

# Liang Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5987900/publications.pdf>

Version: 2024-02-01

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	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
2	Global transcriptome profiles of <i>Camellia sinensis</i> during cold acclimation. <i>BMC Genomics</i> , 2013, 14, 415.	2.8	268
3	Global transcriptome and gene regulation network for secondary metabolite biosynthesis of tea plant ( <i>Camellia sinensis</i> ). <i>BMC Genomics</i> , 2015, 16, 560.	2.8	174
4	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
5	Population sequencing enhances understanding of tea plant evolution. <i>Nature Communications</i> , 2020, 11, 4447.	12.8	123
6	Biochemical and transcriptomic analyses reveal different metabolite biosynthesis profiles among three color and developmental stages in "Anji Baicha"™ ( <i>Camellia sinensis</i> ). <i>BMC Plant Biology</i> , 2016, 16, 195.	3.6	93
7	Diversity distribution and population structure of tea germplasms in China revealed by EST-SSR markers. <i>Tree Genetics and Genomes</i> , 2012, 8, 205-220.	1.6	87
8	Metabolite signatures of diverse <i>Camellia sinensis</i> tea populations. <i>Nature Communications</i> , 2020, 11, 5586.	12.8	78
9	Construction of a SSR-Based Genetic Map and Identification of QTLs for Catechins Content in Tea Plant ( <i>Camellia sinensis</i> ). <i>PLoS ONE</i> , 2014, 9, e93131.	2.5	75
10	Determination of Catechin Content in Representative Chinese Tea Germplasms. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 9436-9441.	5.2	74
11	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
12	Large-Scale SNP Discovery and Genotyping for Constructing a High-Density Genetic Map of Tea Plant Using Specific-Locus Amplified Fragment Sequencing (SLAF-seq). <i>PLoS ONE</i> , 2015, 10, e0128798.	2.5	68
13	Transcriptomic Analysis of Tea Plant Responding to Drought Stress and Recovery. <i>PLoS ONE</i> , 2016, 11, e0147306.	2.5	67
14	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
15	Drought stress triggers proteomic changes involving lignin, flavonoids and fatty acids in tea plants. <i>Scientific Reports</i> , 2020, 10, 15504.	3.3	62
16	Natural allelic variations of TCS1 play a crucial role in caffeine biosynthesis of tea plant and its related species. <i>Plant Physiology and Biochemistry</i> , 2016, 100, 18-26.	5.8	56
17	Regulation of Growth and Flavonoid Formation of Tea Plants ( <i>Camellia sinensis</i> ) by Blue and Green Light. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 2408-2419.	5.2	56
18	Quantitative Succinyl-Proteome Profiling of <i>Camellia sinensis</i> cv. "Anji Baicha"™ During Periodic Albinism. <i>Scientific Reports</i> , 2017, 7, 1873.	3.3	54

#	ARTICLE	IF	CITATIONS
19	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
20	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. <i>Physiologia Plantarum</i> , 2016, 158, 435-451.	5.2	51
21	Comprehensive Dissection of Metabolic Changes in Albino and Green Tea Cultivars. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 2040-2048.	5.2	51
22	Differential expression analysis of different albescent stages of "Anji Baicha"™ ( <i>Camellia sinensis</i> (L.) O.) Tj ETQq0 0 0 rgBT /Overlock	3.6	48
23	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
24	Physiological changes and differential gene expression of tea plant under dehydration and rehydration conditions. <i>Scientia Horticulturae</i> , 2015, 184, 129-141.	3.6	46
25	A transcriptomic analysis of bermudagrass ( <i>Cynodon dactylon</i> ) provides novel insights into the basis of low temperature tolerance. <i>BMC Plant Biology</i> , 2015, 15, 216.	3.6	45
26	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
27	Differential Metabolic Profiles during the Albescent Stages of "Anji Baicha"™ ( <i>Camellia sinensis</i> ). <i>PLoS ONE</i> , 2015, 10, e0139996.	2.5	43
28	Global Tea Breeding. <i>Advanced Topics in Science and Technology in China</i> , 2012, , .	0.1	42
29	Identification and expression profiling of the auxin response factors (ARFs) in the tea plant ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	5.8	42
30	Generation and characterization of 24 novel EST derived microsatellites from tea plant ( <i>Camellia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 <i>Genetics</i> , 2008, 9, 1327-1331.	1.5	40
31	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
32	Transcriptome and metabolome analysis reveal candidate genes and biochemicals involved in tea geometrid defense in <i>Camellia sinensis</i> . <i>PLoS ONE</i> , 2018, 13, e0201670.	2.5	38
33	Hongyacha, a Naturally Caffeine-Free Tea Plant from Fujian, China. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 11311-11319.	5.2	37
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. <i>Frontiers in Plant Science</i> , 2017, 8, 2104.	3.6	33
35	Metabolomics for a Millenniums-Old Crop: Tea Plant ( <i>Camellia sinensis</i> ). <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 6445-6457.	5.2	32
36	Functional natural allelic variants of flavonoid 3,5-hydroxylase gene governing catechin traits in tea plant and its relatives. <i>Planta</i> , 2017, 245, 523-538.	3.2	30

#	ARTICLE	IF	CITATIONS
37	Association mapping of caffeine content with TCS1 in tea plant and its related species. <i>Plant Physiology and Biochemistry</i> , 2016, 105, 251-259.	5.8	28
38	Microsatellite markers from tea plant expressed sequence tags (ESTs) and their applicability for cross-species/genera amplification and genetic mapping. <i>Scientia Horticulturae</i> , 2012, 134, 167-175.	3.6	27
39	Quantitative Trait Loci Mapping for Theobromine and Caffeine Contents in Tea Plant ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	5.2	26
40	Repressed Gene Expression of Photosynthetic Antenna Proteins Associated with Yellow Leaf Variation as Revealed by Bulk 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
41	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
42	Novel insights into the molecular mechanisms underlying the resistance of <i>Camellia sinensis</i> to <i>Ectropis oblique</i> provided by strategic transcriptomic comparisons. <i>Scientia Horticulturae</i> , 2015, 192, 429-440.	3.6	24
43	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
44	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
45	A Novel F3â€²5â€²H Allele with 14 bp Deletion Is Associated with High Catechin Index Trait of Wild Tea Plants and Has Potential Use in Enhancing Tea Quality. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 10470-10478.	5.2	17
46	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
47	Tea Germplasm and Breeding in China. , 2012, , 13-68.		15
48	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
49	Isolation and Characterization of CsWRKY7, a Subgroup IId WRKY Transcription Factor from <i>Camellia sinensis</i> , Linked to Development in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2815.	4.1	14
50	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
51	Novel insight into theacrine metabolism revealed by transcriptome analysis in bitter tea (Kucha,) Tj ETQq1 1 0.784314 rgBT /Overlock	3.3	12
52	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
53	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
54	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. <i>Biochemical Genetics</i> , 2019, 57, 555-570.	1.7	10

#	ARTICLE	IF	CITATIONS
55	The tea plant <i>CsWRKY26</i> promotes drought tolerance in transgenic Arabidopsis plants. Beverage Plant Research, 2021, 1, 1-11.	1.9	10
56	Preparation of the UPOV Guidelines for the Conduct of Tests for Distinctness, Uniformity and Stability-Tea Plant [ <i>Camellia sinensis</i> (L.) O. Kuntze]. Agricultural Sciences in China, 2008, 7, 224-231.	0.6	9
57	DNA-based diversity of tea plants grown in Italy. Genetic Resources and Crop Evolution, 2017, 64, 1905-1915.	1.6	7
58	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
59	Delicious and Healthy Tea: An Overview. , 2012, , 1-11.		7
60	Baiyacha, a wild tea plant naturally occurring high contents of theacrine and 3-methyl-epigallocatechin gallate from Fujian, China. Scientific Reports, 2020, 10, 9715.	3.3	6
61	Genetic, morphological, and chemical discrepancies between <i>Camellia sinensis</i> (L.) O. Kuntze and its close relatives. Journal of Food Composition and Analysis, 2022, 108, 104417.	3.9	5
62	Characteristics of non-volatile metabolites in fresh shoots from tea plant ( <i>Camellia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 T	1.9	5
63	Recent progress in the molecular biology of tea ( <i>Camellia sinensis</i> ) based on the expressed sequence tag strategy: a review. Journal of Horticultural Science and Biotechnology, 2009, 84, 476-482.	1.9	4
64	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
65	Identifying Conserved Functional Gene Modules Underlying the Dynamic Regulation of Tea Plant Development and Secondary Metabolism. Journal of Agricultural and Food Chemistry, 2020, 68, 11026-11037.	5.2	4
66	EST-SSR Genetic Diversity and Population Structure of Tea Landraces and Developed Cultivars (Lines) in Zhejiang Province, China. Acta Agronomica Sinica(China), 2010, 36, 744-753.	0.3	4
67	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
68	Non-Volatile Metabolic Profiling and Regulatory Network Analysis in Fresh Shoots of Tea Plant and Its Wild Relatives. Frontiers in Plant Science, 2021, 12, 746972.	3.6	2
69	Germplasm and Breeding Research of Tea Plant Based on DNA Marker Approaches. Advanced Topics in Science and Technology in China, 2012, , 361-376.	0.1	2
70	Transcriptomic and Metabolomic Analyses Provide Insights Into an Aberrant Tissue of Tea Plant ( <i>Camellia sinensis</i> ). Frontiers in Plant Science, 2021, 12, 730651.	3.6	1
71	Rebuttal to the Comment on Metabolomics for a Millenniums-Old Crop: Tea Plant ( <i>Camellia sinensis</i> ). Journal of Agricultural and Food Chemistry, 2020, 68, 699-699.	5.2	0