Zhongchi Liu

List of Publications by Year
in descending order

83 papers	4,818 citations	76196 40 h-index	106150 65 g-index
91 all docs	91 docs citations	91 times ranked	4710 citing authors

#	Article	IF	Citations
1	Genome-Scale Transcriptomic Insights into Early-Stage Fruit Development in Woodland Strawberry Fragaria vesca. Plant Cell, 2013, 25, 1960-1978.	3.1	268
2	<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
3	APETALA1 and SEPALLATA3 interact with SEUSS to mediate transcription repression during flower development. Development (Cambridge), 2006, 133, 3159-3166.	1.2	171
4	Floral Transcriptomes in Woodland Strawberry Uncover Developing Receptacle and Anther Gene Networks. Plant Physiology, 2014, 165, 1062-1075.	2.3	167
5	Global identification of alternative splicing via comparative analysis of <scp>SMRT</scp>â€•and Illuminaâ€based <scp>RNA</scp>â€seq in strawberry. Plant Journal, 2017, 90, 164-176.	2.8	161
6	MicroRNA Superfamilies Descended from miR390 and Their Roles in Secondary Small Interfering RNA Biogenesis in Eudicots. Plant Cell, 2013, 25, 1555-1572.	3.1	141
7	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
8	Reduced Anthocyanins in Petioles codes for a GST anthocyanin transporter that is essential for the foliage and fruit coloration in strawberry. Journal of Experimental Botany, 2018, 69, 2595-2608.	2.4	138
9	Arabidopsis Ribonucleotide Reductases Are Critical for Cell Cycle Progression, DNA Damage Repair, and Plant Development. Plant Cell, 2006, 18, 350-365.	3.1	129
10	Repression of AGAMOUS by BELLRINGER in Floral and Inflorescence Meristems. Plant Cell, 2004, 16, 1478-1489.	3.1	126
11	Groucho/Tup1 family co-repressors in plant development. Trends in Plant Science, 2008, 13, 137-144.	4.3	122
12	Regulation of Gynoecium Marginal Tissue Formation by LEUNIG and AINTEGUMENTA. Plant Cell, 2000, 12, 1879-1891.	3.1	113
13	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. Plant Cell, 2020, 32, 3723-3749.	3.1	111
14	Global identification and analysis of long non-coding RNAs in diploid strawberry Fragaria vesca during flower and fruit development. BMC Genomics, 2015, 16, 815.	1.2	106
15	24-nt reproductive phasiRNAs are broadly present in angiosperms. Nature Communications, 2019, 10, 627.	5.8	106
16	Flower and early fruit development in a diploid strawberry, Fragaria vesca. Planta, 2012, 235, 1123-1139.	1.6	105
17	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
18	Updated annotation of the wild strawberry Fragaria vesca V4 genome. Horticulture Research, 2019, 6, 61.	2.9	102

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19	Efficient genome editing of wild strawberry genes, vector development and validation. Plant Biotechnology Journal, 2018, 16, 1868-1877.	4.1	97
20	LEUNIG and SEUSS co-repressors regulate <i>miR172</i> expression in <i>Arabidopsis</i> flowers. Development (Cambridge), 2011, 138, 2451-2456.	1.2	79
21	Regulatory mechanisms for floral homeotic gene expression. Seminars in Cell and Developmental Biology, 2010, 21, 80-86.	2.3	77
22	SEUSS and LEUNIG regulate cell proliferation, vascular development and organ polarity in Arabidopsis petals. Planta, 2006, 224, 801-811.	1.6	75
23	Novel and Recently Evolved MicroRNA Clusters Regulate Expansive <i>F-BOX</i> Gene Networks through Phased Small Interfering RNAs in Wild Diploid Strawberry. Plant Physiology, 2015, 169, 594-610.	2.3	73
24	Genome-wide transcriptome profiling provides insights into floral bud development of summer-flowering Camellia azalea. Scientific Reports, 2015, 5, 9729.	1.6	72
25	FvbHLH9 Functions as a Positive Regulator of Anthocyanin Biosynthesis by Forming a HY5â€“bHLH9 Transcription Complex in Strawberry Fruits. Plant and Cell Physiology, 2020, 61, 826-837.	1.5	72
26	Genome-scale DNA variant analysis and functional validation of a SNP underlying yellow fruit color in wild strawberry. Scientific Reports, 2016, 6, 29017.	1.6	70
27	Genome re-annotation of the wild strawberry Fragaria vesca using extensive Illumina- and SMRT-based RNA-seq datasets. DNA Research, 2018, 25, 61-70.	1.5	67
28	An eFP browser for visualizing strawberry fruit and flower transcriptomes. Horticulture Research, 2017, 4, 17029.	2.9	63
29	Genetic modulation of <i>RAP</i> alters fruit coloration in both wild and cultivated strawberry. Plant Biotechnology Journal, 2020, 18, 1550-1561.	4.1	61
30	Re-annotation of the woodland strawberry (Fragaria vesca) genome. BMC Genomics, 2015, 16, 29.	1.2	60
31	Suppressor of Runnerless Encodes a DELLA Protein that Controls Runner Formation for Asexual Reproduction in Strawberry. Molecular Plant, 2018, 11, 230-233.	3.9	60
32	Consensus Coexpression Network Analysis Identifies Key Regulators of Flower and Fruit Development in Wild Strawberry. Plant Physiology, 2018, 178, 202-216.	2.3	57
33	Reporter gene expression reveals precise auxin synthesis sites during fruit and root development in wild strawberry. Journal of Experimental Botany, 2019, 70, 563-574.	2.4	56
34	<i>LEUNIG_HOMOLOG</i>and<i>LEUNIG</i>Perform Partially Redundant Functions during Arabidopsis Embryo and Floral Development Â Â Â. Plant Physiology, 2008, 147, 672-681.	2.3	55
35	The making of virgin fruit: the molecular and genetic basis of parthenocarpy. Journal of Experimental Botany, 2018, 69, 955-962.	2.4	53
36	Loss of a highly conserved sterile alpha motif domain gene (<i>WEEP</i>) results in pendulous branch growth in peach trees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E4690-E4699.	3.3	52

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37	Application and future perspective of CRISPR/Cas9 genome editing in fruit crops. Journal of Integrative Plant Biology, 2020, 62, 269-286.	4.1	52
38	Integrated analysis of high-throughput sequencing data shows abscisic acid-responsive genes and miRNAs in strawberry receptacle fruit ripening. Horticulture Research, 2019, 6, 26.	2.9	51
39	SEUSS Integrates Gibberellin Signaling with Transcriptional Inputs from the SHR-SCR-SCL3 Module to Regulate Middle Cortex Formation in the Arabidopsis Root. Plant Physiology, 2016, 170, 1675-1683.	2.3	48
40	Conserved and novel roles of <i>miR164â€<scp>CUC</scp>2</i> regulatory module in specifying leaf and floral organ morphology in strawberry. New Phytologist, 2019, 224, 480-492.	3.5	46
41	Reannotation of the cultivated strawberry genome and establishment of a strawberry genome database. Horticulture Research, 2021, 8, 41.	2.9	46
42	SGR: an online genomic resource for the woodland strawberry. BMC Plant Biology, 2013, 13, 223.	1.6	45
43	A model for an early role of auxin in Arabidopsis gynoecium morphogenesis. Frontiers in Plant Science, 2014, 5, 327.	1.7	43
44	Distinct double flower varieties in Camellia japonica exhibit both expansion and contraction of C-class gene expression. BMC Plant Biology, 2014, 14, 288.	1.6	40
45	Gibberellin and auxin signaling genes <i>RGA1</i> and <i>ARF8</i> repress accessory fruit initiation in diploid strawberry. Plant Physiology, 2021, 185, 1059-1075.	2.3	40
46	SOL1 and SOL2 regulate fate transition and cell divisions in the Arabidopsis stomatal lineage. Development (Cambridge), 2019, 146, .	1.2	39
47	Developmental regulation of stolon and rhizome. Current Opinion in Plant Biology, 2021, 59, 101970.	3.5	39
48	The second intron of AGAMOUS drives carpel- and stamen-specific expression sufficient to induce complete sterility in Arabidopsis. Plant Cell Reports, 2008, 27, 855-863.	2.8	38
49	<i>Arabidopsis</i> TSO1 and MYB3R1 form a regulatory module to coordinate cell proliferation with differentiation in shoot and root. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3045-E3054.	3.3	38
50	Developmental Mechanisms of Fleshy Fruit Diversity in Rosaceae. Annual Review of Plant Biology, 2020, 71, 547-573.	8.6	38
51	Recessive Antimorphic Alleles Overcome Functionally Redundant Loci to Reveal TSO1 Function in Arabidopsis Flowers and Meristems. PLoS Genetics, 2011, 7, e1002352.	1.5	35
52	LEUNIG_HOMOLOG and LEUNIG Regulate Seed Mucilage Extrusion inâ€,ArabidopsisF. Journal of Integrative Plant Biology, 2011, 53, 399-408.	4.1	34
53	SUI-family genes encode phosphatidylserine synthases and regulate stem development in rice. Planta, 2013, 237, 15-27.	1.6	33
54	Phylogenetic tree-informed microRNAome analysis uncovers conserved and lineage-specific miRNAs in<i>Camellia</i>during floral organ development. Journal of Experimental Botany, 2016, 67, 2641-2653.	2.4	33

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55	Transcript Assembly and Quantification by RNA-Seq Reveals Differentially Expressed Genes between Soft-Endocarp and Hard-Endocarp Hawthorns. PLoS ONE, 2013, 8, e72910.	1.1	30
56	The MADS-box gene FveSEP3 plays essential roles in flower organogenesis and fruit development in woodland strawberry. Horticulture Research, 2021, 8, 247.	2.9	30
57	Transcriptome sequencing reveals role of light in promoting anthocyanin accumulation of strawberry fruit. Plant Growth Regulation, 2018, 86, 121-132.	1.8	29
58	Gibberellic acid induced parthenocarpic â€˜Honeycrispâ€™ apples (Malus domestica) exhibit reduced ovary width and lower acidity. Horticulture Research, 2019, 6, 41.	2.9	29
59	Mechanism of fertilization-induced auxin synthesis in the endosperm for seed and fruit development. Nature Communications, 2022, 13, .	5.8	28
60	<i>PHOSPHATIDYLSERINE SYNTHASE1</i> is Required for Inflorescence Meristem and Organ Development in <i>Arabidopsis</i>. Journal of Integrative Plant Biology, 2013, 55, 682-695.	4.1	26
61	Global gene expression defines faded whorl specification of double flower domestication in Camellia. Scientific Reports, 2017, 7, 3197.	1.6	21
62	GRAS transcription factor <i>LOSS OF AXILLARY MERISTEMS</i> is essential for stamen and runner formation in wild strawberry. Plant Physiology, 2021, 186, 1970-1984.	2.3	21
63	A MFS-like plasma membrane transporter required for Leishmania virulence protects the parasites from iron toxicity. PLoS Pathogens, 2018, 14, e1007140.	2.1	20
64	Novel Insights from Liveâ€imaging in Shoot Meristem Development. Journal of Integrative Plant Biology, 2010, 52, 393-399.	4.1	19
65	Floral-dip Transformation of Arabidopsis thaliana to Examine pTSO2::β-glucuronidase Reporter Gene Expression. Journal of Visualized Experiments, 2010, , .	0.2	19
66	Woodland strawberry axillary bud fate is dictated by a crosstalk of environmental and endogenous factors. Plant Physiology, 2021, 187, 1221-1234.	2.3	18
67	Bimolecular Fluorescence Complementation (BiFC) Assay for Protein-Protein Interaction in Onion Cells Using the Helios Gene Gun. Journal of Visualized Experiments, 2010, , .	0.2	12
68	Plant genetics enters the nano age?. Journal of Integrative Plant Biology, 2018, 60, 446-447.	4.1	11
69	Bacterial diketopiperazines stimulate diatom growth and lipid accumulation. Plant Physiology, 2021, 186, 1159-1170.	2.3	11
70	Gene Expression Profiling of the Shoot Meristematic Tissues in Woodland Strawberry Fragaria vesca. Frontiers in Plant Science, 2019, 10, 1624.	1.7	9
71	Chromosome-Scale Genome for a Red-Fruited, Perpetual Flowering and Runnerless Woodland Strawberry (Fragaria vesca). Frontiers in Genetics, 2021, 12, 671371.	1.1	8
72	Highly interactive nature of flowerâ€specific enhancers and promoters, and its potential impact on tissueâ€specific expression and engineering of multiple genes or agronomic traits. Plant Biotechnology Journal, 2014, 12, 951-962.	4.1	6

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73	Identification of genes preferentially expressed in wild strawberry receptacle fruit and demonstration of their promoter activities. Horticulture Research, 2019, 6, 50.	2.9	6
74	An Easy-to-Follow Pipeline for Long Noncoding RNA Identification: A Case Study in Diploid Strawberry Fragaria vesca. Methods in Molecular Biology, 2019, 1933, 223-243.	0.4	6
75	An Atlas of Genomic Resources for Studying Rosaceae Fruits and Ornamentals. Frontiers in Plant Science, 2021, 12, 644881.	1.7	5
76	Molecular basis of fruit development. Frontiers in Plant Science, 2015, 6, 28.	1.7	4
77	Pyrite cloning: a single tube and programmed reaction cloning with restriction enzymes. Plant Methods, 2018, 14, 91.	1.9	4
78	Comparative transcriptomic analysis of apple and peach fruits: insights into fruit type specification. Plant Journal, 2022, 109, 1614-1629.	2.8	4
79	Plant development: Unveiling cytokininâ€™s role in the end of flowering. Current Biology, 2022, 32, R168-R170.	1.8	1
80	Global nuclear radiation monitoring using plants. Proceedings of SPIE, 2005, 9486, 119.	0.8	0
81	Nuclear Radiation Monitoring Using Plants. Journal of Nuclear Engineering and Radiation Science, 2018, 4, .	0.2	0
82	Editorial overview: Not your average plant: shining a light on developmental diversity. Current Opinion in Plant Biology, 2021, 59, 102016.	3.5	0
83	Editorial: Rosaceae Fruit Development and Quality. Frontiers in Plant Science, 2021, 12, 837300.	1.7	0