

Jungmin Ha

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9938739/publications.pdf>

Version: 2024-02-01

18
papers

366
citations

1163117

8
h-index

888059

17
g-index

18
all docs

18
docs citations

18
times ranked

546
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of QTLs for branching in soybean (<i>Glycine max</i> (L.) Merrill). <i>Euphytica</i> , 2017, 213, 1.	1.2	114
2	Overexpression of the Soybean NAC Gene GmNAC109 Increases Lateral Root Formation and Abiotic Stress Tolerance in Transgenic <i>Arabidopsis</i> Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 1036.	3.6	63
3	Genome sequence of <i>Jatropha curcas</i> L., a non-edible biodiesel plant, provides a resource to improve seed-related traits. <i>Plant Biotechnology Journal</i> , 2019, 17, 517-530.	8.3	56
4	Comprehensive RNA sequencing and co-expression network analysis to complete the biosynthetic pathway of coumestrol, a phytoestrogen. <i>Scientific Reports</i> , 2019, 9, 1934.	3.3	25
5	GmBRC1 is a Candidate Gene for Branching in Soybean (<i>Glycine max</i> (L.) Merrill). <i>International Journal of Molecular Sciences</i> , 2019, 20, 135.	4.1	23
6	Transcriptomic variation in proanthocyanidin biosynthesis pathway genes in soybean (<i>Glycine</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.5	14
7	A candidate flowering gene in mungbean is homologous to a soybean Phytochrome A gene. <i>Euphytica</i> , 2017, 213, 1.	1.2	12
8	Genetic Diversity and Genome-Wide Association Study of Seed Aspect Ratio Using a High-Density SNP Array in Peanut (<i>Arachis hypogaea</i> L.). <i>Genes</i> , 2021, 12, 2.	2.4	12
9	QTL Analysis of Resistance to High-Intensity UV-B Irradiation in Soybean (<i>Glycine max</i> [L.] Merr.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 3287.	4.1	9
10	Comprehensive transcriptome analysis of <i>Lactuca indica</i> , a traditional medicinal wild plant. <i>Molecular Breeding</i> , 2017, 37, 1.	2.1	7
11	Biosynthetic Pathway of Proanthocyanidins in Major Cash Crops. <i>Plants</i> , 2021, 10, 1792.	3.5	7
12	Genetic diversity of <i>Jatropha curcas</i> collections from different islands in Indonesia. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 334-342.	0.8	6
13	Updates on Legume Genome Sequencing. <i>Methods in Molecular Biology</i> , 2020, 2107, 1-18.	0.9	6
14	Genome-Wide Association Study of Leaf Chlorophyll Content Using High-Density SNP Array in Peanuts (<i>Arachis hypogaea</i> L.). <i>Agronomy</i> , 2022, 12, 152.	3.0	4
15	Soybean-VCF2Genomes: a database to identify the closest accession in soybean germplasm collection. <i>BMC Bioinformatics</i> , 2019, 20, 384.	2.6	3
16	Transcriptomic profiling of soybean in response to UV-B and <i>Xanthomonas axonopodis</i> treatment reveals shared gene components in stress defense pathways. <i>Genes and Genomics</i> , 2017, 39, 225-236.	1.4	2
17	Detection of large sequence insertions by a hybrid approach that combine de novo assembly and resequencing of medium-coverage genome sequences. <i>Genome</i> , 2018, 61, 745-754.	2.0	2
18	Analysis of genetic variability and agronomic performance of Indian lettuce (<i>Lactuca indica</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1313-1327.	1.6	1