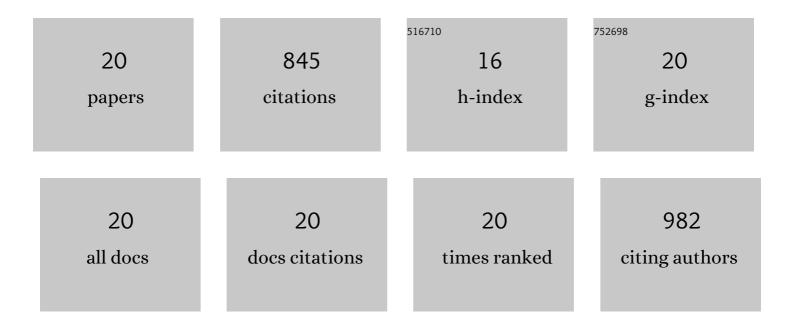
## Rugang Yu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8840047/publications.pdf Version: 2024-02-01



#	Article	lF	CITATIONS
1	Assessing alfalfa ( <i>Medicago sativa</i> L.) tolerance to salinity at seedling stage and screening of the salinity tolerance traits. Plant Biology, 2021, 23, 664-674.	3.8	20
2	Comparative transcriptomics reveals osmotic and ionic stress key genes contributing to the difference in the salinity tolerance of two pak choi cultivars. Environmental and Experimental Botany, 2021, 191, 104621.	4.2	3
3	Identification and differential expression analysis of anthocyanin biosynthetic genes in root-skin color variants of radish (Raphanus sativus L.). Genes and Genomics, 2020, 42, 413-424.	1.4	9
4	Comparative transcriptome analysis reveals gene network regulating cadmium uptake and translocation in peanut roots under iron deficiency. BMC Plant Biology, 2019, 19, 35.	3.6	35
5	Comparative proteomics analysis of peanut roots reveals differential mechanisms of cadmium detoxification and translocation between two cultivars differing in cadmium accumulation. BMC Plant Biology, 2019, 19, 137.	3.6	32
6	Comparative transcriptome analysis revealed key factors for differential cadmium transport and retention in roots of two contrasting peanut cultivars. BMC Genomics, 2018, 19, 938.	2.8	31
7	Variations in root morphology among 18 herbaceous species and their relationship with cadmium accumulation. Environmental Science and Pollution Research, 2017, 24, 4731-4740.	5.3	14
8	Effects of drought on the accumulation and redistribution of cadmium in peanuts at different developmental stages. Archives of Agronomy and Soil Science, 2017, 63, 1049-1057.	2.6	25
9	Comparative transcriptomic analysis reveals the roles of ROS scavenging genes in response to cadmium in two pak choi cultivars. Scientific Reports, 2017, 7, 9217.	3.3	36
10	Comparative transcriptome analysis reveals key cadmium transport-related genes in roots of two pak choi (Brassica rapa L. ssp. chinensis) cultivars. BMC Genomics, 2017, 18, 587.	2.8	43
11	De novo Taproot Transcriptome Sequencing and Analysis of Major Genes Involved in Sucrose Metabolism in Radish (Raphanus sativus L.). Frontiers in Plant Science, 2016, 7, 585.	3.6	36
12	Transcriptome Profiling of Taproot Reveals Complex Regulatory Networks during Taproot Thickening in Radish (Raphanus sativus L.). Frontiers in Plant Science, 2016, 7, 1210.	3.6	29
13	Transcriptome-wide analysis of chromium-stress responsive microRNAs to explore miRNA-mediated regulatory networks in radish (Raphanus sativus L.). Scientific Reports, 2015, 5, 14024.	3.3	76
14	Transcriptome-Wide Characterization of Novel and Heat-Stress-Responsive microRNAs in Radish (Raphanus Sativus L.) Using Next-Generation Sequencing. Plant Molecular Biology Reporter, 2015, 33, 867-880.	1.8	35
15	Transcriptome-based gene profiling provides novel insights into the characteristics of radish root response to Cr stress with next-generation sequencing. Frontiers in Plant Science, 2015, 6, 202.	3.6	65
16	Identification of novel and salt-responsive miRNAs to explore miRNA-mediated regulatory network of salt stress response in radish (Raphanus sativus L.). BMC Genomics, 2015, 16, 197.	2.8	110
17	Transcriptome profiling of root microRNAs reveals novel insights into taproot thickening in radish (Raphanus sativus L.). BMC Plant Biology, 2015, 15, 30.	3.6	24
18	De novo sequencing of root transcriptome reveals complex cadmium-responsive regulatory networks in radish (Raphanus sativus L.). Plant Science, 2015, 236, 313-323.	3.6	75

#	Article	IF	CITATIONS
19	Genome-Wide Identification of Embryogenesis-Associated microRNAs in Radish (Raphanus sativus L.) by High-Throughput Sequencing. Plant Molecular Biology Reporter, 2014, 32, 900-915.	1.8	30
20	Genome-wide identification and characterization of cadmium-responsive microRNAs and their target genes in radish (Raphanus sativus L.) roots. Journal of Experimental Botany, 2013, 64, 4271-4287.	4.8	117