

Yanchao Yuan

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

303
citations

1163117

8
h-index

996975

15
g-index

15
all docs

15
docs citations

15
times ranked

294
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis of codon usage bias in four sequenced cotton species. <i>PLoS ONE</i> , 2018, 13, e0194372.	2.5	104
2	Genome-wide association and differential expression analysis of salt tolerance in <i>Gossypium hirsutum</i> L at the germination stage. <i>BMC Plant Biology</i> , 2019, 19, 394.	3.6	44
3	Genome-Wide Association Study Identifies Candidate Genes Related to Seed Oil Composition and Protein Content in <i>Gossypium hirsutum</i> L.. <i>Frontiers in Plant Science</i> , 2018, 9, 1359.	3.6	34
4	Molecular Mapping and Validation of a Major QTL Conferring Resistance to a Defoliating Isolate of <i>Verticillium Wilt</i> in Cotton (<i>Gossypium hirsutum</i> L.). <i>PLoS ONE</i> , 2014, 9, e96226.	2.5	24
5	Application of 5-azacytidine induces DNA hypomethylation and accelerates dormancy release in buds of tree peony. <i>Plant Physiology and Biochemistry</i> , 2020, 147, 91-100.	5.8	21
6	Metabolomics analysis reveals Embden Meyerhof Parnas pathway activation and flavonoids accumulation during dormancy transition in tree peony. <i>BMC Plant Biology</i> , 2020, 20, 484.	3.6	15
7	Cotton stubble effects on yield and nutrient assimilation in coastal saline soil. <i>Field Crops Research</i> , 2019, 239, 71-81.	5.1	12
8	Candidate quantitative trait loci and genes for fiber quality in <i>Gossypium hirsutum</i> L. detected using single- and multi-locus association mapping. <i>Industrial Crops and Products</i> , 2019, 134, 356-369.	5.2	12
9	Chilling and gibberellin acids hyperinduce β -1,3-glucanases to reopen transport corridor and break endodormancy in tree peony (<i>Paeonia suffruticosa</i>). <i>Plant Physiology and Biochemistry</i> , 2021, 167, 771-784.	5.8	9
10	Molecular tagging and marker-assisted selection of fiber quality traits using chromosome segment introgression lines (CSILs) in cotton. <i>Euphytica</i> , 2014, 200, 239-250.	1.2	8
11	Multi-environments and multi-models association mapping identified candidate genes of lint percentage and seed index in <i>Gossypium hirsutum</i> L.. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	7
12	Genome-wide identification and analysis of Oleosin gene family in four cotton species and its involvement in oil accumulation and germination. <i>BMC Plant Biology</i> , 2021, 21, 569.	3.6	7
13	Changes of DNA Methylation Patterns Reveal Epigenetic Modification of Dormancy Release-Related Genes Is Induced by Chilling in Tree Peony. <i>DNA and Cell Biology</i> , 2021, 40, 606-617.	1.9	3
14	Estimation of Protein and Fatty Acid Composition in Shell-Intact Cottonseed by Near Infrared Reflectance Spectroscopy. <i>JAOCs, Journal of the American Oil Chemists' Society</i> , 2020, 97, 331-340.	1.9	2
15	Genetic analysis of a novel fiber developmental mutant ligo-lintless-Sd (LiSd) in <i>Gossypium hirsutum</i> L.. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1119-1127.	1.6	1