

# Gibum Yi

## List of Publications by Year in descending order

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34  
papers

1,091  
citations

623734

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414414

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docs citations

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times ranked

1544  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Admixture of divergent genomes facilitates hybridization across species in the family Brassicaceae. <i>New Phytologist</i> , 2022, 235, 743-758.	7.3	3
3	Reduced fertility caused by meiotic defects and micronuclei formation during microsporogenesis in <i>xBrassicoraphanus</i> . <i>Genes and Genomics</i> , 2021, 43, 251-258.	1.4	8
4	Expanded transcriptomic view of strawberry fruit ripening through meta-analysis. <i>PLoS ONE</i> , 2021, 16, e0252685.	2.5	1
5	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
6	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
7	Timing and Pattern of Anthocyanin Accumulation during Grain Filling in Purple Waxy Corn ( <i>Zea mays</i> L.) Inbred Line BTx623. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1077-1086.	3.5	11
8	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
9	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
10	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
11	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
12	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
13	Meiotic Chromosome Stability and Suppression of Crossover Between Non-homologous Chromosomes in <i>xBrassicoraphanus</i> , an Intergeneric Allotetraploid Derived From a Cross Between <i>Brassica rapa</i> and <i>Raphanus sativus</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 851.	3.6	13
14	Comparative transcriptome and metabolome analyses of two strawberry cultivars with different storability. <i>PLoS ONE</i> , 2020, 15, e0242556.	2.5	16
15	“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
16	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
17	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
18	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

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19	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
20	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
21	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
22	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
23	The naked endosperm 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
24	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
25	Genomics-Assisted Breeding. , 2015, , 145-173.		1
26	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
27	Maize opaque5 Encodes Monogalactosyldiacylglycerol Synthase and Specifically Affects Galactolipids Necessary for Amyloplast and Chloroplast Function. <i>Plant Cell</i> , 2011, 23, 2331-2347.	6.6	85
28	Regulation of aleurone development in cereal grains. <i>Journal of Experimental Botany</i> , 2011, 62, 1669-1675.	4.8	115
29	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
30	High-throughput linkage analysis of Mutator insertion sites in maize. <i>Plant Journal</i> , 2009, 58, 883-892.	5.7	16
31	Selection of nptII transgenic sweetpotato plants using G418 and paromomycin. <i>Journal of Plant Biology</i> , 2007, 50, 206-212.	2.1	7
32	Production of herbicide-resistant sweet potato plants transformed with the bar gene. <i>Biotechnology Letters</i> , 2007, 29, 669-675.	2.2	28
33	Exploitation of pepper EST-SSRs and an SSR-based linkage map. <i>Theoretical and Applied Genetics</i> , 2006, 114, 113-130.	3.6	175
34	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