

Nai-Xing Ye

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

1,211
citations

304743

22
h-index

414414

32
g-index

45
all docs

45
docs citations

45
times ranked

781
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolite profiling in albino tea mutant <i>Camellia sinensis</i> ‘Fuyun 6’™ using LC-ESI-MS/MS. <i>Trees - Structure and Function</i> , 2022, 36, 261-272.	1.9	3
2	Macro-composition quantification combined with metabolomics analysis uncovered key dynamic chemical changes of aging white tea. <i>Food Chemistry</i> , 2022, 366, 130593.	8.2	17
3	Aroma analysis of Fuyun 6 and Jinguanyin black tea in the Fu'an area based on E-nose and GC-MS. <i>European Food Research and Technology</i> , 2022, 248, 947-961.	3.3	15
4	Identification of PAL genes related to anthocyanin synthesis in tea plants and its correlation with anthocyanin content. <i>Horticultural Plant Journal</i> , 2022, 8, 381-394.	5.0	31
5	Changes in Non-Volatile and Volatile Metabolites Associated with Heterosis in Tea Plants (<i>Camellia</i>) Tj ETQq1 1 0.784314 rgBT /Over	5.2	38
6	Genomes of single- and double-petal jasmines (<i>Jasminum sambac</i>) provide insights into their divergence time and structural variations. <i>Plant Biotechnology Journal</i> , 2022, 20, 1232-1234.	8.3	11
7	Lipidomics analysis unravels changes from flavor precursors in different processing treatments of purple-leaf tea. <i>Journal of the Science of Food and Agriculture</i> , 2022, 102, 3730-3741.	3.5	17
8	Volatile metabolomics and coexpression network analyses provide insight into the formation of the characteristic cultivar aroma of oolong tea (<i>Camellia sinensis</i>). <i>LWT - Food Science and Technology</i> , 2022, 164, 113666.	5.2	21
9	Integrated transcriptomics and metabolomics provide novel insight into changes in specialized metabolites in an albino tea cultivar (<i>Camellia sinensis</i> (L.) O. Kuntz). <i>Plant Physiology and Biochemistry</i> , 2021, 160, 27-36.	5.8	27
10	Chromatin accessibility and translational landscapes of tea plants under chilling stress. <i>Horticulture Research</i> , 2021, 8, 96.	6.3	28
11	Genetic basis of high aroma and stress tolerance in the oolong tea cultivar genome. <i>Horticulture Research</i> , 2021, 8, 107.	6.3	80
12	R2R3-MYB transcription factor family in tea plant (<i>Camellia sinensis</i>): Genome-wide characterization, phylogeny, chromosome location, structure and expression patterns. <i>Genomics</i> , 2021, 113, 1565-1578.	2.9	45
13	Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant <i>Camellia sinensis</i> . <i>Nature Genetics</i> , 2021, 53, 1250-1259.	21.4	157
14	Architecture and Dynamics of the Wounding-Induced Gene Regulatory Network During the Oolong Tea Manufacturing Process (<i>Camellia sinensis</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 788469.	3.6	11
15	Identification of Co-Expressed Genes Related to Theacrine Synthesis in Tea Flowers at Different Developmental Stages. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13394.	4.1	6
16	Genetic diversity of oolong tea (<i>Camellia sinensis</i>) germplasms based on the nanofluidic array of single-nucleotide polymorphism (SNP) markers. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	24
17	Rapid and direct identification of the origin of white tea with proton transfer reaction time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8830.	1.5	10
18	Comparison of Metabolome and Transcriptome of Flavonoid Biosynthesis Pathway in a Purple-Leaf Tea Germplasm Jinmingzao and a Green-Leaf Tea Germplasm Huangdan reveals Their Relationship with Genetic Mechanisms of Color Formation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4167.	4.1	40

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19	Transcriptome and metabolite analyses provide insights into zigzag-shaped stem formation in tea plants (<i>Camellia sinensis</i>). <i>BMC Plant Biology</i> , 2020, 20, 98.	3.6	9
20	Comparative transcriptomic analysis of resistant and susceptible tea cultivars in response to <i>Empoasca onukii</i> (Matsuda) damage. <i>Planta</i> , 2020, 252, 10.	3.2	7
21	Exploration of the Effects of Different Blue LED Light Intensities on Flavonoid and Lipid Metabolism in Tea Plants via Transcriptomics and Metabolomics. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4606.	4.1	52
22	Widely Targeted Metabolomic and Transcriptomic Analyses of a Novel Albino Tea Mutant of ‘Rougui’ Forests, 2020, 11, 229.	2.1	25
23	Integrative Transcriptomic and Metabolic Analyses Provide Insights into the Role of Trichomes in Tea Plant (<i>Camellia Sinensis</i>). <i>Biomolecules</i> , 2020, 10, 311.	4.0	16
24	Comparison of Volatiles in Different Jasmine Tea Grade Samples Using Electronic Nose and Automatic Thermal Desorption-Gas Chromatography-Mass Spectrometry Followed by Multivariate Statistical Analysis. <i>Molecules</i> , 2020, 25, 380.	3.8	28
25	Genome-wide and expression pattern analysis of JAZ family involved in stress responses and postharvest processing treatments in <i>Camellia sinensis</i> . <i>Scientific Reports</i> , 2020, 10, 2792.	3.3	23
26	Identification, expression, and putative target gene analysis of nuclear factor-Y (NF-Y) transcription factors in tea plant (<i>Camellia sinensis</i>). <i>Planta</i> , 2019, 250, 1671-1686.	3.2	26
27	Identification of CBF Transcription Factors in Tea Plants and a Survey of Potential CBF Target Genes under Low Temperature. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5137.	4.1	34
28	Transcriptome and Metabolite Profiling Reveal Novel Insights into Volatile Heterosis in the Tea Plant (<i>Camellia Sinensis</i>). <i>Molecules</i> , 2019, 24, 3380.	3.8	27
29	Determination of 21 free amino acids in 5 types of tea by ultra-high performance liquid chromatography coupled with tandem mass spectrometry (UHPLC-MS/MS) using a modified 6-aminoquinolyl-N-hydroxysuccinimidyl carbamate (AQC) method. <i>Journal of Food Composition and Analysis</i> . 2019, 81, 46-54.	3.9	30
30	Genome-wide identification of WOX genes and their expression patterns under different hormone and abiotic stress treatments in tea plant (<i>Camellia sinensis</i>). <i>Trees - Structure and Function</i> , 2019, 33, 1129-1142.	1.9	22
31	Identification and comparison of oligopeptides during withering process of White tea by ultra-high pressure liquid chromatography coupled with quadrupole-orbitrap ultra-high resolution mass spectrometry. <i>Food Research International</i> , 2019, 121, 825-834.	6.2	18
32	Non-targeted metabolomics reveals distinct chemical compositions among different grades of Bai Mudan white tea. <i>Food Chemistry</i> , 2019, 277, 289-297.	8.2	67
33	Genome-wide identification of WRKY family genes and their response to abiotic stresses in tea plant (<i>Camellia sinensis</i>). <i>Genes and Genomics</i> , 2019, 41, 17-33.	1.4	59
34	Differential expression of gibberellin- and abscisic acid-related genes implies their roles in the bud activity-dormancy transition of tea plants. <i>Plant Cell Reports</i> , 2018, 37, 425-441.	5.6	34
35	Identification and Expression Analyses of SBP-Box Genes Reveal Their Involvement in Abiotic Stress and Hormone Response in Tea Plant (<i>Camellia sinensis</i>). <i>International Journal of Molecular Sciences</i> , 2018, 19, 3404.	4.1	25
36	Comparative transcriptome study of hairy and hairless tea plant (<i>Camellia sinensis</i>) shoots. <i>Journal of Plant Physiology</i> , 2018, 229, 41-52.	3.5	16

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37	Hydrophilic interaction liquid chromatography coupled with quadrupole-orbitrap ultra high resolution mass spectrometry to quantitate nucleobases, nucleosides, and nucleotides during white tea withering process. <i>Food Chemistry</i> , 2018, 266, 343-349.	8.2	29
38	Identification of the Origin of White Tea Based on Mineral Element Content. <i>Food Analytical Methods</i> , 2017, 10, 191-199.	2.6	36
39	Volatiles Emitted at Different Flowering Stages of <i>Jasminum sambac</i> and Expression of Genes Related to Δ^1 -Farnesene Biosynthesis. <i>Molecules</i> , 2017, 22, 546.	3.8	53