

Gibum Yi

List of Publications by Year in descending order

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34
papers

1,091
citations

623734

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docs citations

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times ranked

1544
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#	ARTICLE	IF	CITATIONS
1	Divergent Roles of a Pair of Homologous Jumonji/Zinc-Finger Class Transcription Factor Proteins in the Regulation of Arabidopsis Flowering Time. <i>Plant Cell</i> , 2004, 16, 2601-2613.	6.6	246
2	Exploitation of pepper EST SSRs and an SSR-based linkage map. <i>Theoretical and Applied Genetics</i> , 2006, 114, 113-130.	3.6	175
3	Regulation of aleurone development in cereal grains. <i>Journal of Experimental Botany</i> , 2011, 62, 1669-1675.	4.8	115
4	Maize <i>opaque5</i> Encodes Monogalactosyldiacylglycerol Synthase and Specifically Affects Galactolipids Necessary for Amyloplast and Chloroplast Function. <i>Plant Cell</i> , 2011, 23, 2331-2347.	6.6	85
5	The <i>naked endosperm</i> Genes Encode Duplicate INDETERMINATE Domain Transcription Factors Required for Maize Endosperm Cell Patterning and Differentiation. <i>Plant Physiology</i> , 2015, 167, 443-456.	4.8	58
6	Integrated transcriptomic-metabolomic analysis reveals cellular responses of harvested strawberry fruit subjected to short-term exposure to high levels of carbon dioxide. <i>Postharvest Biology and Technology</i> , 2019, 148, 120-131.	6.0	44
7	Root Glucosinolate Profiles for Screening of Radish (<i>Raphanus sativus</i> L.) Genetic Resources. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 61-70.	5.2	43
8	Seed browning in pepper (<i>Capsicum annuum</i> L.) fruit during cold storage is inhibited by methyl jasmonate or induced by methyl salicylate. <i>Postharvest Biology and Technology</i> , 2020, 166, 111210.	6.0	33
9	The thick aleurone1 Mutant Defines a Negative Regulation of Maize Aleurone Cell Fate That Functions Downstream of defective kernel1. <i>Plant Physiology</i> , 2011, 156, 1826-1836.	4.8	32
10	Production of herbicide-resistant sweet potato plants transformed with the bar gene. <i>Biotechnology Letters</i> , 2007, 29, 669-675.	2.2	28
11	MYB1 transcription factor is a candidate responsible for red root skin in radish (<i>Raphanus sativus</i> L.). <i>PLoS ONE</i> , 2018, 13, e0204241.	2.5	23
12	Identification of three FLOWERING LOCUS C genes responsible for vernalization response in radish (<i>Raphanus sativus</i> L.). <i>Horticulture Environment and Biotechnology</i> , 2014, 55, 548-556.	2.1	22
13	A putative plant organelle RNA recognition protein gene is essential for maize kernel development. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 236-246.	8.5	17
14	High-throughput linkage analysis of <i>Mutator</i> insertion sites in maize. <i>Plant Journal</i> , 2009, 58, 883-892.	5.7	16
15	Comparative transcriptome and metabolome analyses of two strawberry cultivars with different storability. <i>PLoS ONE</i> , 2020, 15, e0242556.	2.5	16
16	Comparison of antioxidant activity assays in fresh purple waxy corn (<i>Zea mays</i> L.) during grain filling. <i>Applied Biological Chemistry</i> , 2022, 65, .	1.9	14
17	The <i>thick aleurone1</i> Gene Encodes a NOT1 Subunit of the CCR4-NOT Complex and Regulates Cell Patterning in Endosperm. <i>Plant Physiology</i> , 2020, 184, 960-972.	4.8	13
18	Revealing biomass heterosis in the allodiploid <i>xBrassicoraphanus</i> , a hybrid between <i>Brassica rapa</i> and <i>Raphanus sativus</i> , through integrated transcriptome and metabolites analysis. <i>BMC Plant Biology</i> , 2020, 20, 252.	3.6	13

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19	Meiotic Chromosome Stability and Suppression of Crossover Between Non-homologous Chromosomes in xBrassicoraphanus, an Intergeneric Allotetraploid Derived From a Cross Between Brassica rapa and Raphanus sativus. <i>Frontiers in Plant Science</i> , 2020, 11, 851.	3.6	13
20	Investigating seed mineral composition in Korean landrace maize (<i>Zea mays</i> L.) and its kernel texture specificity. <i>Journal of Integrative Agriculture</i> , 2019, 18, 1996-2005.	3.5	11
21	Timing and Pattern of Anthocyanin Accumulation during Grain Filling in Purple Waxy Corn (<i>Zea mays</i> L.) Inbred Line BTx623. <i>Journal of Agricultural Science</i> , 2021, 152, 1-10.	3.5	11
22	Analyses of targeted/untargeted metabolites and reactive oxygen species of pepper fruits provide insights into seed browning induced by chilling. <i>Food Chemistry</i> , 2020, 332, 127406.	8.2	11
23	Jasmonic acid and ERF family genes are involved in chilling sensitivity and seed browning of pepper fruit after harvest. <i>Scientific Reports</i> , 2020, 10, 17949.	3.3	10
24	Reduced fertility caused by meiotic defects and micronuclei formation during microsporogenesis in xBrassicoraphanus. <i>Genes and Genomics</i> , 2021, 43, 251-258.	1.4	8
25	Selection of nptII transgenic sweetpotato plants using G418 and paromomycin. <i>Journal of Plant Biology</i> , 2007, 50, 206-212.	2.1	7
26	Measuring antioxidant activity in yellow corn (<i>Zea mays</i> L.) inbreds from three different geographic regions. <i>Applied Biological Chemistry</i> , 2021, 64, .	1.9	7
27	Glycolysis stimulation and storage protein accumulation are hallmarks of maize (<i>Zea mays</i> L.) grain filling. <i>Applied Biological Chemistry</i> , 2020, 63, .	1.9	6
28	Properties of self-sterile but cross-fertile allopolyploids synthesized between <i>Brassica rapa</i> and <i>Raphanus sativus</i> . <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 163-171.	2.1	4
29	Admixture of divergent genomes facilitates hybridization across species in the family Brassicaceae. <i>New Phytologist</i> , 2022, 235, 743-758.	7.3	3
30	Genome divergence in <i>Brassica rapa</i> subspecies revealed by whole genome analysis on a doubled-haploid line of turnip. <i>Plant Biotechnology Reports</i> , 2019, 13, 677-687.	1.5	2
31	“Hwanggeummatchal”, a Single Cross Hybrid Waxy Corn with High Carotenoid Content and Good Eating Quality. <i>Han'guk Yukchong Hakhoe Chi</i> , 2020, 52, 467-472.	0.5	2
32	Genomics-Assisted Breeding. , 2015, , 145-173.		1
33	A genetic characterization of Korean waxy maize (<i>Zea mays</i> L.) landraces having flowering time variation by RNA sequencing. <i>Scientific Reports</i> , 2019, 9, 20023.	3.3	1
34	Expanded transcriptomic view of strawberry fruit ripening through meta-analysis. <i>PLoS ONE</i> , 2021, 16, e0252685.	2.5	1