

Jie Luo

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

7,174
citations

147801

31
h-index

206112

48
g-index

50
all docs

50
docs citations

50
times ranked

7279
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of a widely targeted volatilomics method for profiling volatilomes in plants. <i>Molecular Plant</i> , 2022, 15, 189-202.	8.3	49
2	OsRLCK160 contributes to flavonoid accumulation and UV-B tolerance by regulating OsbZIP48 in rice. <i>Science China Life Sciences</i> , 2022, 65, 1380-1394.	4.9	11
3	Novel Transcriptome Study and Detection of Metabolic Variations in UV-B-Treated Date Palm (Phoenix) Tj ETQq1 1 0.784314 rgBT /Ov	4.1	13
4	Domestication of Crop Metabolomes: Desired and Unintended Consequences. <i>Trends in Plant Science</i> , 2021, 26, 650-661.	8.8	60
5	Integrated de novo Analysis of Transcriptional and Metabolic Variations in Salt-Treated <i>Solenostemma argel</i> Desert Plants. <i>Frontiers in Plant Science</i> , 2021, 12, 744699.	3.6	3
6	Comparative Metabolomics Reveals Two Metabolic Modules Affecting Seed Germination in Rice (<i>Oryza</i>) Tj ETQq0 0.0 rgBT /Oyerlock 10	2.9	7
7	Trichome regulator SIMIXTA-like directly manipulates primary metabolism in tomato fruit. <i>Plant Biotechnology Journal</i> , 2020, 18, 354-363.	8.3	50
8	Genome-wide Dissection of Co-selected UV-B Responsive Pathways in the UV-B Adaptation of Qingke. <i>Molecular Plant</i> , 2020, 13, 112-127.	8.3	106
9	Natural variation in the <i>Os</i> bZIP18 promoter contributes to branched-chain amino acid levels in rice. <i>New Phytologist</i> , 2020, 228, 1548-1558.	7.3	30
10	Integrative Metabolomic and Transcriptomic Analyses Reveal Metabolic Changes and Its Molecular Basis in Rice Mutants of the Strigolactone Pathway. <i>Metabolites</i> , 2020, 10, 425.	2.9	8
11	A UV-B-responsive glycosyltransferase, <i>Os</i> UGT706C2, modulates flavonoid metabolism in rice. <i>Science China Life Sciences</i> , 2020, 63, 1037-1052.	4.9	30
12	Metabolite-based genome-wide association study enables dissection of the flavonoid decoration pathway of wheat kernels. <i>Plant Biotechnology Journal</i> , 2020, 18, 1722-1735.	8.3	94
13	Exploiting Natural Variation in Tomato to Define Pathway Structure and Metabolic Regulation of Fruit Polyphenolics in the <i>Lycopersicon</i> Complex. <i>Molecular Plant</i> , 2020, 13, 1027-1046.	8.3	56
14	A simple and efficient cloning system for CRISPR/Cas9-mediated genome editing in rice. <i>PeerJ</i> , 2020, 8, e8491.	2.0	12
15	Comparative analysis of metabolome of rice seeds at three developmental stages using a recombinant inbred line population. <i>Plant Journal</i> , 2019, 100, 908-922.	5.7	24
16	The Structure and Function of Major Plant Metabolite Modifications. <i>Molecular Plant</i> , 2019, 12, 899-919.	8.3	250
17	Branched-chain amino acids regulate plant growth by affecting the homeostasis of mineral elements in rice. <i>Science China Life Sciences</i> , 2019, 62, 1107-1110.	4.9	17
18	<i>Os</i> TSD2-mediated cell wall modification affects ion homeostasis and salt tolerance. <i>Plant, Cell and Environment</i> , 2019, 42, 1503-1512.	5.7	22

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19	Exploring the Diversity of Plant Metabolism. <i>Trends in Plant Science</i> , 2019, 24, 83-98.	8.8	203
20	Measurement of metabolite variations and analysis of related gene expression in Chinese liquorice (<i>Glycyrrhiza uralensis</i>) plants under UV-B irradiation. <i>Scientific Reports</i> , 2018, 8, 6144.	3.3	39
21	Comparative transcriptomics provides novel insights into the mechanisms of selenium tolerance in the hyperaccumulator plant <i>Cardamine hupingshanensis</i> . <i>Scientific Reports</i> , 2018, 8, 2789.	3.3	41
22	Rewiring of the Fruit Metabolome in Tomato Breeding. <i>Cell</i> , 2018, 172, 249-261.e12.	28.9	606
23	OsATX1 Interacts with Heavy Metal P1B-Type ATPases and Affects Copper Transport and Distribution. <i>Plant Physiology</i> , 2018, 178, 329-344.	4.8	96
24	Metabolome Analysis of Multi-Connected Biparental Chromosome Segment Substitution Line Populations. <i>Plant Physiology</i> , 2018, 178, 612-625.	4.8	25
25	Aromatic Decoration Determines the Formation of Anthocyanic Vacuolar Inclusions. <i>Current Biology</i> , 2017, 27, 945-957.	3.9	49
26	The Tomato DOF Daily Fluctuations 1, TDDF1 acts as flowering accelerator and protector against various stresses. <i>Scientific Reports</i> , 2017, 7, 10299.	3.3	30
27	Characterization and Metabolic Diversity of Flavonoids in Citrus Species. <i>Scientific Reports</i> , 2017, 7, 10549.	3.3	103
28	Differentially evolved glucosyltransferases determine natural variation of rice flavone accumulation and UV-tolerance. <i>Nature Communications</i> , 2017, 8, 1975.	12.8	233
29	OsPT4 Contributes to Arsenate Uptake and Transport in Rice. <i>Frontiers in Plant Science</i> , 2017, 8, 2197.	3.6	116
30	Imprinted gene <i>OsFIE1</i> modulates rice seed development by influencing nutrient metabolism and modifying genome H3K27me3. <i>Plant Journal</i> , 2016, 87, 305-317.	5.7	37
31	Evolutionarily Distinct BAHD N-acyltransferases are Responsible for Natural Variation of Aromatic Amine Conjugates in Rice. <i>Plant Cell</i> , 2016, 28, tpc.00265.2016.	6.6	42
32	Control of Leaf Senescence by an MeOH-Jasmonates Cascade that Is Epigenetically Regulated by OsSRT1 in Rice. <i>Molecular Plant</i> , 2016, 9, 1366-1378.	8.3	60
33	Rice putative methyltransferase gene <i>OsTSD2</i> is required for root development involving pectin modification. <i>Journal of Experimental Botany</i> , 2016, 67, 5349-5362.	4.8	25
34	Comparative and parallel genome-wide association studies for metabolic and agronomic traits in cereals. <i>Nature Communications</i> , 2016, 7, 12767.	12.8	224
35	Identification of a peroxisomal-targeted aldolase involved in chlorophyll biosynthesis and sugar metabolism in rice. <i>Plant Science</i> , 2016, 250, 205-215.	3.6	10
36	Spatio-temporal distribution and natural variation of metabolites in citrus fruits. <i>Food Chemistry</i> , 2016, 199, 8-17.	8.2	134

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37	Combining Quantitative Genetics Approaches with Regulatory Network Analysis to Dissect the Complex Metabolism of the Maize Kernel. <i>Plant Physiology</i> , 2016, 170, 136-146.	4.8	62
38	Metabolite-based genome-wide association studies in plants. <i>Current Opinion in Plant Biology</i> , 2015, 24, 31-38.	7.1	204
39	Spatiotemporal Distribution of Phenolamides and the Genetics of Natural Variation of Hydroxycinnamoyl Spermidine in Rice. <i>Molecular Plant</i> , 2015, 8, 111-121.	8.3	112
40	Interaction between carbon metabolism and phosphate accumulation is revealed by a mutation of a cellulose synthase-like protein, CSLF6. <i>Journal of Experimental Botany</i> , 2015, 66, 2557-2567.	4.8	16
41	Multi-level engineering facilitates the production of phenylpropanoid compounds in tomato. <i>Nature Communications</i> , 2015, 6, 8635.	12.8	303
42	Breeding signatures of rice improvement revealed by a genomic variation map from a large germplasm collection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5411-9.	7.1	165
43	Spatio-temporal distribution of phenolamides and the genetics of natural variation of hydroxycinnamoyl spermidine in rice. <i>Molecular Plant</i> , 2014, , .	8.3	0
44	Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. <i>Nature Communications</i> , 2014, 5, 3438.	12.8	402
45	Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism. <i>Nature Genetics</i> , 2014, 46, 714-721.	21.4	560
46	Genetic analysis of the metabolome exemplified using a rice population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20320-20325.	7.1	155
47	A Novel Integrated Method for Large-Scale Detection, Identification, and Quantification of Widely Targeted Metabolites: Application in the Study of Rice Metabolomics. <i>Molecular Plant</i> , 2013, 6, 1769-1780.	8.3	1,107
48	A Novel Polyamine Acyltransferase Responsible for the Accumulation of Spermidine Conjugates in <i>Arabidopsis</i> Seed. <i>Plant Cell</i> , 2009, 21, 318-333.	6.6	139
49	Enrichment of tomato fruit with health-promoting anthocyanins by expression of select transcription factors. <i>Nature Biotechnology</i> , 2008, 26, 1301-1308.	17.5	1,030