

Mei-Liang Zhou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/83878/publications.pdf>

Version: 2024-02-01

66
papers

2,783
citations

201385

27
h-index

189595

50
g-index

67
all docs

67
docs citations

67
times ranked

2716
citing authors

#	ARTICLE	IF	CITATIONS
1	Acceleration of the genetic gain for nutraceutical improvement of adlay (<i>Coix</i> L.) through genomic approaches: current status and future prospects. <i>Food Reviews International</i> , 2023, 39, 5377-5401.	4.3	2
2	Tartary Buckwheat: An Under-utilized Edible and Medicinal Herb for Food and Nutritional Security. <i>Food Reviews International</i> , 2022, 38, 440-454.	4.3	32
3	MeJA-responsive bHLH transcription factor LjbHLH7 regulates cyanogenic glucoside biosynthesis in <i>Lotus japonicus</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 2650-2665.	2.4	12
4	Buckwheat in Tissue Culture Research: Current Status and Future Perspectives. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2298.	1.8	9
5	Metal Tolerance Protein Encoding Gene Family in <i>Fagopyrum tartaricum</i> : Genome-Wide Identification, Characterization and Expression under Multiple Metal Stresses. <i>Plants</i> , 2022, 11, 850.	1.6	3
6	Rutin Promotes Pancreatic Cancer Cell Apoptosis by Upregulating miRNA-877-3p Expression. <i>Molecules</i> , 2022, 27, 2293.	1.7	8
7	Identification of Tartary Buckwheat Varieties Suitable for Forage via Nutrient Value Analysis at Different Growth Stages. <i>International Journal of Plant Biology</i> , 2022, 13, 31-43.	1.1	0
8	Inflorescence Transcriptome Sequencing and Development of New EST-SSR Markers in Common Buckwheat (<i>Fagopyrum esculentum</i>). <i>Plants</i> , 2022, 11, 742.	1.6	6
9	Beyond a reference genome: pangenomes and population genomics of underutilized and orphan crops for future food and nutrition security. <i>New Phytologist</i> , 2022, 234, 1583-1597.	3.5	23
10	JA-induced FtBPM3 accumulation promotes FtERF ^{EAR3} degradation and rutin biosynthesis in Tartary buckwheat. <i>Plant Journal</i> , 2022, 111, 323-334.	2.8	10
11	Comparison of buckwheat genomes reveals the genetic basis of metabolomic divergence and ecotype differentiation. <i>New Phytologist</i> , 2022, 235, 1927-1943.	3.5	18
12	Roles of Arbuscular mycorrhizal Fungi as a Biocontrol Agent in the Control of Plant Diseases. <i>Microorganisms</i> , 2022, 10, 1266.	1.6	43
13	Treasure from garden: Bioactive compounds of buckwheat. <i>Food Chemistry</i> , 2021, 335, 127653.	4.2	117
14	First Report of <i>Nigrospora osmanthi</i> Causing Leaf Spot on Tartary Buckwheat in China. <i>Plant Disease</i> , 2021, 105, 1227-1227.	0.7	4
15	First Report of <i>Rhizoctonia solani</i> AG-4 HGI Causing Stem Canker on <i>Fagopyrum tataricum</i> (Tartary Buckwheat) in China. <i>Plant Disease</i> , 2021, 105, 505-505.	0.7	5
16	Resequencing of global Tartary buckwheat accessions reveals multiple domestication events and key loci associated with agronomic traits. <i>Genome Biology</i> , 2021, 22, 23.	3.8	69
17	<i>Fagopyrum longistylum</i> (Polygonaceae), a new species from Sichuan, China. <i>Phytotaxa</i> , 2021, 482, 173-182.	0.1	7
18	<i>Streptomyces liangshanensis</i> sp. nov., a novel actinomycete isolated from rhizosphere soil of <i>Fagopyrum tataricum</i> . <i>Archives of Microbiology</i> , 2021, 203, 3055-3059.	1.0	6

#	ARTICLE	IF	CITATIONS
19	FtBPM3 modulates the orchestration of FtMYB11-mediated flavonoids biosynthesis in Tartary buckwheat. <i>Plant Biotechnology Journal</i> , 2021, 19, 1285-1287.	4.1	14
20	First Report of <i>Alternaria alternata</i> Causing Leaf Spot of Tartary Buckwheat in China. <i>Plant Disease</i> , 2021, 105, 3751.	0.7	0
21	Elucidation of the Regulatory Network of Flavonoid Biosynthesis by Profiling the Metabolome and Transcriptome in Tartary Buckwheat. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 7218-7229.	2.4	25
22	Ubiquitin Proteins and the Orchestration of Transcription Factors Activity. <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 366-377.	2.7	1
23	Jasmonic acid-responsive RRTF1 transcription factor controls <i>DTX18</i> gene expression in hydroxycinnamic acid amide secretion. <i>Plant Physiology</i> , 2021, 185, 369-384.	2.3	9
24	Breeding Buckwheat for Increased Levels and Improved Quality of Protein. <i>Plants</i> , 2021, 10, 14.	1.6	22
25	JAZ8 Interacts With VirE3 Attenuating Agrobacterium Mediated Root Tumorigenesis. <i>Frontiers in Plant Science</i> , 2021, 12, 685533.	1.7	6
26	The Complete Chloroplast Genome Sequences of Eight Fagopyrum Species: Insights Into Genome Evolution and Phylogenetic Relationships. <i>Frontiers in Plant Science</i> , 2021, 12, 799904.	1.7	17
27	Newly discovered tetraploid Fagopyrum homotropicum in Tibet, China. <i>Phytotaxa</i> , 2021, 528, 202-208.	0.1	0
28	Effects of phosphate fertiliser on the physicochemical properties of Tartary buckwheat (Fagopyrum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	4.2	14
29	Strategic enhancement of genetic gain for nutraceutical development in buckwheat: A genomics-driven perspective. <i>Biotechnology Advances</i> , 2020, 39, 107479.	6.0	67
30	Breeding buckwheat for nutritional quality. <i>Breeding Science</i> , 2020, 70, 67-73.	0.9	47
31	Fagopyrum esculentum ssp. ancestrale-A Hybrid Species Between Diploid F. cymosum and F. esculentum. <i>Frontiers in Plant Science</i> , 2020, 11, 1073.	1.7	6
32	MYB Transcription Repressors Regulate Plant Secondary Metabolism. <i>Critical Reviews in Plant Sciences</i> , 2019, 38, 159-170.	2.7	65
33	Jasmonic Acid Signaling Pathway in Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2479.	1.8	417
34	Ft MYB 16 interacts with Ftimportin-1 to regulate rutin biosynthesis in tartary buckwheat. <i>Plant Biotechnology Journal</i> , 2019, 17, 1479-1481.	4.1	20
35	Revisiting the versatile buckwheat: reinvigorating genetic gains through integrated breeding and genomics approach. <i>Planta</i> , 2019, 250, 783-801.	1.6	79
36	Jasmonate-responsive MYB factors spatially repress rutin biosynthesis in Fagopyrum tataricum. <i>Journal of Experimental Botany</i> , 2018, 69, 1955-1966.	2.4	74

#	ARTICLE	IF	CITATIONS
37	Biosynthesis and regulation of cyanogenic glycoside production in forage plants. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9-16.	1.7	31
38	Co-expression of PeDREB2a and KcERF Improves Drought and Salt Tolerance in Transgenic <i>Lotus corniculatus</i> . <i>Journal of Plant Growth Regulation</i> , 2018, 37, 550-559.	2.8	9
39	Description of Cultivated Tartary Buckwheat. , 2018, , 45-52.		2
40	Integrated omics data of two annual ryegrass (<i>Lolium multiflorum</i> L.) genotypes reveals core metabolic processes under drought stress. <i>BMC Plant Biology</i> , 2018, 18, 26.	1.6	30
41	Jasmonic acid/ethylene signaling coordinates hydroxycinnamic acid amides biosynthesis through <i>ORA59</i> transcription factor. <i>Plant Journal</i> , 2018, 95, 444-457.	2.8	63
42	<i>Fagopyrum longzhoushanense</i> , a new species of Polygonaceae from Sichuan, China. <i>Phytotaxa</i> , 2017, 291, 73.	0.1	8
43	LNK1 and LNK2 Corepressors Interact with the MYB3 Transcription Factor in Phenylpropanoid Biosynthesis. <i>Plant Physiology</i> , 2017, 174, 1348-1358.	2.3	95
44	FtSAD2 and FtJAZ1 regulate activity of the FtMYB11 transcription repressor of the phenylpropanoid pathway in <i>Fagopyrum tataricum</i> . <i>New Phytologist</i> , 2017, 216, 814-828.	3.5	66
45	Comparative Analysis of Four Buckwheat Species Based on Morphology and Complete Chloroplast Genome Sequences. <i>Scientific Reports</i> , 2017, 7, 6514.	1.6	34
46	Transcriptional Profiles of Drought-Related Genes in Modulating Metabolic Processes and Antioxidant Defenses in <i>Lolium multiflorum</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 519.	1.7	81
47	Jasmonate-responsive transcription factors regulating plant secondary metabolism. <i>Biotechnology Advances</i> , 2016, 34, 441-449.	6.0	346
48	Identification of JAZ1-MYC2 Complex in <i>Lotus corniculatus</i> . <i>Journal of Plant Growth Regulation</i> , 2016, 35, 440-448.	2.8	4
49	Plantlet Regeneration of Tartary Buckwheat (<i>Fagopyrum tataricum</i> Gaertn.) in Vitro Tissue Cultures. <i>Protein and Peptide Letters</i> , 2016, 23, 468-477.	0.4	4
50	The <i>Agrobacterium tumefaciens</i> virulence protein VirE3 is a transcriptional activator of the <i>VBF</i> gene. <i>Plant Journal</i> , 2015, 84, 914-924.	2.8	27
51	Ectopic Expression of <i>Fagopyrum tataricum</i> FtMYB12 Improves Cold Tolerance in <i>Arabidopsis thaliana</i> . <i>Journal of Plant Growth Regulation</i> , 2015, 34, 362-371.	2.8	31
52	High-efficiency <i>Agrobacterium</i> -mediated transformation of <i>Lotus corniculatus</i> L. using phosphomannose isomerase positive selection. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 121, 413-422.	1.2	12
53	<i>Fagopyrum luojishanense</i> , a New Species of Polygonaceae from Sichuan, China. <i>Novon</i> , 2015, 24, 22-26.	0.3	19
54	Production and transcriptional regulation of proanthocyanidin biosynthesis in forage legumes. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 3797-3806.	1.7	23

#	ARTICLE	IF	CITATIONS
55	Changing a conserved amino acid in R2R3-MYB transcription repressors results in cytoplasmic accumulation and abolishes their repressive activity in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2015, 84, 395-403.	2.8	59
56	<i>Fagopyrum hailuogouense</i> (Polygonaceae), One New Species from Sichuan, China. <i>Novon</i> , 2015, 24, 222-224.	0.3	16
57	Genome-wide analysis of AP2/ERF family genes from <i>Lotus corniculatus</i> shows LcERF054 enhances salt tolerance. <i>Functional and Integrative Genomics</i> , 2014, 14, 453-466.	1.4	55
58	Phylogenetic relationship of four new species related to southwestern Sichuan <i>Fagopyrum</i> based on morphological and molecular characterization. <i>Biochemical Systematics and Ecology</i> , 2014, 57, 403-409.	0.6	17
59	Cotton proteomics for deciphering the mechanism of environment stress response and fiber development. <i>Journal of Proteomics</i> , 2014, 105, 74-84.	1.2	34
60	Bioactive compounds in functional buckwheat food. <i>Food Research International</i> , 2012, 49, 389-395.	2.9	210
61	Improvement of drought and salt tolerance in <i>Arabidopsis</i> and <i>Lotus corniculatus</i> by overexpression of a novel DREB transcription factor from <i>Populus euphratica</i> . <i>Gene</i> , 2012, 506, 10-17.	1.0	63
62	Genetic diversity of four new species related to southwestern Sichuan buckwheats as revealed by karyotype, ISSR and allozyme characterization. <i>Plant Systematics and Evolution</i> , 2012, 298, 751-759.	0.3	29
63	<i>Fagopyrum wenchuanense</i> and <i>Fagopyrum qiangcai</i> , Two New Species of Polygonaceae from Sichuan, China. <i>Novon</i> , 2011, 21, 256-261.	0.3	27
64	Soybean transcription factor GmMYBZ2 represses catharanthine biosynthesis in hairy roots of <i>Catharanthus roseus</i> . <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1095-1105.	1.7	32
65	Transcriptional response of the catharanthine biosynthesis pathway to methyl jasmonate/nitric oxide elicitation in <i>Catharanthus roseus</i> hairy root culture. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 737-750.	1.7	75
66	<i>Fagopyrum pugense</i> (Polygonaceae), a New Species from Sichuan, China. <i>Novon</i> , 2010, 20, 239-242.	0.3	24