7, 131.	6.3	21
22	A bacterial Fâ€xbox effector suppresses SAR immunity through mediating the proteasomal degradation of OsTrxh2 in rice. Plant Journal, 2020, 104, 1054-1072.	5.7	12
23	Comparative Transcriptome and Proteome Analysis of Salt-Tolerant and Salt-Sensitive Sweet Potato and Overexpression of IbNAC7 Confers Salt Tolerance in Arabidopsis. Frontiers in Plant Science, 2020, 11, 572540.	3.6	42
24	Genome-wide analysis of expression quantitative trait loci (eQTLs) reveals the regulatory architecture of gene expression variation in the storage roots of sweet potato. Horticulture Research, 2020, 7, 90.	6.3	38
25	Selection of stable reference genes for gene expression analysis in sweet potato (<i>Ipomoea batatas</i> L.). Molecular and Cellular Probes, 2020, 53, 101610.	2.1	9
26	Chilling and Heat Stress-Induced Physiological Changes and MicroRNA-Related Mechanism in Sweetpotato (<i>Ipomoea batatas</i> L.). Frontiers in Plant Science, 2020, 11, 687.	3.6	30
27	<i>SISTE1</i> promotes abscisic acid-dependent salt stress-responsive pathways via improving ion homeostasis and reactive oxygen species scavenging in tomato. Journal of Integrative Plant Biology, 2020, 62, 1942-1966.	8.5	19
28	Identification of candidate miRNAs related in storage root development of sweet potato by high throughput sequencing. Journal of Plant Physiology, 2020, 251, 153224.	3.5	17
29	Characterization of a Novel Chitinase from Sweet Potato and Its Fungicidal Effect against <i>Ceratocystis fimbriata</i> . Journal of Agricultural and Food Chemistry, 2020, 68, 7591-7600.	5.2	23
30	Improving CRISPR-Cas-mediated RNA targeting and gene editing using SPLCV replicon-based expression vectors in <i>Nicotiana benthamiana</i> . Plant Biotechnology Journal, 2020, 18, 1993-1995.	8.3	15
31	High-throughput deep sequencing reveals the important role that microRNAs play in the salt response in sweet potato (<i>Ipomoea batatas</i> L.). BMC Genomics, 2020, 21, 164.	2.8	46
32	High throughput sequencing identifies chilling responsive genes in sweetpotato (<i>Ipomoea batatas</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.9	24
33	Involvement of Phosphatidylserine and Triacylglycerol in the Response of Sweet Potato Leaves to Salt Stress. Frontiers in Plant Science, 2019, 10, 1086.	3.6	28
34	Research Progress of Betalain in Response to Adverse Stresses and Evolutionary Relationship Compared with Anthocyanin. Molecules, 2019, 24, 3078.	3.8	43
35	Expression of IbVPE1 from sweet potato in Arabidopsis affects leaf development, flowering time and chlorophyll catabolism. BMC Plant Biology, 2019, 19, 184.	3.6	10
36	Genome-wide identification, structural and gene expression analysis of the bZIP transcription factor family in sweet potato wild relative <i>Ipomoea trifida</i> . BMC Genetics, 2019, 20, 41.	2.7	63

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37	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
38	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
39	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
40	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
41	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
42	Comparative Analysis of the Complete Mitochondrial Genomes for Development Application. <i>Frontiers in Genetics</i> , 2019, 9, 651.	2.3	4
43	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
44	A systematic comparison of eight new plastome sequences from <i>Ipomoea</i> L. PeerJ, 2019, 7, e6563.	2.0	10
45	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
46	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
47	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
48	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
49	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
50	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
51	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
52	NaCl-induced changes of ion homeostasis and nitrogen metabolism in two sweet potato (<i>Ipomoea</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 <i>Experimental Botany</i> , 2016, 129, 23-36.	4.2	70
53	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
54	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

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55	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
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	A high-resolution cucumber cytogenetic map integrated with the genome assembly. <i>BMC Genomics</i> , 2013, 14, 461.	2.8	33