

Weiwei Wen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4030123/publications.pdf>

Version: 2024-02-01

28
papers

1,808
citations

430874

18
h-index

552781

26
g-index

28
all docs

28
docs citations

28
times ranked

2050
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Genome-wide association of the metabolic shifts underpinning dark-induced senescence in Arabidopsis. <i>Plant Cell</i> , 2022, 34, 557-578. | 6.6 | 29 |
| 2 | Combining novel technologies with interdisciplinary basic research to enhance horticultural crops. <i>Plant Journal</i> , 2022, 109, 35-46. | 5.7 | 17 |
| 3 | Genome-wide association studies of Arabidopsis dark-induced senescence reveals signatures of autophagy in metabolic reprogramming. <i>Autophagy</i> , 2022, 18, 457-458. | 9.1 | 2 |
| 4 | Understanding carotenoid biosynthetic pathway control points using metabolomic analysis and natural genetic variation. <i>Methods in Enzymology</i> , 2022, , . | 1.0 | 0 |
| 5 | Population genomics of Zea species identifies selection signatures during maize domestication and adaptation. <i>BMC Plant Biology</i> , 2022, 22, 72. | 3.6 | 9 |
| 6 | Integrated multi-omics analysis of developing "Newhall" orange and its glossy mutant provide insights into citrus fragrance formation. <i>Horticultural Plant Journal</i> , 2022, 8, 435-449. | 5.0 | 7 |
| 7 | Camellia sinensis (Tea). <i>Trends in Genetics</i> , 2021, 37, 201-202. | 6.7 | 10 |
| 8 | A phased genome based on single sperm sequencing reveals crossover pattern and complex relatedness in tea plants. <i>Plant Journal</i> , 2021, 105, 197-208. | 5.7 | 15 |
| 9 | Multimiomics-based dissection of citrus flavonoid metabolism using a Citrus reticulata "Poncirus trifoliata" population. <i>Horticulture Research</i> , 2021, 8, 56. | 6.3 | 24 |
| 10 | Domestication of Crop Metabolomes: Desired and Unintended Consequences. <i>Trends in Plant Science</i> , 2021, 26, 650-661. | 8.8 | 60 |
| 11 | Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756. | 19.0 | 403 |
| 12 | Dissection of the domestication-shaped genetic architecture of lettuce primary metabolism. <i>Plant Journal</i> , 2020, 104, 613-630. | 5.7 | 24 |
| 13 | Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. <i>Nature Communications</i> , 2020, 11, 3719. | 12.8 | 108 |
| 14 | A NAC transcription factor and its interaction protein hinder abscisic acid biosynthesis by synergistically repressing NCED5 in Citrus reticulata. <i>Journal of Experimental Botany</i> , 2020, 71, 3613-3625. | 4.8 | 39 |
| 15 | Editorial overview: Evolution of metabolic diversity. <i>Current Opinion in Plant Biology</i> , 2020, 55, A1-A4. | 7.1 | 0 |
| 16 | Lipidomic and transcriptomic analysis reveals reallocation of carbon flux from cuticular wax into plastid membrane lipids in a glossy "Newhall" navel orange mutant. <i>Horticulture Research</i> , 2020, 7, 41. | 6.3 | 23 |
| 17 | Parallel Metabolomic and Transcriptomic Analysis Reveals Key Factors for Quality Improvement of Tea Plants. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 5483-5495. | 5.2 | 9 |
| 18 | Conservation and diversification of flavonoid metabolism in the plant kingdom. <i>Current Opinion in Plant Biology</i> , 2020, 55, 100-108. | 7.1 | 137 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Metabolomics analysis reveals differences in evolution between maize and rice. <i>Plant Journal</i> , 2020, 103, 1710-1722. | 5.7 | 41 |
| 20 | Large-scale metabolite quantitative trait locus analysis provides new insights for high-quality maize improvement. <i>Plant Journal</i> , 2019, 99, 216-230. | 5.7 | 37 |
| 21 | Finding Noemi: The Transcription Factor Mutations Underlying Trait Differentiation Amongst Citrus. <i>Trends in Plant Science</i> , 2019, 24, 384-386. | 8.8 | 9 |
| 22 | Fatty acid metabolic flux and lipid peroxidation homeostasis maintain the biomembrane stability to improve citrus fruit storage performance. <i>Food Chemistry</i> , 2019, 292, 314-324. | 8.2 | 33 |
| 23 | An integrated multi-layered analysis of the metabolic networks of different tissues uncovers key genetic components of primary metabolism in maize. <i>Plant Journal</i> , 2018, 93, 1116-1128. | 5.7 | 38 |
| 24 | Integrated transcriptomic and metabolomic analyses of a wax deficient citrus mutant exhibiting jasmonic acid-mediated defense against fungal pathogens. <i>Horticulture Research</i> , 2018, 5, 43. | 6.3 | 49 |
| 25 | 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 |
| 26 | Genomic, Transcriptomic, and Phenomic Variation Reveals the Complex Adaptation of Modern Maize Breeding. <i>Molecular Plant</i> , 2015, 8, 871-884. | 8.3 | 72 |
| 27 | Genetic Determinants of the Network of Primary Metabolism and Their Relationships to Plant Performance in a Maize Recombinant Inbred Line Population. <i>Plant Cell</i> , 2015, 27, 1839-1856. | 6.6 | 149 |
| 28 | Metabolome-based genome-wide association study of maize kernel leads to novel biochemical insights. <i>Nature Communications</i> , 2014, 5, 3438. | 12.8 | 402 |