Meng Zhang

List of Publications by Year
in descending order

41 papers	1,402 citations	430754 18 h-index	345118 36 g-index
45 all docs	45 docs citations	45 times ranked	1660 citing authors

#	Article	IF	Citations
1	<i>DGAT1</i>and<i>PDAT1</i>Acyltransferases Have Overlapping Functions in<i>Arabidopsis</i>Triacylglycerol Biosynthesis and Are Essential for Normal Pollen and Seed Development Â. Plant Cell, 2010, 21, 3885-3901.	3.1	407
2	MYB89 Transcription Factor Represses Seed Oil Accumulation. Plant Physiology, 2017, 173, 1211-1225.	2.3	87
3	<i><scp>FUSCA</scp>3</i> activates triacylglycerol accumulation in Arabidopsis seedlings and tobacco <scp>BY</scp>2 cells. Plant Journal, 2016, 88, 95-107.	2.8	71
4	Evaluation of the reference genes for expression analysis using quantitative realâ€time polymerase chain reaction in the green peach aphid, <i>Myzus persicae</i>. Insect Science, 2017, 24, 222-234.	1.5	69
5	Two jasmonate-responsive factors, TcERF12 and TcERF15, respectively act as repressor and activator of tasy gene of taxol biosynthesis in Taxus chinensis. Plant Molecular Biology, 2015, 89, 463-473.	2.0	57
6	Reducing Isozyme Competition Increases Target Fatty Acid Accumulation in Seed Triacylglycerols of Transgenic Arabidopsis Â. Plant Physiology, 2015, 168, 36-46.	2.3	51
7	An annotated database of Arabidopsis mutants of acyl lipid metabolism. Plant Cell Reports, 2015, 34, 519-532.	2.8	44
8	TcMYC2a, a Basic Helixâ€“Loopâ€“Helix Transcription Factor, Transduces JA-Signals and Regulates Taxol Biosynthesis in Taxus chinensis. Frontiers in Plant Science, 2018, 9, 863.	1.7	43
9	Transcriptome-wide identification and screening of WRKY factors involved in the regulation of taxol biosynthesis in Taxus chinensis. Scientific Reports, 2018, 8, 5197.	1.6	41
10	MYC2, MYC3, and MYC4 function redundantly in seed storage protein accumulation in Arabidopsis. Plant Physiology and Biochemistry, 2016, 108, 63-70.	2.8	40
11	Genomic analysis and expression investigation of caleosin gene family in Arabidopsis. Biochemical and Biophysical Research Communications, 2014, 448, 365-371.	1.0	37
12	Transcriptome Assembly and Systematic Identification of Novel Cytochrome P450s in Taxus chinensis. Frontiers in Plant Science, 2017, 8, 1468.	1.7	37
13	Deciphering the Mechanism of Î²-Aminobutyric Acid-Induced Resistance in Wheat to the Grain Aphid, Sitobion avenae. PLoS ONE, 2014, 9, e91768.	1.1	35
14	High-throughput sequencing reveals miRNA effects on the primary and secondary production properties in long-term subcultured Taxus cells. Frontiers in Plant Science, 2015, 6, 604.	1.7	34
15	Insulin-Related Peptide 5 is Involved in Regulating Embryo Development and Biochemical Composition in Pea Aphid with Wing Polyphenism. Frontiers in Physiology, 2016, 7, 31.	1.3	30
16	MOLECULAR CLONING, EXPRESSION PATTERN OF MULTIDRUG RESISTANCE ASSOCIATED PROTEIN 1 (MRP1,) Tj ETQq0 0 0 rgBT /Overlc BIRD CHERRYâ€OAT APHID. Archives of Insect Biochemistry and Physiology, 2016, 92, 65-84.	0.6	26
17	Strong co-suppression impedes an increase in polyunsaturated fatty acids in seeds overexpressing <i>FAD2</i>. Journal of Experimental Botany, 2019, 70, 985-994.	2.4	26
18	WRINKLED1 homologs highly and functionally express in oil-rich endosperms of oat and castor. Plant Science, 2019, 287, 110193.	1.7	24

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19	Enhancing Taxol Biosynthesis by Overexpressing a 9-Cis-Epoxycarotenoid Dioxygenase Gene in Transgenic Cell Lines of Taxus chinensis. Plant Molecular Biology Reporter, 2012, 30, 1125-1130.	1.0	19
20	Mechanisms and effective control of physiological browning phenomena in plant cell cultures. Physiologia Plantarum, 2016, 156, 13-28.	2.6	18
21	Evaluation of duplicated reference genes for quantitative real-time PCR analysis in genome unknown hexaploid oat (Avena sativa L.). Plant Methods, 2020, 16, 138.	1.9	17
22	Genome-wide analysis reveals the evolution and structural features of WRINKLED1 in plants. Molecular Genetics and Genomics, 2019, 294, 329-341.	1.0	16
23	ABA-INSENSITIVE 3 with or without FUSCA3 highly up-regulates lipid droplet proteins and activates oil accumulation. Journal of Experimental Botany, 2022, 73, 2077-2092.	2.4	16
24	Identification, duplication, evolution and expression analyses of caleosins in Brassica plants and Arabidopsis subspecies. Molecular Genetics and Genomics, 2016, 291, 971-988.	1.0	15
25	Molecular, structural, and phylogenetic analyses of Taxus chinensis JAZs. Gene, 2017, 620, 66-74.	1.0	15
26	Molecular Cloning and Characterization of Two 9-Lipoxygenase Genes from Taxus chinensis. Plant Molecular Biology Reporter, 2012, 30, 1283-1290.	1.0	13
27	A 3-ketoacyl-CoA synthase 11 (KCS11) homolog from Malania oleifera synthesizes nervonic acid in plants rich in 11Z-eicosenoic acid. Tree Physiology, 2021, 41, 331-342.	1.4	13
28	Transcriptome Analysis Reveals Candidate Genes for Petroselinic Acid Biosynthesis in Fruits of <i>Coriandrum sativum</i> L.. Journal of Agricultural and Food Chemistry, 2020, 68, 5507-5520.	2.4	12
29	New different origins and evolutionary processes of AP2/EREBP transcription factors in Taxus chinensis. BMC Plant Biology, 2019, 19, 413.	1.6	11
30	Accelerating gene function discovery by rapid phenotyping of fatty acid composition and oil content of single transgenic T₁ Arabidopsis and camelina seeds. Plant Direct, 2020, 4, e00253.	0.8	11
31	Cloning of eight Rhopalosiphum padi (Hemiptera: Aphididae) nAChR subunit genes and mutation detection of the î²1 subunit in field samples from China. Pesticide Biochemistry and Physiology, 2016, 132, 89-95.	1.6	9
32	Investigation of Plant Species with Identified Seed Oil Fatty Acids in Chinese Literature and Analysis of Five Unsurveyed Chinese Endemic Species. Frontiers in Plant Science, 2017, 8, 224.	1.7	9
33	Salicylic Acid-Responsive Factor TcWRKY33 Positively Regulates Taxol Biosynthesis in Taxus chinensis in Direct and Indirect Ways. Frontiers in Plant Science, 2021, 12, 697476.	1.7	9
34	Transcriptional reprogramming strategies and miRNA-mediated regulation networks of Taxus media induced into callus cells from tissues. BMC Genomics, 2020, 21, 168.	1.2	8
35	Concerted increases of <i>FAE1</i> expression level and substrate availability improve and singularize the production of veryâ€longâ€chain fatty acids in Arabidopsis seeds. Plant Direct, 2021, 5, e00331.	0.8	8
36	BnDGAT1s Function Similarly in Oil Deposition and Are Expressed with Uniform Patterns in Tissues of Brassica napus. Frontiers in Plant Science, 2017, 8, 2205.	1.7	7

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37	Multiple caleosins have overlapping functions in oil accumulation and embryo development. Journal of Experimental Botany, 2022, 73, 3946-3962.	2.4	6
38	A novel glycosylated solution from Dioscorea zingiberensis C.H. Wright significantly improves the solvent productivity of Clostridium beijerinckii. Bioresource Technology, 2017, 241, 317-324.	4.8	3
39	Genome-wide characterization and phylogenetic and expression analyses of the caleosin gene family in soybean, common bean and barrel medic. Archives of Biological Sciences, 2016, 68, 575-585.	0.2	3
40	New insights into phenotypic heterogeneity for the distinct lipid accumulation of Schizochytrium sp. H016. , 2022, 15, 33.		3
41	Functional characterization of Brassica napus DNA topoisomerase Iα-1 and its effect on flowering time when expressed in Arabidopsis thaliana. Biochemical and Biophysical Research Communications, 2017, 486, 124-129.	1.0	2