

Jingyin Yu

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

5,981
citations

159585

30
h-index

182427

51
g-index

52
all docs

52
docs citations

52
times ranked

5442
citing authors

#	ARTICLE	IF	CITATIONS
1	High-resolution temporal transcriptome sequencing unravels ERF and WRKY as the master players in the regulatory networks underlying sesame responses to waterlogging and recovery. <i>Genomics</i> , 2021, 113, 276-290.	2.9	21
2	Sinbase 2.0: An Updated Database to Study Multi-Omics in <i>Sesamum indicum</i> . <i>Plants</i> , 2021, 10, 272.	3.5	6
3	Transcriptome Dynamics during Black and White Sesame (<i>Sesamum indicum</i> L.) Seed Development and Identification of Candidate Genes Associated with Black Pigmentation. <i>Genes</i> , 2020, 11, 1399.	2.4	25
4	Transcriptomic profiling of sesame during waterlogging and recovery. <i>Scientific Data</i> , 2019, 6, 204.	5.3	18
5	Transcriptomic and metabolomic profiling of drought-tolerant and susceptible sesame genotypes in response to drought stress. <i>BMC Plant Biology</i> , 2019, 19, 267.	3.6	162
6	Gene expression profiles that shape high and low oil content sesames. <i>BMC Genetics</i> , 2019, 20, 45.	2.7	18
7	Transcriptome and metabolome analyses of two contrasting sesame genotypes reveal the crucial biological pathways involved in rapid adaptive response to salt stress. <i>BMC Plant Biology</i> , 2019, 19, 66.	3.6	98
8	The genetic basis of drought tolerance in the high oil crop <i>Sesamum indicum</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 1788-1803.	8.3	63
9	Insight into the evolution and functional characteristics of the pan-genome assembly from sesame landraces and modern cultivars. <i>Plant Biotechnology Journal</i> , 2019, 17, 881-892.	8.3	79
10	Syntenic quantitative trait loci and genomic divergence for <i>Sclerotinia</i> resistance and flowering time in <i>Brassica napus</i> . <i>Journal of Integrative Plant Biology</i> , 2019, 61, 75-88.	8.5	34
11	Genome-Wide Identification of Flowering-Time Genes in Brassica Species and Reveals a Correlation between Selective Pressure and Expression Patterns of Vernalization-Pathway Genes in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3632.	4.1	20
12	Genome-Wide Association Studies of 39 Seed Yield-Related Traits in Sesame (<i>Sesamum indicum</i> L.). <i>International Journal of Molecular Sciences</i> , 2018, 19, 2794.	4.1	30
13	Genome-wide identification and comprehensive analysis of the NAC transcription factor family in <i>Sesamum indicum</i> . <i>PLoS ONE</i> , 2018, 13, e0199262.	2.5	29
14	Identification and characterization of the bZIP transcription factor family and its expression in response to abiotic stresses in sesame. <i>PLoS ONE</i> , 2018, 13, e0200850.	2.5	57
15	Genetic dissection and fine mapping of a novel dt gene associated with determinate growth habit in sesame. <i>BMC Genetics</i> , 2018, 19, 38.	2.7	16
16	Dynamic transcriptome landscape of sesame (<i>Sesamum indicum</i> L.) under progressive drought and after rewatering. <i>Genomics Data</i> , 2017, 11, 122-124.	1.3	24
17	Development of SSR markers and identification of major quantitative trait loci controlling shelling percentage in cultivated peanut (<i>Arachis hypogaea</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1635-1648.	3.6	48
18	The high-quality genome of <i>Brassica napus</i> cultivar 'ZS11' reveals the introgression history in semi-winter morphotype. <i>Plant Journal</i> , 2017, 92, 452-468.	5.7	233

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19	Transcriptomic, biochemical and physio-anatomical investigations shed more light on responses to drought stress in two contrasting sesame genotypes. <i>Scientific Reports</i> , 2017, 7, 8755.	3.3	62
20	SesameFG: an integrated database for the functional genomics of sesame. <i>Scientific Reports</i> , 2017, 7, 2342.	3.3	22
21	Genome evolutionary dynamics followed by diversifying selection explains the complexity of the <i>Sesamum indicum</i> genome. <i>BMC Genomics</i> , 2017, 18, 257.	2.8	17
22	Genome-wide analysis of UDP-glycosyltransferase super family in <i>Brassica rapa</i> and <i>Brassica oleracea</i> reveals its evolutionary history and functional characterization. <i>BMC Genomics</i> , 2017, 18, 474.	2.8	54
23	The Emerging Oilseed Crop <i>Sesamum indicum</i> Enters the "Omics" Era. <i>Frontiers in Plant Science</i> , 2017, 8, 1154.	3.6	107
24	Development of Highly Informative Genome-Wide Single Sequence Repeat Markers for Breeding Applications in Sesame and Construction of a Web Resource: SisatBase. <i>Frontiers in Plant Science</i> , 2017, 8, 1470.	3.6	29
25	Evolutionary history and functional divergence of the cytochrome P450 gene superfamily between <i>Arabidopsis thaliana</i> and <i>Brassica</i> species uncover effects of whole genome and tandem duplications. <i>BMC Genomics</i> , 2017, 18, 733.	2.8	37
26	Genome-wide analysis of WRKY gene family in the sesame genome and identification of the WRKY genes involved in responses to abiotic stresses. <i>BMC Plant Biology</i> , 2017, 17, 152.	3.6	94
27	PMDBase: a database for studying microsatellite DNA and marker development in plants. <i>Nucleic Acids Research</i> , 2017, 45, D1046-D1053.	14.5	46
28	Identification of Sesame Genomic Variations from Genome Comparison of Landrace and Variety. <i>Frontiers in Plant Science</i> , 2016, 7, 1169.	3.6	48
29	Transcriptomic comparison between <i>Brassica oleracea</i> and rice (<i>Oryza sativa</i>) reveals diverse modulations on cell death in response to <i>Sclerotinia sclerotiorum</i> . <i>Scientific Reports</i> , 2016, 6, 33706.	3.3	11
30	Insight into the AP2/ERF transcription factor superfamily in sesame and expression profiling of DREB subfamily under drought stress. <i>BMC Plant Biology</i> , 2016, 16, 171.	3.6	116
31	Updated sesame genome assembly and fine mapping of plant height and seed coat color QTLs using a new high-density genetic map. <i>BMC Genomics</i> , 2016, 17, 31.	2.8	84
32	Tolerant and Susceptible Sesame Genotypes Reveal Waterlogging Stress Response Patterns. <i>PLoS ONE</i> , 2016, 11, e0149912.	2.5	42
33	EST-based in silico identification and in vitro test of antimicrobial peptides in <i>Brassica napus</i> . <i>BMC Genomics</i> , 2015, 16, 653.	2.8	7
34	PTGBase: an integrated database to study tandem duplicated genes in plants. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	46
35	ocsESTdb: a database of oil crop seed EST sequences for comparative analysis and investigation of a global metabolic network and oil accumulation metabolism. <i>BMC Plant Biology</i> , 2015, 15, 19.	3.6	15
36	Genome-wide identification and analysis of the MADS-box gene family in sesame. <i>Gene</i> , 2015, 569, 66-76.	2.2	37

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37	Sinbase: An Integrated Database to Study Genomics, Genetics and Comparative Genomics in <i>Sesamum indicum</i> . <i>Plant and Cell Physiology</i> , 2015, 56, e2-e2.	3.1	46
38	Identification of a Novel Proline-Rich Antimicrobial Peptide from <i>Brassica napus</i> . <i>PLoS ONE</i> , 2015, 10, e0137414.	2.5	31
39	Genome-wide comparative analysis of NBS-encoding genes between <i>Brassica</i> species and <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2014, 15, 3.	2.8	147
40	Cysteine Protease 51 (CP51), an anther-specific cysteine protease gene, is essential for pollen exine formation in <i>Arabidopsis</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 119, 383-397.	2.3	26
41	Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. <i>Genome Biology</i> , 2014, 15, R39.	9.6	245
42	Genome-Wide Microsatellite Characterization and Marker Development in the Sequenced <i>Brassica</i> Crop Species. <i>DNA Research</i> , 2014, 21, 53-68.	3.4	71
43	BnEPFL6, an EPIDERMAL PATTERNING FACTOR-LIKE (EPFL) secreted peptide gene, is required for filament elongation in <i>Brassica napus</i> . <i>Plant Molecular Biology</i> , 2014, 85, 505-517.	3.9	7
44	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
45	Comprehensive analysis of RNA-seq data reveals the complexity of the transcriptome in <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2013, 14, 689.	2.8	172
46	Bolbase: a comprehensive genomics database for <i>Brassica oleracea</i> . <i>BMC Genomics</i> , 2013, 14, 664.	2.8	99
47	Transcriptome profile analysis of young floral buds of fertile and sterile plants from the self-pollinated offspring of the hybrid between novel restorer line NR1 and Nsa CMS line in <i>Brassica napus</i> . <i>BMC Genomics</i> , 2013, 14, 26.	2.8	77
48	Shifts in the evolutionary rate and intensity of purifying selection between two <i>Brassica</i> genomes revealed by analyses of orthologous transposons and relics of a whole genome triplication. <i>Plant Journal</i> , 2013, 76, 211-222.	5.7	38
49	Functional Identification and Characterization of the <i>Brassica Napus</i> Transcription Factor Gene BnAP2, the Ortholog of <i>Arabidopsis Thaliana</i> APETALA2. <i>PLoS ONE</i> , 2012, 7, e33890.	2.5	28
50	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
51	PMRD: plant microRNA database. <i>Nucleic Acids Research</i> , 2010, 38, D806-D813.	14.5	326