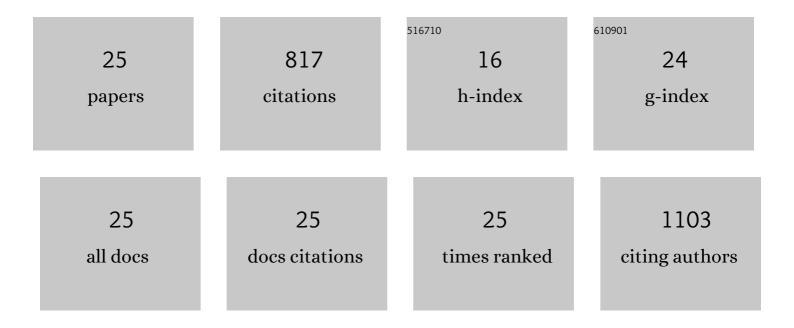
Zhiyong Pan

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	OsADK1, a novel kinase regulating arbuscular mycorrhizal symbiosis in rice. New Phytologist, 2022, 234, 256-268.	7.3	15
2	Current Understandings on Magnesium Deficiency and Future Outlooks for Sustainable Agriculture. International Journal of Molecular Sciences, 2021, 22, 1819.	4.1	34
3	Effects of phosphorus on fruit soluble sugar and citric acid accumulations in citrus. Plant Physiology and Biochemistry, 2021, 160, 73-81.	5.8	40
4	TGF-β1 Facilitates TAp63α Protein Lysosomal Degradation to Promote Pancreatic Cancer Cell Migration. Biology, 2021, 10, 597.	2.8	5
5	Microbiome and Metagenome Analysis Reveals Huanglongbing Affects the Abundance of Citrus Rhizosphere Bacteria Associated with Resistance and Energy Metabolism. Horticulturae, 2021, 7, 151.	2.8	6
6	Influence of Citrus Scion/Rootstock Genotypes on Arbuscular Mycorrhizal Community Composition under Controlled Environment Condition. Plants, 2020, 9, 901.	3.5	9
7	Phosphoproteomic changes in root cells of Poncirus trifoliata (L.) Raf. induced by Rhizophagus intraradices inoculation. Tree Genetics and Genomes, 2019, 15, 1.	1.6	1
8	Natural Variation in CCD4 Promoter Underpins Species-Specific Evolution of Red Coloration in Citrus Peel. Molecular Plant, 2019, 12, 1294-1307.	8.3	102
9	A <i>Medicago truncatula </i> <scp>SWEET</scp> transporter implicated in arbuscule maintenance during arbuscular mycorrhizal symbiosis. New Phytologist, 2019, 224, 396-408.	7.3	101
10	SLAF-Based Construction of a High-Density Genetic Map and Its Application in QTL Mapping of Carotenoids Content in Citrus Fruit. Journal of Agricultural and Food Chemistry, 2019, 67, 994-1002.	5.2	27
11	Comparative genome analyses reveal sequence features reflecting distinct modes of host-adaptation between dicot and monocot powdery mildew. BMC Genomics, 2018, 19, 705.	2.8	39
12	Small RNA profiling reveals involvement of microRNA-mediated gene regulation in response to mycorrhizal symbiosis in Poncirus trifoliata L. Raf Tree Genetics and Genomes, 2018, 14, 1.	1.6	9
13	Comparative transcriptome analysis of Poncirus trifoliata identifies a core set of genes involved in arbuscular mycorrhizal symbiosis. Journal of Experimental Botany, 2018, 69, 5255-5264.	4.8	19
14	Physiological and Transcriptional Changes of Three Citrus Rootstock Seedlings under Iron Deficiency. Frontiers in Plant Science, 2017, 8, 1104.	3.6	21
15	Boron deficiency alters root growth and development and interacts with auxin metabolism by influencing the expression of auxin synthesis and transport genes. Biotechnology and Biotechnological Equipment, 2016, 30, 661-668.	1.3	28
16	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. Frontiers in Microbiology, 2015, 6, 1372.	3.5	24
17	Boron deficiency in woody plants: various responses and tolerance mechanisms. Frontiers in Plant Science, 2015, 6, 916.	3.6	82
18	A Comprehensive Analysis of Chromoplast Differentiation Reveals Complex Protein Changes Associated with Plastoglobule Biogenesis and Remodeling of Protein Systems in Sweet Orange Flesh. Plant Physiology, 2015, 168, 1648-1665.	4.8	43

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19	miRNAome analysis associated with anatomic and transcriptomic investigations reveal the polar exhibition of corky split vein in boron deficient Citrus sinensis. Molecular Genetics and Genomics, 2015, 290, 1639-1657.	2.1	8
20	Transcriptome responses to phosphate deficiency in Poncirus trifoliata (L.) Raf. Acta Physiologiae Plantarum, 2014, 36, 3207-3215.	2.1	7
21	Phosphoproteomic analysis of chromoplasts from sweet orange during fruit ripening. Physiologia Plantarum, 2014, 150, 252-270.	5.2	20
22	Non-targeted metabolomic analysis of orange (Citrus sinensis [L.] Osbeck) wild type and bud mutant fruits by direct analysis in real-time and HPLC-electrospray mass spectrometry. Metabolomics, 2014, 10, 508-523.	3.0	40
23	Array-comparative genome hybridization reveals genome variations between a citrus bud mutant and its parental cultivar. Tree Genetics and Genomes, 2012, 8, 1379-1387.	1.6	7
24	An integrative analysis of transcriptome and proteome provides new insights into carotenoid biosynthesis and regulation in sweet orange fruits. Journal of Proteomics, 2012, 75, 2670-2684.	2.4	74
25	A proteomic analysis of the chromoplasts isolated from sweet orange fruits [Citrus sinensis (L.) Osbeck], Journal of Experimental Botany, 2011, 62, 5297-5309.	4.8	56