Houqing Zeng

List of Publications by Year
in descending order

38 papers	1,908 citations	304743 22 h-index	315739 38 g-index
38 all docs	38 docs citations	38 times ranked	2309 citing authors

#	Article	IF	Citations
1	Involvement of calmodulin and calmodulin-like proteins in plant responses to abiotic stresses. Frontiers in Plant Science, 2015, 6, 600.	3.6	241
2	Genomeâ€wide identification of <i>Medicago truncatula</i> microRNAs and their targets reveals their differential regulation by heavy metal. Plant, Cell and Environment, 2012, 35, 86-99.	5.7	182
3	Transcriptome profiling of early developing cotton fiber by deep-sequencing reveals significantly differential expression of genes in a fuzzless/lintless mutant. Genomics, 2010, 96, 369-376.	2.9	154
4	Adaptation of plasma membrane H⁺â€ATPase of rice roots to low pH as related to ammonium nutrition. Plant, Cell and Environment, 2009, 32, 1428-1440.	5.7	137
5	Plasma membrane H+-ATPase overexpression increases rice yield via simultaneous enhancement of nutrient uptake and photosynthesis. Nature Communications, 2021, 12, 735.	12.8	97
6	Analysis of phosphorus-deficient responsive miRNAs and cis-elements from soybean (Glycine max L.). Journal of Plant Physiology, 2010, 167, 1289-1297.	3.5	96
7	Role of microRNAs in plant responses to nutrient stress. Plant and Soil, 2014, 374, 1005-1021.	3.7	96
8	A cotton miRNA is involved in regulation of plant response to salt stress. Scientific Reports, 2016, 6, 19736.	3.3	79
9	Analysis of EF-Hand Proteins in Soybean Genome Suggests Their Potential Roles in Environmental and Nutritional Stress Signaling. Frontiers in Plant Science, 2017, 8, 877.	3.6	69
10	microRNA expression profiles associated with phosphorus deficiency in white lupin (Lupinus albus L.). Plant Science, 2010, 178, 23-29.	3.6	68
11	Stimulation of phosphorus uptake by ammonium nutrition involves plasma membrane H+ ATPase in rice roots. Plant and Soil, 2012, 357, 205-214.	3.7	56
12	Identification and expression analyses of calmodulin-binding transcription activator genes in soybean. Plant and Soil, 2015, 386, 205-221.	3.7	52
13	Genome-wide identification of phosphate-deficiency-responsive genes in soybean roots by high-throughput sequencing. Plant and Soil, 2016, 398, 207-227.	3.7	52
14	Rhizobia-inoculation enhances the soybeanâ€™s tolerance to salt stress. Plant and Soil, 2016, 400, 209-222.	3.7	49
15	H⁺-ATPases in Plant Growth and Stress Responses. Annual Review of Plant Biology, 2022, 73, 495-521.	18.7	45
16	Adaptation of plasma membrane H+ ATPase and H+ pump to P deficiency in rice roots. Plant and Soil, 2011, 349, 3-11.	3.7	36
17	Genome-wide identification, expression analysis of GH3 family genes in Medicago truncatula under stress-related hormones and Sinorhizobium meliloti infection. Applied Microbiology and Biotechnology, 2015, 99, 841-854.	3.6	36
18	Molecular regulation of zinc deficiency responses in plants. Journal of Plant Physiology, 2021, 261, 153419.	3.5	34

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19	Interplay among NH 4 + uptake, rhizosphere pH and plasma membrane H+-ATPase determine the release of BNIs in sorghum roots â€“ possible mechanisms and underlying hypothesis. Plant and Soil, 2012, 358, 131-141.	3.7	33
20	miRNA778 and SUVH6 are involved in phosphate homeostasis in Arabidopsis. Plant Science, 2015, 238, 273-285.	3.6	33
21	Integrated analyses of miRNAome and transcriptome reveal zinc deficiency responses in rice seedlings. BMC Plant Biology, 2019, 19, 585.	3.6	27
22	Transcriptome profiles of soybean leaves and roots in response to zinc deficiency. Physiologia Plantarum, 2019, 167, 330-351.	5.2	27
23	Loss of two families of SPX domain-containing proteins required for vacuolar polyphosphate accumulation coincides with the transition to phosphate storage in green plants. Molecular Plant, 2021, 14, 838-846.	8.3	24
24	Transcriptional response of plasma membrane H+-ATPase genes to ammonium nutrition and its functional link to the release of biological nitrification inhibitors from sorghum roots. Plant and Soil, 2016, 398, 301-312.	3.7	22
25	Early Transcriptomic Response to Phosphate Deprivation in Soybean Leaves as Revealed by RNA-Sequencing. International Journal of Molecular Sciences, 2018, 19, 2145.	4.1	19
26	Sucrose rather than <scp>GA</scp> transported by <scp>AtSWEET13</scp> and <scp>AtSWEET14</scp> supports pollen fitness at late anther development stages. New Phytologist, 2022, 236, 525-537.	7.3	17
27	Insights of intracellular/intercellular phosphate transport and signaling in unicellular green algae and multicellular land plants. New Phytologist, 2021, 232, 1566-1571.	7.3	16
28	Comprehensive In Silico Characterization and Expression Profiling of Nine Gene Families Associated with Calcium Transport in Soybean. Agronomy, 2020, 10, 1539.	3.0	15
29	Involvement of plasma membrane H⁺â€ATPase in the ammoniumâ€nutrition response of barley roots. Journal of Plant Nutrition and Soil Science, 2018, 181, 878-885.	1.9	13
30	Molecular basis of plasma membrane H+-ATPase function and potential application in the agricultural production. Plant Physiology and Biochemistry, 2021, 168, 10-16.	5.8	13
31	Citrate exudation induced by aluminum is independent of plasma membrane H+-ATPase activity and coupled with potassium efflux from cluster roots of phosphorus-deficient white lupin. Plant and Soil, 2013, 366, 389-400.	3.7	12
32	BNI-release mechanisms in plant root systems: current status of understanding. Biology and Fertility of Soils, 2022, 58, 225-233.	4.3	12
33	Arabidopsis CAMTA3/SR1 is involved in drought stress tolerance and ABA signaling. Plant Science, 2022, 319, 111250.	3.6	11
34	Genome-Wide Identification, Expression Profiling, and Evolution of Phosphate Transporter Gene Family in Green Algae. Frontiers in Genetics, 2020, 11, 590947.	2.3	10
35	Post-translational regulation of plasma membrane H+-ATPase is involved in the release of biological nitrification inhibitors from sorghum roots. Plant and Soil, 2020, 450, 357-372.	3.7	9
36	A Simplified Hydroponic Culture of Arabidopsis. Bio-protocol, 2018, 8, .	0.4	6

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37	Combined analyses of translatome and transcriptome in <i>Arabidopsis</i> reveal new players responding to magnesium deficiency. Journal of Integrative Plant Biology, 2021, 63, 2075-2092.	8.5	5
38	Genome-Wide Identification, Characterization, and Expression Analyses of P-Type ATPase Superfamily Genes in Soybean. Agronomy, 2021, 11, 71.	3.0	5