

Yuling Lin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3789950/publications.pdf>

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 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | Molecular characterization of miRNA genes and their expression in <i>Dimocarpus longan</i> Lour. <i>Planta</i> , 2021, 253, 41. | 3.2 | 3 |
| 11 | 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 |
| 12 | 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 |
| 13 | Molecular evolution and expression analysis of ADP-ribosylation factors (ARFs) from longan embryogenic callus. <i>Gene</i> , 2021, 777, 145461. | 2.2 | 2 |
| 14 | Genome-Wide Investigation of N6-Methyladenosine Regulatory Genes and Their Roles in Tea (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 | 3.6 | 18 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 ETQq0 0 0 rgBT /Overlock 10 Tj 50 62 Td 12749-12767. | 5.2 | 35 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Genome-wide identification and expression analysis of the SR gene family in longan (<i>Dimocarpus</i>) Tj ETQq1 1 0.784314 rgBT 5/Overloc | 2.5 | 5 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Exploration of the effect of blue light on microRNAs involved in the accumulation of functional metabolites of longan embryonic calli through RNA-seq. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 1533-1547. | 3.5 | 10 |
| 26 | 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 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | Isolation and characterisation of a MYB transcription factor associated with epigallocatechin-3-gallate biosynthesis in <i>Camellia sinensis</i> L.. <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 94, 41-48. | 1.9 | 4 |
| 35 | 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 |
| 36 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Genome-wide identification and characterization of the CKII gene family in the cultivated banana cultivar (<i>Musa spp. cv. Tianbaojiao</i>) and the wild banana (<i>Musa itinerans</i>). PLoS ONE, 2018, 13, e0200149. | 2.5 | 2 |
| 38 | Genome-wide identification and characterization of mRNAs and lncRNAs involved in cold stress in the wild banana (<i>Musa itinerans</i>). PLoS ONE, 2018, 13, e0200002. | 2.5 | 61 |
| 39 | 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.. International Journal of Molecular Sciences, 2018, 19, 2403. | 4.1 | 23 |
| 40 | Effects of blue light on flavonoid accumulation linked to the expression of miR393, miR394 and miR395 in longan embryogenic calli. PLoS ONE, 2018, 13, e0191444. | 2.5 | 26 |
| 41 | Genome-wide sequencing of longan (<i>Dimocarpus longan</i> Lour.) provides insights into molecular basis of its polyphenol-rich characteristics. GigaScience, 2017, 6, 1-14. | 6.4 | 103 |
| 42 | Combined small RNA and degradome sequencing reveals complex microRNA regulation of catechin biosynthesis in tea (<i>Camellia sinensis</i>). PLoS ONE, 2017, 12, e0171173. | 2.5 | 33 |
| 43 | Identification of drought-responsive miRNAs and physiological characterization of tea plant (<i>Camellia</i>) Tj ETQq1 1 0,784314 rBT /Overl | 3.6 | 75 |
| 44 | Molecular Characterization of MaCCS, a Novel Copper Chaperone Gene Involved in Abiotic and Hormonal Stress Responses in <i>Musa acuminata</i> cv. Tianbaojiao. International Journal of Molecular Sciences, 2016, 17, 441. | 4.1 | 11 |
| 45 | Ras-Related Nuclear Protein Ran3B Gene Is Involved in Hormone Responses in the Embryogenic Callus of <i>Dimocarpus longan</i> Lour.. International Journal of Molecular Sciences, 2016, 17, 873. | 4.1 | 5 |
| 46 | Cloning and expression analysis of betalain biosynthesis genes in <i>Amaranthus tricolor</i> . Biotechnology Letters, 2016, 38, 723-729. | 2.2 | 26 |
| 47 | Genome-wide identification and characterization of the superoxide dismutase gene family in <i>Musa acuminata</i> cv. Tianbaojiao (AAA group). BMC Genomics, 2015, 16, 823. | 2.8 | 74 |
| 48 | Molecular cloning and expression analysis of KIN10 and cold-acclimation related genes in wild banana "Huanxi"™ (<i>Musa itinerans</i>). SpringerPlus, 2015, 4, 829. | 1.2 | 7 |
| 49 | Endogenous target mimics, microRNA167, and its targets ARF6 and ARF8 during somatic embryo development in <i>Dimocarpus longan</i> Lour.. Molecular Breeding, 2015, 35, 1. | 2.1 | 21 |
| 50 | DIRan3A is involved in hormone, light, and abiotic stress responses in embryogenic callus of <i>Dimocarpus longan</i> Lour.. Gene, 2015, 569, 267-275. | 2.2 | 11 |
| 51 | Growth Promotion-Related miRNAs in <i>Oncidium</i> Orchid Roots Colonized by the Endophytic Fungus <i>Piriformospora indica</i> . PLoS ONE, 2014, 9, e84920. | 2.5 | 48 |