

Liang Chen

List of Publications by Year in descending order

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71
papers

3,292
citations

126907

33
h-index

155660

55
g-index

73
all docs

73
docs citations

73
times ranked

2378
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative trait loci mapping for free amino acid content using an albino population and SNP markers provides insight into the genetic improvement of tea plants. <i>Horticulture Research</i> , 2022, 9, .	6.3	23
2	Genetic, morphological, and chemical discrepancies between <i>Camellia sinensis</i> (L.) O. Kuntze and its close relatives. <i>Journal of Food Composition and Analysis</i> , 2022, 108, 104417.	3.9	5
3	Characteristics of non-volatile metabolites in fresh shoots from tea plant (<i>Camellia) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	1.9	5
4	Genome-wide identification of PME gene family and expression of candidate genes associated with aluminum tolerance in tea plant (<i>Camellia sinensis</i>). <i>BMC Plant Biology</i> , 2022, 22, .	3.6	12
5	The tea plant <i>CsWRKY26</i>; promotes drought tolerance in transgenic <i>Arabidopsis</i> plants. <i>Beverage Plant Research</i> , 2021, 1, 1-11.	1.9	10
6	Transcriptomic and Metabolomic Analyses Provide Insights Into an Aberrant Tissue of Tea Plant (<i>Camellia sinensis</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 730651.	3.6	1
7	Non-Volatile Metabolic Profiling and Regulatory Network Analysis in Fresh Shoots of Tea Plant and Its Wild Relatives. <i>Frontiers in Plant Science</i> , 2021, 12, 746972.	3.6	2
8	Rebuttal to the Comment on Metabolomics for a Millenniums-Old Crop: Tea Plant (<i>Camellia sinensis</i>). <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 699-699.	5.2	0
9	Drought stress triggers proteomic changes involving lignin, flavonoids and fatty acids in tea plants. <i>Scientific Reports</i> , 2020, 10, 15504.	3.3	62
10	Population sequencing enhances understanding of tea plant evolution. <i>Nature Communications</i> , 2020, 11, 4447.	12.8	123
11	Identifying Conserved Functional Gene Modules Underlying the Dynamic Regulation of Tea Plant Development and Secondary Metabolism. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 11026-11037.	5.2	4
12	Metabolite signatures of diverse <i>Camellia sinensis</i> tea populations. <i>Nature Communications</i> , 2020, 11, 5586.	12.8	78
13	Baiyacha, a wild tea plant naturally occurring high contents of theacrine and 3<sup>â€³</sup>-methyl-epigallocatechin gallate from Fujian, China. <i>Scientific Reports</i> , 2020, 10, 9715.	3.3	6
14	Repressed Gene Expression of Photosynthetic Antenna Proteins Associated with Yellow Leaf Variation as Revealed by Bulked Segregant RNA-seq in Tea Plant <i>Camellia sinensis</i>. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 8068-8079.	5.2	26
15	Identification and distribution of a single nucleotide polymorphism responsible for the catechin content in tea plants. <i>Horticulture Research</i> , 2020, 7, 24.	6.3	25
16	The chromosome-scale genome reveals the evolution and diversification after the recent tetraploidization event in tea plant. <i>Horticulture Research</i> , 2020, 7, 63.	6.3	63
17	Novel insight into theacrine metabolism revealed by transcriptome analysis in bitter tea (Kucha,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	3.3	12
18	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.	5.2	20

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19	The complete chloroplast genome sequence of <i>Camellia tachangensis</i> F. C. Zhang (Theaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 3344-3345.	0.4	4
20	The complete chloroplast genome of an albino tea, <i>Camellia sinensis</i> cultivar "Baiye 1". Mitochondrial DNA Part B: Resources, 2019, 4, 3143-3144.	0.4	3
21	Regulation of Growth and Flavonoid Formation of Tea Plants (<i>Camellia sinensis</i>) by Blue and Green Light. Journal of Agricultural and Food Chemistry, 2019, 67, 2408-2419.	5.2	56
22	Isolation and Characterization of CsWRKY7, a Subgroup IId WRKY Transcription Factor from <i>Camellia sinensis</i> , Linked to Development in Arabidopsis. International Journal of Molecular Sciences, 2019, 20, 2815.	4.1	14
23	Metabolomics for a Millenniums-Old Crop: Tea Plant (<i>Camellia sinensis</i>). Journal of Agricultural and Food Chemistry, 2019, 67, 6445-6457.	5.2	32
24	Analysis of Genetic Diversity and Development of a SCAR Marker for Green Tea (<i>Camellia sinensis</i>) Cultivars in Zhejiang Province: The Most Famous Green Tea-Producing Area in China. Biochemical Genetics, 2019, 57, 555-570.	1.7	10
25	Cloning and expression patterns of VQ-motif-containing proteins under abiotic stress in tea plant. Plant Growth Regulation, 2019, 87, 277-286.	3.4	7
26	Comprehensive Dissection of Metabolic Changes in Albino and Green Tea Cultivars. Journal of Agricultural and Food Chemistry, 2018, 66, 2040-2048.	5.2	51
27	Quantitative Trait Loci Mapping for Theobromine and Caffeine Contents in Tea Plant (<i>Camellia</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	5.2	26
28	A Novel F3 ²⁵ H Allele with 14 bp Deletion Is Associated with High Catechin Index Trait of Wild Tea Plants and Has Potential Use in Enhancing Tea Quality. Journal of Agricultural and Food Chemistry, 2018, 66, 10470-10478.	5.2	17
29	Hongyacha, a Naturally Caffeine-Free Tea Plant from Fujian, China. Journal of Agricultural and Food Chemistry, 2018, 66, 11311-11319.	5.2	37
30	Transcriptome and metabolome analysis reveal candidate genes and biochemicals involved in tea geometrid defense in <i>Camellia sinensis</i> . PLoS ONE, 2018, 13, e0201670.	2.5	38
31	Functional natural allelic variants of flavonoid 3 ² ,5 ² -hydroxylase gene governing catechin traits in tea plant and its relatives. Planta, 2017, 245, 523-538.	3.2	30
32	Quantitative Succinyl-Proteome Profiling of <i>Camellia sinensis</i> cv. "Anji Baicha" During Periodic Albinism. Scientific Reports, 2017, 7, 1873.	3.3	54
33	DNA-based diversity of tea plants grown in Italy. Genetic Resources and Crop Evolution, 2017, 64, 1905-1915.	1.6	7
34	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. Frontiers in Plant Science, 2017, 8, 2104.	3.6	33
35	Small <i>scp</i> RNA and degradome profiling reveals important roles for <i>scp</i> microRNAs and their targets in tea plant response to drought stress. Physiologia Plantarum, 2016, 158, 435-451.	5.2	51
36	Association mapping of caffeine content with TCS1 in tea plant and its related species. Plant Physiology and Biochemistry, 2016, 105, 251-259.	5.8	28

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37	Biochemical and transcriptomic analyses reveal different metabolite biosynthesis profiles among three color and developmental stages in "Anji Baicha"™ (Camellia sinensis). BMC Plant Biology, 2016, 16, 195.	3.6	93
38	Natural allelic variations of TCS1 play a crucial role in caffeine biosynthesis of tea plant and its related species. Plant Physiology and Biochemistry, 2016, 100, 18-26.	5.8	56
39	Identification and expression profiling of the auxin response factors (ARFs) in the tea plant (Camellia) Tj ETQq1 1 0.784314 rgBT /Ove 46-56.	5.8	42
40	Transcriptomic Analysis of Tea Plant Responding to Drought Stress and Recovery. PLoS ONE, 2016, 11, e0147306.	2.5	67
41	A transcriptomic analysis of bermudagrass (Cynodon dactylon) provides novel insights into the basis of low temperature tolerance. BMC Plant Biology, 2015, 15, 216.	3.6	45
42	Differential Metabolic Profiles during the Albescent Stages of "Anji Baicha"™ (Camellia sinensis). PLoS ONE, 2015, 10, e0139996.	2.5	43
43	Large-Scale SNP Discovery and Genotyping for Constructing a High-Density Genetic Map of Tea Plant Using Specific-Locus Amplified Fragment Sequencing (SLAF-seq). PLoS ONE, 2015, 10, e0128798.	2.5	68
44	Physiological changes and differential gene expression of tea plant under dehydration and rehydration conditions. Scientia Horticulturae, 2015, 184, 129-141.	3.6	46
45	Novel insights into the molecular mechanisms underlying the resistance of Camellia sinensis to Ectropis oblique provided by strategic transcriptomic comparisons. Scientia Horticulturae, 2015, 192, 429-440.	3.6	24
46	Global transcriptome and gene regulation network for secondary metabolite biosynthesis of tea plant (Camellia sinensis). BMC Genomics, 2015, 16, 560.	2.8	174
47	Construction of a SSR-Based Genetic Map and Identification of QTLs for Catechins Content in Tea Plant (Camellia sinensis). PLoS ONE, 2014, 9, e93131.	2.5	75
48	Determination of Catechin Content in Representative Chinese Tea Germplasms. Journal of Agricultural and Food Chemistry, 2014, 62, 9436-9441.	5.2	74
49	Global transcriptome profiles of Camellia sinensis during cold acclimation. BMC Genomics, 2013, 14, 415.	2.8	268
50	Microsatellite markers from tea plant expressed sequence tags (ESTs) and their applicability for cross-species/genera amplification and genetic mapping. Scientia Horticulturae, 2012, 134, 167-175.	3.6	27
51	Differential expression analysis of different albescent stages of "Anji Baicha"™ (Camellia sinensis (L.) O.) Tj ETQq1 1 0.784314 rgBT /Ove 3.6 48	3.6	48
52	Global Tea Breeding. Advanced Topics in Science and Technology in China, 2012, , .	0.1	42
53	Diversity distribution and population structure of tea germplasms in China revealed by EST-SSR markers. Tree Genetics and Genomes, 2012, 8, 205-220.	1.6	87
54	Delicious and Healthy Tea: An Overview. , 2012, , 1-11.		7

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55	Germplasm and Breeding Research of Tea Plant Based on DNA Marker Approaches. <i>Advanced Topics in Science and Technology in China</i> , 2012, , 361-376.	0.1	2
56	Tea Germplasm and Breeding in China. , 2012, , 13-68.		15
57	Establishment of core collection for Chinese tea germplasm based on cultivated region grouping and phenotypic data. <i>Frontiers of Agriculture in China</i> , 2011, 5, 344-350.	0.2	11
58	Genotypic variation of beta-carotene and lutein contents in tea germplasms, <i>Camellia sinensis</i> (L.) O. Kuntze. <i>Journal of Food Composition and Analysis</i> , 2010, 23, 9-14.	3.9	14
59	Identification and characterization of 74 novel polymorphic EST-SSR markers in the tea plant, <i>Camellia sinensis</i> (Theaceae). <i>American Journal of Botany</i> , 2010, 97, e153-6.	1.7	44
60	EST-SSR Genetic Diversity and Population Structure of Tea Landraces and Developed Cultivars (Lines) in Zhejiang Province, China. <i>Acta Agronomica Sinica</i> (China), 2010, 36, 744-753.	0.3	4
61	Recent progress in the molecular biology of tea (<i>Camellia sinensis</i>) based on the expressed sequence tag strategy: a review. <i>Journal of Horticultural Science and Biotechnology</i> , 2009, 84, 476-482.	1.9	4
62	Generation and characterization of 24 novel EST derived microsatellites from tea plant (<i>Camellia</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 4 Genetics, 2008, 9, 1327-1331.	1.5	40
63	Preparation of the UPOV Guidelines for the Conduct of Tests for Distinctness, Uniformity and Stability-Tea Plant [<i>Camellia sinensis</i> (L.) O. Kuntze]. <i>Agricultural Sciences in China</i> , 2008, 7, 224-231.	0.6	9
64	Germplasm and breeding research of tea plant based on DNA marker approaches. <i>Frontiers of Agriculture in China</i> , 2008, 2, 200-207.	0.2	16
65	Genetic improvement and breeding of tea plant (<i>Camellia sinensis</i>) in China: from individual selection to hybridization and molecular breeding. <i>Euphytica</i> , 2007, 154, 239-248.	1.2	124
66	Research progress on isolation and cloning of functional genes in tea plants. <i>Frontiers of Agriculture in China</i> , 2007, 1, 449-455.	0.2	12
67	Genome-Wide Analysis of Basic/Helix-Loop-Helix Transcription Factor Family in Rice and Arabidopsis. <i>Plant Physiology</i> , 2006, 141, 1167-1184.	4.8	527
68	The use of RAPD markers for detecting genetic diversity, relationship and molecular identification of Chinese elite tea genetic resources [<i>Camellia sinensis</i> (L.) O. Kuntze] preserved in a tea germplasm repository. <i>Biodiversity and Conservation</i> , 2005, 14, 1433-1444.	2.6	47
69	Variations of Main Quality Components of Tea Genetic Resources [<i>Camellia sinensis</i> (L.) O. Kuntze] Preserved in the China National Germplasm Tea Repository. <i>Plant Foods for Human Nutrition</i> , 2005, 60, 31-35.	3.2	71
70	Generation and analysis of expressed sequence tags from the tender shoots cDNA library of tea plant (<i>Camellia sinensis</i>). <i>Plant Science</i> , 2005, 168, 359-363.	3.6	52
71	Genetic diversity and phylogeny of tea plant (<i>Camellia sinensis</i>) and its related species and varieties in the section <i>Thea</i> genus <i>Camellia</i> determined by randomly amplified polymorphic DNA analysis. <i>Journal of Horticultural Science and Biotechnology</i> , 2002, 77, 729-732.	1.9	38