

Yuling Lin

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

1,149
citations

361413

20
h-index

414414

32
g-index

64
all docs

64
docs citations

64
times ranked

1129
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide sequencing of longan (<i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. <i>GigaScience</i> , 2017, 6, 1-14.	6.4	103
2	Identification of drought-responsive miRNAs and physiological characterization of tea plant (<i>Camellia</i>) Tj ETQq0 0 0,rgBT /Overlock 10 T	3.6	75
3	Genome-wide identification and characterization of the superoxide dismutase gene family in <i>Musa acuminata</i> cv. Tianbaojiao (AAA group). <i>BMC Genomics</i> , 2015, 16, 823.	2.8	74
4	Genome-wide investigation of superoxide dismutase (SOD) gene family and their regulatory miRNAs reveal the involvement in abiotic stress and hormone response in tea plant (<i>Camellia sinensis</i>). <i>PLoS ONE</i> , 2019, 14, e0223609.	2.5	69
5	Genome-wide identification and characterization of mRNAs and lncRNAs involved in cold stress in the wild banana (<i>Musa itinerans</i>). <i>PLoS ONE</i> , 2018, 13, e0200002.	2.5	61
6	Transcriptome and Phytochemical Analyses Provide New Insights Into Long Non-Coding RNAs Modulating Characteristic Secondary Metabolites of Oolong Tea (<i>Camellia sinensis</i>) in Solar-Withering. <i>Frontiers in Plant Science</i> , 2019, 10, 1638.	3.6	51
7	Growth Promotion-Related miRNAs in <i>Oncidium</i> Orchid Roots Colonized by the Endophytic Fungus <i>Piriformospora indica</i> . <i>PLoS ONE</i> , 2014, 9, e84920.	2.5	48
8	De novo transcriptome and phytochemical analyses reveal differentially expressed genes and characteristic secondary metabolites in the original oolong tea (<i>Camellia sinensis</i>) cultivar "Tieguanyin"™ compared with cultivar "Benshan"™. <i>BMC Genomics</i> , 2019, 20, 265.	2.8	46
9	Genome-wide identification and characterization of long non-coding RNAs involved in the early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>BMC Genomics</i> , 2018, 19, 805.	2.8	45
10	De novo transcriptome combined with spectrophotometry and gas chromatography-mass spectrometer (GC-MS) reveals differentially expressed genes during accumulation of secondary metabolites in purple-leaf tea (<i>Camellia sinensis</i> cv Hongyafoshou). <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 349-367.	1.9	36
11	Integrated Transcriptome, microRNA, and Phytochemical Analyses Reveal Roles of Phytohormone Signal Transduction and ABC Transporters in Flavor Formation of Oolong Tea (<i>Camellia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 12749-12767.	3.2	35
12	Combined small RNA and degradome sequencing reveals complex microRNA regulation of catechin biosynthesis in tea (<i>Camellia sinensis</i>). <i>PLoS ONE</i> , 2017, 12, e0171173.	2.5	33
13	Global scale transcriptome analysis reveals differentially expressed genes involve in early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>BMC Genomics</i> , 2020, 21, 4.	2.8	32
14	Genome-wide investigation and transcriptional analysis of cytosine-5 DNA methyltransferase and DNA demethylase gene families in tea plant (<i>Camellia sinensis</i>) under abiotic stress and withering processing. <i>PeerJ</i> , 2020, 8, e8432.	2.0	28
15	Genome-wide identification, molecular evolution, and expression analysis provide new insights into the APETALA2/ethylene responsive factor (AP2/ERF) superfamily in <i>Dimocarpus longan</i> Lour. <i>BMC Genomics</i> , 2020, 21, 62.	2.8	27
16	Cloning and expression analysis of betalain biosynthesis genes in <i>Amaranthus tricolor</i> . <i>Biotechnology Letters</i> , 2016, 38, 723-729.	2.2	26
17	High-throughput sequencing of small RNAs revealed the diversified cold-responsive pathways during cold stress in the wild banana (<i>Musa itinerans</i>). <i>BMC Plant Biology</i> , 2018, 18, 308.	3.6	26
18	Effects of blue light on flavonoid accumulation linked to the expression of miR393, miR394 and miR395 in longan embryogenic calli. <i>PLoS ONE</i> , 2018, 13, e0191444.	2.5	26

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19	Genome-wide identification of miRNAs and their targets during early somatic embryogenesis in <i>Dimocarpus longan</i> Lour.. <i>Scientific Reports</i> , 2020, 10, 4626.	3.3	26
20	Seed-Specific Gene MOTHER of FT and TFL1 ^{1/4} MFT1 ^{1/4} Involved in Embryogenesis, Hormones and Stress Responses in <i>Dimocarpus longan</i> Lour.. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2403.	4.1	23
21	Endogenous target mimics, microRNA167, and its targets ARF6 and ARF8 during somatic embryo development in <i>Dimocarpus longan</i> Lour.. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	21
22	Exploration of the Effect of Blue Light on Functional Metabolite Accumulation in Longan Embryonic Calli via RNA Sequencing. <i>International Journal of Molecular Sciences</i> , 2019, 20, 441.	4.1	20
23	Genome-Wide Investigation of N6-Methyladenosine Regulatory Genes and Their Roles in Tea (<i>Camellia</i>) Tj ETQq1 1 0,784314 18 BT /Over	3.6	18
24	RNA-Seq analysis reveals an essential role of tyrosine metabolism pathway in response to root-rot infection in <i>Gerbera hybrida</i> . <i>PLoS ONE</i> , 2019, 14, e0223519.	2.5	16
25	RNA-sequencing analysis reveals betalains metabolism in the leaf of <i>Amaranthus tricolor</i> L.. <i>PLoS ONE</i> , 2019, 14, e0216001.	2.5	15
26	Comparative transcriptome analysis reveals a role for anthocyanin biosynthesis genes in the formation of purple peel in Minhou wild banana (<i>Musa itinerans</i> Cheesman). <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 184-200.	1.9	12
27	Genome-wide investigation of DNA methylation dynamics reveals a critical role of DNA demethylation during the early somatic embryogenesis of <i>Dimocarpus longan</i> Lour. <i>Tree Physiology</i> , 2020, 40, 1807-1826.	3.1	12
28	DIRan3A is involved in hormone, light, and abiotic stress responses in embryogenic callus of <i>Dimocarpus longan</i> Lour.. <i>Gene</i> , 2015, 569, 267-275.	2.2	11
29	Molecular Characterization of MaCCS, a Novel Copper Chaperone Gene Involved in Abiotic and Hormonal Stress Responses in <i>Musa acuminata</i> cv. Tianbaojiao. <i>International Journal of Molecular Sciences</i> , 2016, 17, 441.	4.1	11
30	Colonisation of <i>Oncidium</i> orchid roots by the endophyte <i>Piriformospora indica</i> restricts <i>Erwinia chrysanthemi</i> infection, stimulates accumulation of NBS-LRR resistance gene transcripts and represses their targeting micro-RNAs in leaves. <i>BMC Plant Biology</i> , 2019, 19, 601.	3.6	11
31	Genome-wide identification, evolution analysis of cytochrome P450 monooxygenase multigene family and their expression patterns during the early somatic embryogenesis in <i>Dimocarpus longan</i> Lour.. <i>Gene</i> , 2022, 826, 146453.	2.2	11
32	Exploration of the effect of blue light on microRNAs involved in the accumulation of functional metabolites of longan embryonic calli through RNA sequencing. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 1533-1547.	3.5	10
33	Genome-Wide Identification and Comprehensive Analyses of TCP Gene Family in Banana (<i>Musa</i> L.). <i>Tropical Plant Biology</i> , 2021, 14, 180-202.	1.9	8
34	Genome-wide identification and characterization of DEAD-box helicase family associated with early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>Journal of Plant Physiology</i> , 2021, 258-259, 153364.	3.5	8
35	Genome-Wide Investigation of the MiR166 Family Provides New Insights into Its Involvement in the Drought Stress Responses of Tea Plants (<i>Camellia sinensis</i> (L.) O. Kuntze). <i>Forests</i> , 2022, 13, 628.	2.1	8
36	Molecular cloning and expression analysis of KIN10 and cold-acclimation related genes in wild banana "Huanxi" (Musa itinerans). <i>SpringerPlus</i> , 2015, 4, 829.	1.2	7

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37	Transcriptome analysis of azacitidine (5-AzaC)-treatment affecting the development of early somatic embryogenesis in longan. <i>Journal of Horticultural Science and Biotechnology</i> , 2021, 96, 311-323.	1.9	7
38	Exploring the Effect of Methyl Jasmonate on the Expression of microRNAs Involved in Biosynthesis of Active Compounds of Rosemary Cell Suspension Cultures through RNA-Sequencing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3704.	4.1	6
39	Ras-Related Nuclear Protein Ran3B Gene Is Involved in Hormone Responses in the Embryogenic Callus of <i>Dimocarpus longan</i> Lour.. <i>International Journal of Molecular Sciences</i> , 2016, 17, 873.	4.1	5
40	Genome-wide identification and expression analysis of the SR gene family in longan (<i>Dimocarpus</i>) Tj ETQq0 0 0 rgBTJ /Overlock 10 Tf 50	2.5	5
41	Genome-wide identification and expression analyses of Sm genes reveal their involvement in early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>PLoS ONE</i> , 2020, 15, e0230795.	2.5	5
42	Genome-wide circular RNA profiling and competing endogenous RNA regulatory network analysis provide new insights into the molecular mechanisms underlying early somatic embryogenesis in <i>Dimocarpus longan</i> Lour.. <i>Tree Physiology</i> , 2022, 42, 1876-1898.	3.1	5
43	Transcriptome Analysis Reveals Differentially Expressed Genes That Regulate Biosynthesis of the Active Compounds with Methyl Jasmonate in Rosemary Suspension Cells. <i>Genes</i> , 2022, 13, 67.	2.4	5
44	Isolation and characterisation of a MYB transcription factor associated with epigallocatechin-3-gallate biosynthesis in <i>Camellia sinensis</i> ÅL.. <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 41-48.	1.9	4
45	PAs Regulate Early Somatic Embryo Development by Changing the Gene Expression Level and the Hormonal Balance in <i>Dimocarpus longan</i> Lour.. <i>Genes</i> , 2022, 13, 317.	2.4	4
46	Genome-wide identification, expression and functional analysis of the core cell cycle gene family during the early somatic embryogenesis of <i>Dimocarpus longan</i> Lour.. <i>Gene</i> , 2022, 821, 146286.	2.2	4
47	Molecular characterization of miRNA genes and their expression in <i>Dimocarpus longan</i> Lour. <i>Planta</i> , 2021, 253, 41.	3.2	3
48	Genome-wide identification and characterization of the CKII gene family in the cultivated banana cultivar (<i>Musa</i> spp. cv Tianbaojiao) and the wild banana (<i>Musa itinerans</i>). <i>PLoS ONE</i> , 2018, 13, e0200149.	2.5	2
49	Molecular evolution and expression analysis of ADP-ribosylation factors (ARFs) from longan embryogenic callus. <i>Gene</i> , 2021, 777, 145461.	2.2	2
50	Identification of microRNAs involved in betalain metabolism in the green and red sectors of amaranth leaves based on Illumina sequencing data. <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 454-469.	1.9	1
51	Genome-wide identification and expression of <i>CYP71</i> gene family in response to low-temperature stress in banana. <i>Journal of Horticultural Science and Biotechnology</i> , 2023, 98, 159-177.	1.9	0