

The Tea Tree Genome Provides Insights into Tea Flavor Caffeine Biosynthesis

Molecular Plant

10, 866-877

DOI: [10.1016/j.molp.2017.04.002](https://doi.org/10.1016/j.molp.2017.04.002)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Harnessing the Potential of the Tea Tree Genome. <i>Molecular Plant</i> , 2017, 10, 788-790.	3.9	2
2	Phosphate stresses affect ionome and metabolome in tea plants. <i>Plant Physiology and Biochemistry</i> , 2017, 120, 30-39.	2.8	51
3	Molecular dissection of transcriptional reprogramming of steviol glycosides synthesis in leaf tissue during developmental phase transitions in <i>Stevia rebaudiana</i> Bert. <i>Scientific Reports</i> , 2017, 7, 11835.	1.6	51
4	Construction and characterization of a bacterial artificial chromosome library for <i>Camellia sinensis</i> . <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	6
6	Proteome and Acetyl-Proteome Profiling of <i>Camellia sinensis</i> cv. 'Anji Baicha'™ during Periodic Albinism Reveals Alterations in Photosynthetic and Secondary Metabolite Biosynthetic Pathways. <i>Frontiers in Plant Science</i> , 2017, 8, 2104.	1.7	33
7	Metabolic Characterization of the Anthocyanidin Reductase Pathway Involved in the Biosynthesis of Flavan-3-ols in Elite Shuchazao Tea (<i>Camellia sinensis</i>) Cultivar in the Field. <i>Molecules</i> , 2017, 22, 2241.	1.7	47
8	Living Organisms Author Their Read-Write Genomes in Evolution. <i>Biology</i> , 2017, 6, 42.	1.3	44
9	Genome-Wide Analysis of the Biosynthesis and Deactivation of Gibberellin-Dioxygenases Gene Family in <i>Camellia sinensis</i> (L.) O. Kuntze. <i>Genes</i> , 2017, 8, 235.	1.0	34
10	Genome-wide identification and expression analysis of GRAS family transcription factors in tea plant (<i>Camellia sinensis</i>). <i>Scientific Reports</i> , 2018, 8, 3949.	1.6	62
11	Next generation crop improvement program: Progress and prospect in tea (<i>Camellia sinensis</i> (L.) O.) Tj ETQq1 1 0.784314 rgBT /Overlo 1.2 18		
12	Draft genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> provides insights into the evolution of the tea genome and tea quality. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4151-E4158.	3.3	730
13	Integrative transcriptional and metabolic analyses provide insights into cold spell response mechanisms in young shoots of the tea plant. <i>Tree Physiology</i> , 2018, 38, 1655-1671.	1.4	31
14	Transcriptome changes and its effect on physiological and metabolic processes in tea plant during mechanical damage. <i>Forest Pathology</i> , 2018, 48, e12432.	0.5	9
15	Tea plant SWEET transporters: expression profiling, sugar transport, and the involvement of CsSWEET16 in modifying cold tolerance in <i>Arabidopsis</i> . <i>Plant Molecular Biology</i> , 2018, 96, 577-592.	2.0	71
16	The validation of two major QTLs related to the timing of spring bud flush in <i>Camellia sinensis</i> . <i>Euphytica</i> , 2018, 214, 1.	0.6	6
17	Characterization and Alternative Splicing Profiles of the Lipxygenase Gene Family in Tea Plant (<i>Camellia sinensis</i>). <i>Plant and Cell Physiology</i> , 2018, 59, 1765-1781.	1.5	110
18	Comparative transcriptomic analysis identifies genes responsible for fruit count and oil yield in the oil tea plant <i>Camellia chekiangoleosa</i> . <i>Scientific Reports</i> , 2018, 8, 6637.	1.6	16
19	Genome-wide identification of simple sequence repeats and development of polymorphic SSR markers for genetic studies in tea plant (<i>Camellia sinensis</i>). <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	44

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20	De novo transcriptome analysis of <i>Rhododendron molle</i> G. Don flowers by Illumina sequencing. <i>Genes and Genomics</i> , 2018, 40, 591-601.	0.5	17
21	Biosynthesis of Jasmine Lactone in Tea (<i>Camellia sinensis</i>) Leaves and Its Formation in Response to Multiple Stresses. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 3899-3909.	2.4	64
22	Insight into Catechins Metabolic Pathways of <i>Camellia sinensis</i> Based on Genome and Transcriptome Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 4281-4293.	2.4	62
23	Implementation of <i>CsLIS/NES</i> in linalool biosynthesis involves transcript splicing regulation in <i>Camellia sinensis</i> . <i>Plant, Cell and Environment</i> , 2018, 41, 176-186.	2.8	106
24	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.	2.8	34
25	The <i>Chrysanthemum nankingense</i> Genome Provides Insights into the Evolution and Diversification of <i>Chrysanthemum</i> Flowers and Medicinal Traits. <i>Molecular Plant</i> , 2018, 11, 1482-1491.	3.9	148
26	Understanding Response of Tea Plants to Heat Stress and the Mechanisms of Adaptation. , 2018, , 25-37.		2
27	Complementary iTRAQ Proteomic and Transcriptomic Analyses of Leaves in Tea Plant (<i>Camellia</i>) Tj ETQq1 1 0.784314 rgBT /Overlock Proteome Research, 2019, 18, 252-264.	1.8	27
28	Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle. <i>Frontiers in Microbiology</i> , 2018, 9, 3160.	1.5	45
29	Genome survey sequencing for the characterization of genetic background of <i>Dracaena cambodiana</i> and its defense response during dragon's blood formation. <i>PLoS ONE</i> , 2018, 13, e0209258.	1.1	16
30	High-density SNP linkage map construction and QTL mapping for flavonoid-related traits in a tea plant (<i>Camellia sinensis</i>) using 2b-RAD sequencing. <i>BMC Genomics</i> , 2018, 19, 955.	1.2	36
31	Genomics Approaches for Biotic and Abiotic Stress Improvement in Tea. , 2018, , 289-312.		1
32	Quantitative Trait Loci Mapping for Theobromine and Caffeine Contents in Tea Plant (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2.4	2.4	26
33	Response and Adaptation Mechanisms of Tea Plant to Low-Temperature Stress. , 2018, , 39-61.		8
34	Toward the Implementation of Climate-Resilient Tea Systems: Agroecological, Physiological, and Molecular Innovations. , 2018, , 333-355.		2
35	Genome-wide identification, classification and expression pattern of LBD gene family in <i>Camellia sinensis</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2018, 32, 1387-1397.	0.5	9
36	Identification, characterization and expression analysis of the VQ motif-containing gene family in tea plant (<i>Camellia sinensis</i>). <i>BMC Genomics</i> , 2018, 19, 710.	1.2	38
37	Discovery of Plant Viruses From Tea Plant (<i>Camellia sinensis</i> (L.) O. Kuntze) by Metagenomic Sequencing. <i>Frontiers in Microbiology</i> , 2018, 9, 2175.	1.5	44

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38	Transcriptomic analyses identify albino-associated genes of a novel albino tea germplasm "Huabai 1"™. Horticulture Research, 2018, 5, 54.	2.9	42
39	Identification of key genes involved in catechin metabolism in tea seedlings based on transcriptomic and HPLC analysis. Plant Physiology and Biochemistry, 2018, 133, 107-115.	2.8	30
40	Identification and Expression Analyses of SBP-Box Genes Reveal Their Involvement in Abiotic Stress and Hormone Response in Tea Plant (Camellia sinensis). International Journal of Molecular Sciences, 2018, 19, 3404.	1.8	25
41	Metabolite profiling and transcriptomic analyses reveal an essential role of UVR8-mediated signal transduction pathway in regulating flavonoid biosynthesis in tea plants (Camellia sinensis) in response to shading. BMC Plant Biology, 2018, 18, 233.	1.6	84
42	CsINV5, a tea vacuolar invertase gene enhances cold tolerance in transgenic Arabidopsis. BMC Plant Biology, 2018, 18, 228.	1.6	45
43	Unraveling the Roles of Regulatory Genes during Domestication of Cultivated Camellia: Evidence and Insights from Comparative and Evolutionary Genomics. Genes, 2018, 9, 488.	1.0	11
44	Genome-Wide Identification, Classification and Expression Analysis of the HSP Gene Superfamily in Tea Plant (Camellia sinensis). International Journal of Molecular Sciences, 2018, 19, 2633.	1.8	60
45	The Integration of Metabolomics and Next-Generation Sequencing Data to Elucidate the Pathways of Natural Product Metabolism in Medicinal Plants. Planta Medica, 2018, 84, 855-873.	0.7	47
46	Genetic engineering of trees: progress and new horizons. In Vitro Cellular and Developmental Biology - Plant, 2018, 54, 341-376.	0.9	47
47	Gene Discovery of Characteristic Metabolic Pathways in the Tea Plant (Camellia sinensis) Using "Omics"-Based Network Approaches: A Future Perspective. Frontiers in Plant Science, 2018, 9, 480.	1.7	33
48	Insights into Tissue-specific Specialized Metabolism in Tieguanyin Tea Cultivar by Untargeted Metabolomics. Molecules, 2018, 23, 1817.	1.7	24
49	Revealing the influence of microbiota on the quality of Pu-erh tea during fermentation process by shotgun metagenomic and metabolomic analysis. Food Microbiology, 2018, 76, 405-415.	2.1	105
50	Flavoalkaloids with a Pyrrolidinone Ring from Chinese Ancient Cultivated Tea Xi-Gui. Journal of Agricultural and Food Chemistry, 2018, 66, 7948-7957.	2.4	46
51	Metabolite Profiling of 14 Wuyi Rock Tea Cultivars Using UPLC-QTOF MS and UPLC-QqQ MS Combined with Chemometrics. Molecules, 2018, 23, 104.	1.7	90
52	Genome of Wild Mandarin and Domestication History of Mandarin. Molecular Plant, 2018, 11, 1024-1037.	3.9	130
53	Genome-wide identification and characterization of ALTERNATIVE OXIDASE genes and their response under abiotic stresses in Camellia sinensis (L.) O. Kuntze. Planta, 2018, 248, 1231-1247.	1.6	9
54	Genome-wide systematic characterization and its regulatory expression reprogramming process of the bZIP transcription factors during trauma response in Camellia sinensis. Canadian Journal of Forest Research, 2018, 48, 1279-1291.	0.8	2
55	Circular RNA architecture and differentiation during leaf bud to young leaf development in tea (Camellia sinensis). Planta, 2018, 248, 1417-1429.	1.6	71

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56	Comparative genomics analysis reveals gene family expansion and changes of expression patterns associated with natural adaptations of flowering time and secondary metabolism in yellow <i>Camellia</i> . <i>Functional and Integrative Genomics</i> , 2018, 18, 659-671.	1.4	14
57	Tea consumption and disease correlations. <i>Trends in Food Science and Technology</i> , 2018, 78, 95-106.	7.8	96
58	Long-read sequencing and de novo genome assembly of <i>Ammopiptanthus nanus</i> , a desert shrub. <i>GigaScience</i> , 2018, 7, .	3.3	22
59	Novel insight into the role of withering process in characteristic flavor formation of teas using transcriptome analysis and metabolite profiling. <i>Food Chemistry</i> , 2019, 272, 313-322.	4.2	133
60	Genomic and transcriptomic analyses of HD-Zip family transcription factors and their responses to abiotic stress in tea plant (<i>Camellia sinensis</i>). <i>Genomics</i> , 2019, 111, 1142-1151.	1.3	62
61	Identification of genes revealed differential expression profiles and lignin accumulation during leaf and stem development in tea plant (<i>Camellia sinensis</i> (L.) O. Kuntze). <i>Protoplasma</i> , 2019, 256, 359-370.	1.0	43
62	Trends in herbgenomics. <i>Science China Life Sciences</i> , 2019, 62, 288-308.	2.3	46
63	Gene Coexpression Networks Reveal Key Drivers of Flavonoid Variation in Eleven Tea Cultivars (<i>Camellia sinensis</i>). <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 9967-9978.	2.4	20
64	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.	1.6	26
65	Molecular Origins of Functional Diversity in Benzylisoquinoline Alkaloid Methyltransferases. <i>Frontiers in Plant Science</i> , 2019, 10, 1058.	1.7	25
66	Comparative transcriptomic analysis reveals gene expression associated with cold adaptation in the tea plant <i>Camellia sinensis</i> . <i>BMC Genomics</i> , 2019, 20, 624.	1.2	82
67	The tea plant reference genome and improved gene annotation using long-read and paired-end sequencing data. <i>Scientific Data</i> , 2019, 6, 122.	2.4	29
68	Genetic diversity, linkage disequilibrium, and population structure analysis of the tea plant (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf genotyping-by-sequencing. <i>BMC Plant Biology</i> , 2019, 19, 328.	1.6	65
69	Chemistry and Biological Activities of Processed <i>Camellia sinensis</i> Teas: A Comprehensive Review. <i>Comprehensive Reviews in Food Science and Food Safety</i> , 2019, 18, 1474-1495.	5.9	283
70	A high-quality <i>Actinidia chinensis</i> (kiwifruit) genome. <i>Horticulture Research</i> , 2019, 6, 117.	2.9	109
71	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.	1.8	34
72	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.	1.1	69
73	The <i>Rhododendron</i> Genome and Chromosomal Organization Provide Insight into Shared Whole-Genome Duplications across the Heath Family (Ericaceae). <i>Genome Biology and Evolution</i> , 2019, 11, 3353-3371.	1.1	47

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74	Effects of parental genetic divergence on gene expression patterns in interspecific hybrids of <i>Camellia</i> . <i>BMC Genomics</i> , 2019, 20, 828.	1.2	11
75	Seasonal Theanine Accumulation and Related Gene Expression in the Roots and Leaf Buds of Tea Plants (<i>Camellia Sinensis</i> L.). <i>Frontiers in Plant Science</i> , 2019, 10, 1397.	1.7	41
76	Structural and functional insights into the LBD family involved in abiotic stress and flavonoid synthases in <i>Camellia sinensis</i> . <i>Scientific Reports</i> , 2019, 9, 15651.	1.6	20
77	Alternative Splicing of Key Genes in LOX Pathway Involves Biosynthesis of Volatile Fatty Acid Derivatives in Tea Plant (<i>Camellia sinensis</i>). <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 13021-13032.	2.4	17
78	Optimized sequencing depth and de novo assembler for deeply reconstructing the transcriptome of the tea plant, an economically important plant species. <i>BMC Bioinformatics</i> , 2019, 20, 553.	1.2	7
79	Deciphering tea tree chloroplast and mitochondrial genomes of <i>Camellia sinensis</i> var. <i>assamica</i> . <i>Scientific Data</i> , 2019, 6, 209.	2.4	26
80	Genomic Analyses Provide Insights Into the Evolutionary History and Genetic Diversity of <i>Auricularia</i> Species. <i>Frontiers in Microbiology</i> , 2019, 10, 2255.	1.5	12
81	Genome-Wide Association Study to Identify Favorable SNP Allelic Variations and Candidate Genes That Control the Timing of Spring Bud Flush of Tea (<i>Camellia sinensis</i>) Using SLAF-seq. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 10380-10391.	2.4	24
82	Functional analysis of flavonoid 3- α -hydroxylase and flavonoid 3,5- α -hydroxylases from tea plant (<i>Camellia sinensis</i>), involved in the B-ring hydroxylation of flavonoids. <i>Gene</i> , 2019, 717, 144046.	1.0	27
83	The growth of tea. <i>Nature</i> , 2019, 566, S2-S4.	13.7	59
84	Genomic focus brings tea research to the boil. <i>Nature</i> , 2019, 566, S12-S13.	13.7	4
85	The involvements of calcium-dependent protein kinases and catechins in tea plant [<i>Camellia sinensis</i> (L.) O. Kuntze] cold responses. <i>Plant Physiology and Biochemistry</i> , 2019, 143, 190-202.	2.8	32
86	Genome-wide identification and expression analyses of the LEA protein gene family in tea plant reveal their involvement in seed development and abiotic stress responses. <i>Scientific Reports</i> , 2019, 9, 14123.	1.6	33
87	Habitat management as a safe and effective approach for improving yield and quality of tea (<i>Camellia</i>) Tj ETQq1 1 0.784314 rgBT /Overl 1.6 18	1.6	18
88	The Quality Control of Tea by Near-Infrared Reflectance (NIR) Spectroscopy and Chemometrics. <i>Journal of Spectroscopy</i> , 2019, 2019, 1-11.	0.6	36
89	Global Transcriptional Insights of Pollen-Pistil Interactions Commencing Self-Incompatibility and Fertilization in Tea [<i>Camellia sinensis</i> (L.) O. Kuntze]. <i>International Journal of Molecular Sciences</i> , 2019, 20, 539.	1.8	34
90	Physiological and iTRAQ-based proteomic analyses reveal the function of exogenous $\hat{1}^3$ -aminobutyric acid (GABA) in improving tea plant (<i>Camellia sinensis</i> L.) tolerance at cold temperature. <i>BMC Plant Biology</i> , 2019, 19, 43.	1.6	54
91	Advances in research on functional genes of tea plant. <i>Gene</i> , 2019, 711, 143940.	1.0	20

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92	Assessment of genome-wide DArT-seq markers for tea <i>Camellia sinensis</i> (L.) O. Kuntze germplasm analysis. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	3
93	Sequencing of a Wild Apple (<i>Malus baccata</i>) Genome Unravels the Differences Between Cultivated and Wild Apple Species Regarding Disease Resistance and Cold Tolerance. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2051-2060.	0.8	47
94	Isolation and expression analysis of CsCML genes in response to abiotic stresses in the tea plant (<i>Camellia sinensis</i>). <i>Scientific Reports</i> , 2019, 9, 8211.	1.6	27
95	Differentially Expressed Protein Are Involved in Dynamic Changes of Catechins Contents in Postharvest Tea Leaves under Different Temperatures. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 7547-7560.	2.4	12
96	A novel data processing method CyC* for quantitative real time polymerase chain reaction minimizes cumulative error. <i>PLoS ONE</i> , 2019, 14, e0218159.	1.1	6
97	Construction and analysis of an interologous protein-protein interaction network of <i>Camellia sinensis</i> leaf (TeaLIPIN) from RNA-Seq data sets. <i>Plant Cell Reports</i> , 2019, 38, 1249-1262.	2.8	9
98	Metabolomics for a Millenniums-Old Crop: Tea Plant (<i>Camellia sinensis</i>). <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 6445-6457.	2.4	32
99	Transcriptional profiling of contrasting genotypes revealed key candidates and nucleotide variations for drought dissection in <i>Camellia sinensis</i> (L.) O. Kuntze. <i>Scientific Reports</i> , 2019, 9, 7487.	1.6	32
100	Diversity of Pestalotiopsis-Like Species Causing Gray Blight Disease of Tea Plants (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf Pathogenicity. <i>Plant Disease</i> , 2019, 103, 2548-2558.	0.7	31
101	Uptake of adenine by purine permeases of <i>Coffea canephora</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 1300-1305.	0.6	7
102	Identification of Tea Plant Purple Acid Phosphatase Genes and Their Expression Responses to Excess Iron. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1954.	1.8	17
103	Expression patterns of alpha-amylase and beta-amylase genes provide insights into the molecular mechanisms underlying the responses of tea plants (<i>Camellia sinensis</i>) to stress and postharvest processing treatments. <i>Planta</i> , 2019, 250, 281-298.	1.6	40
104	Response of leaf color and the expression of photoreceptor genes of <i>Camellia sinensis</i> cv. Huangjinya to different light quality conditions. <i>Scientia Horticulturae</i> , 2019, 251, 225-232.	1.7	29
105	Herbgenomics: A stepping stone for research into herbal medicine. <i>Science China Life Sciences</i> , 2019, 62, 913-920.	2.3	22
106	Tea Plant Information Archive: a comprehensive genomics and bioinformatics platform for tea plant. <i>Plant Biotechnology Journal</i> , 2019, 17, 1938-1953.	4.1	220
107	Tissue specific long non-coding RNAs are involved in aroma formation of black tea. <i>Industrial Crops and Products</i> , 2019, 133, 79-89.	2.5	48
109	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.	0.9	22
110	Conserved MicroRNA Act Boldly During Sprout Development and Quality Formation in Pingyang Tezaocha (<i>Camellia sinensis</i>). <i>Frontiers in Genetics</i> , 2019, 10, 237.	1.1	21

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111	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.	1.2	46
112	Comprehensive identification of the full-length transcripts and alternative splicing related to the secondary metabolism pathways in the tea plant (<i>Camellia sinensis</i>). <i>Scientific Reports</i> , 2019, 9, 2709.	1.6	51
113	Functional annotation of putative QTL associated with black tea quality and drought tolerance traits. <i>Scientific Reports</i> , 2019, 9, 1465.	1.6	22
114	Environmental Impact and Carbon Footprint Assessment of Taiwanese Agricultural Products: A Case Study on Taiwanese Dongshan Tea. <i>Energies</i> , 2019, 12, 138.	1.6	12
115	Cloning and expression patterns of VQ-motif-containing proteins under abiotic stress in tea plant. <i>Plant Growth Regulation</i> , 2019, 87, 277-286.	1.8	7
116	Tung Tree (<i>Vernicia fordii</i>) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 558-575.	3.0	43
117	Genomic Variance and Transcriptional Comparisons Reveal the Mechanisms of Leaf Color Affecting Palatability and Stressed Defense in Tea Plant. <i>Genes</i> , 2019, 10, 929.	1.0	14
118	Dissection of Chemical Composition and Associated Gene Expression in the Pigment-Deficient Tea Cultivar 'Xiaoxueya'™ Reveals an Albino Phenotype and Metabolite Formation. <i>Frontiers in Plant Science</i> , 2019, 10, 1543.	1.7	30
119	Establishing a System for Functional Characterization of Full-Length cDNAs of <i>Camellia sinensis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 5929.	1.8	0
120	First nitrosoproteomic profiling deciphers the cysteine S-nitrosylation involved in multiple metabolic pathways of tea leaves. <i>Scientific Reports</i> , 2019, 9, 17525.	1.6	13
121	Characterization of genome-wide genetic variations between two varieties of tea plant (<i>Camellia</i>) Tj ETQq0 0 0 rBT J/Overlock 10 Tf 50	1.2	38
122	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.	1.7	51
123	The late embryogenesis abundant gene family in tea plant (<i>Camellia sinensis</i>): Genome-wide characterization and expression analysis in response to cold and dehydration stress. <i>Plant Physiology and Biochemistry</i> , 2019, 135, 277-286.	2.8	48
124	Fast sensing of imidacloprid residue in tea using surface-enhanced Raman scattering by comparative multivariate calibration. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2019, 211, 86-93.	2.0	50
125	Classification of tea (<i>Camellia sinensis</i>) landraces and cultivars in Kyoto, Japan and other regions, based on simple sequence repeat markers and restriction site-associated DNA sequencing analysis. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 441-451.	0.8	8
126	Comprehensive Analysis Revealed the Close Relationship between N/P/K Status and Secondary Metabolites in Tea Leaves. <i>ACS Omega</i> , 2019, 4, 176-184.	1.6	29
127	AtHB2, a class II HD-ZIP protein, negatively regulates the expression of CsANS, which encodes a key enzyme in <i>Camellia sinensis</i> catechin biosynthesis. <i>Physiologia Plantarum</i> , 2019, 166, 936-945.	2.6	14
128	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.	0.5	59

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129	<sc>DNA</sc> methylome analysis provides evidence that the expansion of the tea genome is linked to <sc>TE</sc> bursts. <i>Plant Biotechnology Journal</i> , 2019, 17, 826-835.	4.1	39
130	<i>De novo</i> 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.	0.9	36
131	Exploiting MATE efflux proteins to improve flavonoid accumulation in <i>Camellia sinensis</i> in silico. <i>International Journal of Biological Macromolecules</i> , 2020, 143, 732-743.	3.6	7
132	Multi-omics research in albino tea plants: Past, present, and future. <i>Scientia Horticulturae</i> , 2020, 261, 108943.	1.7	36
133	Genome-wide identification, characterization, and expression analysis of nucleotide-binding leucine-rich repeats gene family under environmental stresses in tea (<i>Camellia sinensis</i>). <i>Genomics</i> , 2020, 112, 1351-1362.	1.3	7
134	<i>De novo</i> assembly of a wild pear (<i>Pyrus betuleafolia</i>) genome. <i>Plant Biotechnology Journal</i> , 2020, 18, 581-595.	4.1	72
135	Plant Alkaloid Engineering. , 2020, , 700-755.		2
136	miRNA precursorâ€derived SSR markerâ€mediated genotyping of tea (<i>Camellia sinensis</i>) cultivars with varying health benefit traits. <i>Plant Breeding</i> , 2020, 139, 804-810.	1.0	8
137	Genome-wide identification and expression analysis of flowering-related genes reveal putative floral induction and differentiation mechanisms in tea plant (<i>Camellia sinensis</i>). <i>Genomics</i> , 2020, 112, 2318-2326.	1.3	21
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