

Zhongchi Liu

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

4,818
citations

87401

40
h-index

120465

65
g-index

91
all docs

91
docs citations

91
times ranked

5186
citing authors

#	ARTICLE	IF	CITATIONS
1	Plant development: Unveiling cytokinin's role in the end of flowering. <i>Current Biology</i> , 2022, 32, R168-R170.	1.8	1
2	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. <i>Plant Journal</i> , 2022, 109, 1614-1629.	2.8	4
3	Mechanism of fertilization-induced auxin synthesis in the endosperm for seed and fruit development. <i>Nature Communications</i> , 2022, 13, .	5.8	28
4	Developmental regulation of stolon and rhizome. <i>Current Opinion in Plant Biology</i> , 2021, 59, 101970.	3.5	39
5	Bacterial diketopiperazines stimulate diatom growth and lipid accumulation. <i>Plant Physiology</i> , 2021, 186, 1159-1170.	2.3	11
6	Editorial overview: Not your average plant: shining a light on developmental diversity. <i>Current Opinion in Plant Biology</i> , 2021, 59, 102016.	3.5	0
7	Reannotation of the cultivated strawberry genome and establishment of a strawberry genome database. <i>Horticulture Research</i> , 2021, 8, 41.	2.9	46
8	GRAS transcription factor <i>LOSS OF AXILLARY MERISTEMS</i> is essential for stamen and runner formation in wild strawberry. <i>Plant Physiology</i> , 2021, 186, 1970-1984.	2.3	21
9	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. <i>Frontiers in Plant Science</i> , 2021, 12, 644881.	1.7	5
10	Chromosome-Scale Genome for a Red-Fruited, Perpetual Flowering and Runnerless Woodland Strawberry (<i>Fragaria vesca</i>). <i>Frontiers in Genetics</i> , 2021, 12, 671371.	1.1	8
11	Woodland strawberry axillary bud fate is dictated by a crosstalk of environmental and endogenous factors. <i>Plant Physiology</i> , 2021, 187, 1221-1234.	2.3	18
12	Gibberellin and auxin signaling genes <i>RGA1</i> and <i>ARF8</i> repress accessory fruit initiation in diploid strawberry. <i>Plant Physiology</i> , 2021, 185, 1059-1075.	2.3	40
13	The MADS-box gene <i>FveSEP3</i> plays essential roles in flower organogenesis and fruit development in woodland strawberry. <i>Horticulture Research</i> , 2021, 8, 247.	2.9	30
14	Editorial: Rosaceae Fruit Development and Quality. <i>Frontiers in Plant Science</i> , 2021, 12, 837300.	1.7	0
15	Application and future perspective of CRISPR/Cas9 genome editing in fruit crops. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 269-286.	4.1	52
16	Genetic modulation of <i>RAP</i> alters fruit coloration in both wild and cultivated strawberry. <i>Plant Biotechnology Journal</i> , 2020, 18, 1550-1561.	4.1	61
17	<i>FvbHLH9</i> Functions as a Positive Regulator of Anthocyanin Biosynthesis by Forming a HY5-bHLH9 Transcription Complex in Strawberry Fruits. <i>Plant and Cell Physiology</i> , 2020, 61, 826-837.	1.5	72
18	Allelic Variation of <i>MYB10</i> Is the Major Force Controlling Natural Variation in Skin and Flesh Color in Strawberry (<i>Fragaria</i> spp.) Fruit. <i>Plant Cell</i> , 2020, 32, 3723-3749.	3.1	111

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19	Developmental Mechanisms of Fleshy Fruit Diversity in Rosaceae. <i>Annual Review of Plant Biology</i> , 2020, 71, 547-573.	8.6	38
20	SOL1 and SOL2 regulate fate transition and cell divisions in the Arabidopsis stomatal lineage. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	39
21	Integrated analysis of high-throughput sequencing data shows abscisic acid-responsive genes and miRNAs in strawberry receptacle fruit ripening. <i>Horticulture Research</i> , 2019, 6, 26.	2.9	51
22	Conserved and novel roles of <i>miR164</i> regulatory module in specifying leaf and floral organ morphology in strawberry. <i>New Phytologist</i> , 2019, 224, 480-492.	3.5	46
23	Updated annotation of the wild strawberry <i>Fragaria vesca</i> V4 genome. <i>Horticulture Research</i> , 2019, 6, 61.	2.9	102
24	Gibberellic acid induced parthenocarpic "Honeycrisp" apples (<i>Malus domestica</i>) exhibit reduced ovary width and lower acidity. <i>Horticulture Research</i> , 2019, 6, 41.	2.9	29
25	Identification of genes preferentially expressed in wild strawberry receptacle fruit and demonstration of their promoter activities. <i>Horticulture Research</i> , 2019, 6, 50.	2.9	6
26	An Easy-to-Follow Pipeline for Long Noncoding RNA Identification: A Case Study in Diploid Strawberry <i>Fragaria vesca</i> . <i>Methods in Molecular Biology</i> , 2019, 1933, 223-243.	0.4	6
27	24-nt reproductive phasiRNAs are broadly present in angiosperms. <i>Nature Communications</i> , 2019, 10, 627.	5.8	106
28	Gene Expression Profiling of the Shoot Meristematic Tissues in Woodland Strawberry <i>Fragaria vesca</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1624.	1.7	9
29	Reporter gene expression reveals precise auxin synthesis sites during fruit and root development in wild strawberry. <i>Journal of Experimental Botany</i> , 2019, 70, 563-574.	2.4	56
30	Plant genetics enters the nano age?. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 446-447.	4.1	11
31	Efficient genome editing of wild strawberry genes, vector development and validation. <i>Plant Biotechnology Journal</i> , 2018, 16, 1868-1877.	4.1	97
32	The making of virgin fruit: the molecular and genetic basis of parthenocarpy. <i>Journal of Experimental Botany</i> , 2018, 69, 955-962.	2.4	53
33	Genome re-annotation of the wild strawberry <i>Fragaria vesca</i> using extensive Illumina- and SMRT-based RNA-seq datasets. <i>DNA Research</i> , 2018, 25, 61-70.	1.5	67
34	Loss of a highly conserved sterile alpha motif domain gene (<i>WEEP</i>) results in pendulous branch growth in peach trees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4690-E4699.	3.3	52
35	Reduced Anthocyanins in Petioles codes for a GST anthocyanin transporter that is essential for the foliage and fruit coloration in strawberry. <i>Journal of Experimental Botany</i> , 2018, 69, 2595-2608.	2.4	138
36	<i>Arabidopsis</i> TSO1 and MYB3R1 form a regulatory module to coordinate cell proliferation with differentiation in shoot and root. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3045-E3054.	3.3	38

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37	Suppressor of Runnerless Encodes a DELLA Protein that Controls Runner Formation for Asexual Reproduction in Strawberry. <i>Molecular Plant</i> , 2018, 11, 230-233.	3.9	60
38	Pyrite cloning: a single tube and programmed reaction cloning with restriction enzymes. <i>Plant Methods</i> , 2018, 14, 91.	1.9	4
39	Nuclear Radiation Monitoring Using Plants. <i>Journal of Nuclear Engineering and Radiation Science</i> , 2018, 4, .	0.2	0
40	Consensus Coexpression Network Analysis Identifies Key Regulators of Flower and Fruit Development in Wild Strawberry. <i>Plant Physiology</i> , 2018, 178, 202-216.	2.3	57
41	A MFS-like plasma membrane transporter required for <i>Leishmania</i> virulence protects the parasites from iron toxicity. <i>PLoS Pathogens</i> , 2018, 14, e1007140.	2.1	20
42	Transcriptome sequencing reveals role of light in promoting anthocyanin accumulation of strawberry fruit. <i>Plant Growth Regulation</i> , 2018, 86, 121-132.	1.8	29
43	Global identification of alternative splicing via comparative analysis of <i>sc</i> RNA-seq and Illumina-based <i>sc</i> RNA-seq in strawberry. <i>Plant Journal</i> , 2017, 90, 164-176.	2.8	161
44	An eFP browser for visualizing strawberry fruit and flower transcriptomes. <i>Horticulture Research</i> , 2017, 4, 17029.	2.9	63
45	Global gene expression defines faded whorl specification of double flower domestication in <i>Camellia</i> . <i>Scientific Reports</i> , 2017, 7, 3197.	1.6	21
46	SEUSS Integrates Gibberellin Signaling with Transcriptional Inputs from the SHR-SCR-SCL3 Module to Regulate Middle Cortex Formation in the Arabidopsis Root. <i>Plant Physiology</i> , 2016, 170, 1675-1683.	2.3	48
47	Genome-scale DNA variant analysis and functional validation of a SNP underlying yellow fruit color in wild strawberry. <i>Scientific Reports</i> , 2016, 6, 29017.	1.6	70
48	Phylogenetic tree-informed microRNAome analysis uncovers conserved and lineage-specific miRNAs in <i>Camellia</i> during floral organ development. <i>Journal of Experimental Botany</i> , 2016, 67, 2641-2653.	2.4	33
49	Global identification and analysis of long non-coding RNAs in diploid strawberry <i>Fragaria vesca</i> during flower and fruit development. <i>BMC Genomics</i> , 2015, 16, 815.	1.2	106
50	Novel and Recently Evolved MicroRNA Clusters Regulate Expansive <i>F-BOX</i> Gene Networks through Phased Small Interfering RNAs in Wild Diploid Strawberry. <i>Plant Physiology</i> , 2015, 169, 594-610.	2.3	73
51	Molecular basis of fruit development. <i>Frontiers in Plant Science</i> , 2015, 6, 28.	1.7	4
52	Re-annotation of the woodland strawberry (<i>Fragaria vesca</i>) genome. <i>BMC Genomics</i> , 2015, 16, 29.	1.2	60
53	Genome-wide transcriptome profiling provides insights into floral bud development of summer-flowering <i>Camellia azalea</i> . <i>Scientific Reports</i> , 2015, 5, 9729.	1.6	72
54	A model for an early role of auxin in Arabidopsis gynoecium morphogenesis. <i>Frontiers in Plant Science</i> , 2014, 5, 327.	1.7	43

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55	Distinct double flower varieties in <i>Camellia japonica</i> exhibit both expansion and contraction of C-class gene expression. <i>BMC Plant Biology</i> , 2014, 14, 288.	1.6	40
56	Floral Transcriptomes in Woodland Strawberry Uncover Developing Receptacle and Anther Gene Networks. <i>Plant Physiology</i> , 2014, 165, 1062-1075.	2.3	167
57	Highly interactive nature of flower-specific enhancers and promoters, and its potential impact on tissue-specific expression and engineering of multiple genes or agronomic traits. <i>Plant Biotechnology Journal</i> , 2014, 12, 951-962.	4.1	6
58	SGR: an online genomic resource for the woodland strawberry. <i>BMC Plant Biology</i> , 2013, 13, 223.	1.6	45
59	<i>PHOSPHATIDYLSERINE SYNTHASE1</i> is Required for Inflorescence Meristem and Organ Development in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2013, 55, 682-695.	4.1	26
60	Genome-Scale Transcriptomic Insights into Early-Stage Fruit Development in Woodland Strawberry <i>Fragaria vesca</i> . <i>Plant Cell</i> , 2013, 25, 1960-1978.	3.1	268
61	SUI-family genes encode phosphatidylserine synthases and regulate stem development in rice. <i>Planta</i> , 2013, 237, 15-27.	1.6	33
62	MicroRNA Superfamilies Descended from miR390 and Their Roles in Secondary Small Interfering RNA Biogenesis in Eudicots. <i>Plant Cell</i> , 2013, 25, 1555-1572.	3.1	141
63	Transcript Assembly and Quantification by RNA-Seq Reveals Differentially Expressed Genes between Soft-Endocarp and Hard-Endocarp Hawthorns. <i>PLoS ONE</i> , 2013, 8, e72910.	1.1	30
64	Flower and early fruit development in a diploid strawberry, <i>Fragaria vesca</i> . <i>Planta</i> , 2012, 235, 1123-1139.	1.6	105
65	LEUNIG_HOMOLOG and LEUNIG Regulate Seed Mucilage Extrusion in <i>Arabidopsis</i> . <i>Journal of Integrative Plant Biology</i> , 2011, 53, 399-408.	4.1	34
66	LEUNIG and SEUSS co-repressors regulate <i>miR172</i> expression in <i>Arabidopsis</i> flowers. <i>Development (Cambridge)</i> , 2011, 138, 2451-2456.	1.2	79
67	Recessive Antimorphic Alleles Overcome Functionally Redundant Loci to Reveal TSO1 Function in <i>Arabidopsis</i> Flowers and Meristems. <i>PLoS Genetics</i> , 2011, 7, e1002352.	1.5	35
68	Bimolecular Fluorescence Complementation (BiFC) Assay for Protein-Protein Interaction in Onion Cells Using the Helios Gene Gun. <i>Journal of Visualized Experiments</i> , 2010, , .	0.2	12
69	Novel Insights from Live-imaging in Shoot Meristem Development. <i>Journal of Integrative Plant Biology</i> , 2010, 52, 393-399.	4.1	19
70	Floral-dip Transformation of <i>Arabidopsis thaliana</i> ; to Examine <i>pTSO2::beta-glucuronidase</i> Reporter Gene Expression. <i>Journal of Visualized Experiments</i> , 2010, , .	0.2	19
71	Regulatory mechanisms for floral homeotic gene expression. <i>Seminars in Cell and Developmental Biology</i> , 2010, 21, 80-86.	2.3	77
72	The second intron of <i>AGAMOUS</i> drives carpel- and stamen-specific expression sufficient to induce complete sterility in <i>Arabidopsis</i> . <i>Plant Cell Reports</i> , 2008, 27, 855-863.	2.8	38

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73	Groucho/Tup1 family co-repressors in plant development. Trends in Plant Science, 2008, 13, 137-144.	4.3	122
74	<i>LEUNIG_HOMOLOG</i> and <i>LEUNIG</i> Perform Partially Redundant Functions during Arabidopsis Embryo and Floral Development. Plant Physiology, 2008, 147, 672-681.	2.3	55
75	APETALA1 and SEPALLATA3 interact with SEUSS to mediate transcription repression during flower development. Development (Cambridge), 2006, 133, 3159-3166.	1.2	171
76	Arabidopsis Ribonucleotide Reductases Are Critical for Cell Cycle Progression, DNA Damage Repair, and Plant Development. Plant Cell, 2006, 18, 350-365.	3.1	129
77	SEUSS and LEUNIG regulate cell proliferation, vascular development and organ polarity in Arabidopsis petals. Planta, 2006, 224, 801-811.	1.6	75
78	Global nuclear radiation monitoring using plants. Proceedings of SPIE, 2005, 9486, 119.	0.8	0
79	Repression of AGAMOUS by BELLRINGER in Floral and Inflorescence Meristems. Plant Cell, 2004, 16, 1478-1489.	3.1	126
80	Transcriptional repression of target genes by LEUNIG and SEUSS, two interacting regulatory proteins for Arabidopsis flower development. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11494-11499.	3.3	139
81	<i>SEUSS</i> , a member of a novel family of plant regulatory proteins, represses floral homeotic gene expression with <i>LEUNIG</i> . Development (Cambridge), 2002, 129, 253-263.	1.2	182
82	SEUSS, a member of a novel family of plant regulatory proteins, represses floral homeotic gene expression with LEUNIG. Development (Cambridge), 2002, 129, 253-63.	1.2	105
83	Regulation of Gynoecium Marginal Tissue Formation by LEUNIG and AINTEGUMENTA. Plant Cell, 2000, 12, 1879-1891.	3.1	113