

Rugang Yu

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

845
citations

516710

16
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752698

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20
docs citations

20
times ranked

982
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#	ARTICLE	IF	CITATIONS
1	Genome-wide identification and characterization of cadmium-responsive microRNAs and their target genes in radish (<i>Raphanus sativus</i> L.) roots. <i>Journal of Experimental Botany</i> , 2013, 64, 4271-4287.	4.8	117
2	Identification of novel and salt-responsive miRNAs to explore miRNA-mediated regulatory network of salt stress response in radish (<i>Raphanus sativus</i> L.). <i>BMC Genomics</i> , 2015, 16, 197.	2.8	110
3	Transcriptome-wide analysis of chromium-stress responsive microRNAs to explore miRNA-mediated regulatory networks in radish (<i>Raphanus sativus</i> L.). <i>Scientific Reports</i> , 2015, 5, 14024.	3.3	76
4	De novo sequencing of root transcriptome reveals complex cadmium-responsive regulatory networks in radish (<i>Raphanus sativus</i> L.). <i>Plant Science</i> , 2015, 236, 313-323.	3.6	75
5	Transcriptome-based gene profiling provides novel insights into the characteristics of radish root response to Cr stress with next-generation sequencing. <i>Frontiers in Plant Science</i> , 2015, 6, 202.	3.6	65
6	Comparative transcriptome analysis reveals key cadmium transport-related genes in roots of two pak choi (<i>Brassica rapa</i> L. ssp. <i>chinensis</i>) cultivars. <i>BMC Genomics</i> , 2017, 18, 587.	2.8	43
7	De novo Taproot Transcriptome Sequencing and Analysis of Major Genes Involved in Sucrose Metabolism in Radish (<i>Raphanus sativus</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 585.	3.6	36
8	Comparative transcriptomic analysis reveals the roles of ROS scavenging genes in response to cadmium in two pak choi cultivars. <i>Scientific Reports</i> , 2017, 7, 9217.	3.3	36
9	Transcriptome-Wide Characterization of Novel and Heat-Stress-Responsive microRNAs in Radish (<i>Raphanus Sativus</i> L.) Using Next-Generation Sequencing. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 867-880.	1.8	35
10	Comparative transcriptome analysis reveals gene network regulating cadmium uptake and translocation in peanut roots under iron deficiency. <i>BMC Plant Biology</i> , 2019, 19, 35.	3.6	35
11	Comparative proteomics analysis of peanut roots reveals differential mechanisms of cadmium detoxification and translocation between two cultivars differing in cadmium accumulation. <i>BMC Plant Biology</i> , 2019, 19, 137.	3.6	32
12	Comparative transcriptome analysis revealed key factors for differential cadmium transport and retention in roots of two contrasting peanut cultivars. <i>BMC Genomics</i> , 2018, 19, 938.	2.8	31
13	Genome-Wide Identification of Embryogenesis-Associated microRNAs in Radish (<i>Raphanus sativus</i> L.) by High-Throughput Sequencing. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 900-915.	1.8	30
14	Transcriptome Profiling of Taproot Reveals Complex Regulatory Networks during Taproot Thickening in Radish (<i>Raphanus sativus</i> L.). <i>Frontiers in Plant Science</i> , 2016, 7, 1210.	3.6	29
15	Effects of drought on the accumulation and redistribution of cadmium in peanuts at different developmental stages. <i>Archives of Agronomy and Soil Science</i> , 2017, 63, 1049-1057.	2.6	25
16	Transcriptome profiling of root microRNAs reveals novel insights into taproot thickening in radish (<i>Raphanus sativus</i> L.). <i>BMC Plant Biology</i> , 2015, 15, 30.	3.6	24
17	Assessing alfalfa (<i>Medicago sativa</i> L.) tolerance to salinity at seedling stage and screening of the salinity tolerance traits. <i>Plant Biology</i> , 2021, 23, 664-674.	3.8	20
18	Variations in root morphology among 18 herbaceous species and their relationship with cadmium accumulation. <i>Environmental Science and Pollution Research</i> , 2017, 24, 4731-4740.	5.3	14

#	ARTICLE	IF	CITATIONS
19	Identification and differential expression analysis of anthocyanin biosynthetic genes in root-skin color variants of radish (<i>Raphanus sativus</i> L.). <i>Genes and Genomics</i> , 2020, 42, 413-424.	1.4	9
20	Comparative transcriptomics reveals osmotic and ionic stress key genes contributing to the difference in the salinity tolerance of two pak choi cultivars. <i>Environmental and Experimental Botany</i> , 2021, 191, 104621.	4.2	3