

Zhiyong Pan

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

817
citations

516710

16
h-index

610901

24
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25
all docs

25
docs citations

25
times ranked

1103
citing authors

#	ARTICLE	IF	CITATIONS
1	OsADK1, a novel kinase regulating arbuscular mycorrhizal symbiosis in rice. <i>New Phytologist</i> , 2022, 234, 256-268.	7.3	15
2	Current Understandings on Magnesium Deficiency and Future Outlooks for Sustainable Agriculture. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1819.	4.1	34
3	Effects of phosphorus on fruit soluble sugar and citric acid accumulations in citrus. <i>Plant Physiology and Biochemistry</i> , 2021, 160, 73-81.	5.8	40
4	TGF- β 1 Facilitates TAp63 \pm Protein Lysosomal Degradation to Promote Pancreatic Cancer Cell Migration. <i>Biology</i> , 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. <i>Horticulturae</i> , 2021, 7, 151.	2.8	6
6	Influence of Citrus Scion/Rootstock Genotypes on Arbuscular Mycorrhizal Community Composition under Controlled Environment Condition. <i>Plants</i> , 2020, 9, 901.	3.5	9
7	Phosphoproteomic changes in root cells of <i>Poncirus trifoliata</i> (L.) Raf. induced by <i>Rhizophagus intraradices</i> inoculation. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	1.6	1
8	Natural Variation in CCD4 Promoter Underpins Species-Specific Evolution of Red Coloration in Citrus Peel. <i>Molecular Plant</i> , 2019, 12, 1294-1307.	8.3	102
9	A <i>Medicago truncatula</i> <i>SWEET</i> transporter implicated in arbuscule maintenance during arbuscular mycorrhizal symbiosis. <i>New Phytologist</i> , 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. <i>Journal of Agricultural and Food Chemistry</i> , 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. <i>BMC Genomics</i> , 2018, 19, 705.	2.8	39
12	Small RNA profiling reveals involvement of microRNA-mediated gene regulation in response to mycorrhizal symbiosis in <i>Poncirus trifoliata</i> L. Raf.. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	9
13	Comparative transcriptome analysis of <i>Poncirus trifoliata</i> identifies a core set of genes involved in arbuscular mycorrhizal symbiosis. <i>Journal of Experimental Botany</i> , 2018, 69, 5255-5264.	4.8	19
14	Physiological and Transcriptional Changes of Three Citrus Rootstock Seedlings under Iron Deficiency. <i>Frontiers in Plant Science</i> , 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. <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 661-668.	1.3	28
16	The Scion/Rootstock Genotypes and Habitats Affect Arbuscular Mycorrhizal Fungal Community in Citrus. <i>Frontiers in Microbiology</i> , 2015, 6, 1372.	3.5	24
17	Boron deficiency in woody plants: various responses and tolerance mechanisms. <i>Frontiers in Plant Science</i> , 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. <i>Plant Physiology</i> , 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 <i>Citrus sinensis</i> . <i>Molecular Genetics and Genomics</i> , 2015, 290, 1639-1657.	2.1	8
20	Transcriptome responses to phosphate deficiency in <i>Poncirus trifoliata</i> (L.) Raf. <i>Acta Physiologiae Plantarum</i> , 2014, 36, 3207-3215.	2.1	7
21	Phosphoproteomic analysis of chromoplasts from sweet orange during fruit ripening. <i>Physiologia Plantarum</i> , 2014, 150, 252-270.	5.2	20
22	Non-targeted metabolomic analysis of orange (<i>Citrus sinensis</i> [L.] Osbeck) wild type and bud mutant fruits by direct analysis in real-time and HPLC-electrospray mass spectrometry. <i>Metabolomics</i> , 2014, 10, 508-523.	3.0	40
23	Array-comparative genome hybridization reveals genome variations between a citrus bud mutant and its parental cultivar. <i>Tree Genetics and Genomes</i> , 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. <i>Journal of Proteomics</i> , 2012, 75, 2670-2684.	2.4	74
25	A proteomic analysis of the chromoplasts isolated from sweet orange fruits [<i>Citrus sinensis</i> (L.) Osbeck]. <i>Journal of Experimental Botany</i> , 2011, 62, 5297-5309.	4.8	56