Hong-Qing Ling

List of Publications by Year
in descending order

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Version: 2024-02-01

33 papers	3,503 citations	331670 21 h-index	414414 32 g-index
35 all docs	35 docs citations	35 times ranked	4097 citing authors

#	Article	IF	Citations
1	Biofortification of iron and zinc in rice and wheat. Journal of Integrative Plant Biology, 2022, 64, 1157-1167.	8.5	13
2	AtCPS V326M significantly affect the biosynthesis of gibberellins.. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2022, 44, 245-252.	0.2	0
3	Iron in plantâ€“pathogen interactions. Journal of Experimental Botany, 2021, 72, 2114-2124.	4.8	35
4	Fine mapping of hybrid necrosis gene Ne1 in common wheat (Triticum aestivum L.). Theoretical and Applied Genetics, 2021, 134, 2603-2611.	3.6	7
5	Ne2 , a typical CCâ€“NBSâ€“LRRâ€type gene, is responsible for hybrid necrosis in wheat. New Phytologist, 2021, 232, 279-289.	7.3	8
6	Cysteine protease RD21A regulated by E3 ligase SINAT4 is required for drought-induced resistance to Pseudomonas syringae in Arabidopsis. Journal of Experimental Botany, 2020, 71, 5562-5576.	4.8	22
7	Glutamate synthase 1 is involved in ironâ€deficiency response and longâ€distance transportation in Arabidopsis. Journal of Integrative Plant Biology, 2020, 62, 1925-1941.	8.5	5
8	FIT-Binding Proteins and Their Functions in the Regulation of Fe Homeostasis. Frontiers in Plant Science, 2019, 10, 844.	3.6	30
9	Arabidopsis BRUTUS-LIKE E3 ligases negatively regulate iron uptake by targeting transcription factor FIT for recycling. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17584-17591.	7.1	91
10	A <scp>FIT</scp>â€binding protein is involved in modulating iron and zinc homeostasis in Arabidopsis. Plant, Cell and Environment, 2018, 41, 1698-1714.	5.7	31
11	Screening wheat genotypes for better performance on reduced phosphorus supply by comparing glasshouse experiments with field trials. Plant and Soil, 2018, 430, 349-360.	3.7	11
12	Four IVa bHLH Transcription Factors Are Novel Interactors of FIT and Mediate JA Inhibition of Iron Uptake in Arabidopsis. Molecular Plant, 2018, 11, 1166-1183.	8.3	134
13	Genome sequence of the progenitor of wheat A subgenome Triticum urartu. Nature, 2018, 557, 424-428.	27.8	354
14	Characterization of theAtSPX3Promoter Elucidates its Complex Regulation in Response to Phosphorus Deficiency. Plant and Cell Physiology, 2016, 57, 1767-1778.	3.1	11
15	Rhizobacterial volatiles and photosynthesisâ€related signals coordinate <scp>MYB</scp>72 expression in Arabidopsis roots during onset of induced systemic resistance and ironâ€deficiency responses. Plant Journal, 2015, 84, 309-322.	5.7	171
16	Dissecting and Enhancing the Contributions of High-Molecular-Weight Glutenin Subunits to Dough Functionality and Bread Quality. Molecular Plant, 2015, 8, 332-334.	8.3	32
17	Genome-wide identification and characterization of the bHLH gene family in tomato. BMC Genomics, 2015, 16, 9.	2.8	193
18	SlbHLH068 interacts with FER to regulate the iron-deficiency response in tomato. Annals of Botany, 2015, 116, 23-34.	2.9	28

#	Article	IF	Citations
19	Genome sequencing of adzuki bean (Vigna angularis) provides insight into high starch and low fat accumulation and domestication. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13213-13218.	7.1	104
20	Fine Physical and Genetic Mapping of Powdery Mildew Resistance Gene MlIW172 Originating from Wild Emmer (Triticum dicoccoides). PLoS ONE, 2014, 9, e100160.	2.5	36
21	Mediator subunit 16 functions in the regulation of iron uptake gene expression in Arabidopsis. New Phytologist, 2014, 203, 770-783.	7.3	65
22	Dissecting and enhancing the contributions of high-molecular-weight glutenin subunits to dough functionality and bread quality. Molecular Plant, 2014, , .	8.3	1
23	Draft genome of the wheat A-genome progenitor Triticum urartu. Nature, 2013, 496, 87-90.	27.8	700
24	Requirement and Functional Redundancy of Ib Subgroup bHLH Proteins for Iron Deficiency Responses and Uptake in Arabidopsis thaliana. Molecular Plant, 2013, 6, 503-513.	8.3	295
25	The cauliflower Orange gene enhances petiole elongation by suppressing expression of eukaryotic release factor 1. New Phytologist, 2011, 190, 89-100.	7.3	41
26	Arsenic biotransformation and volatilization in transgenic rice. New Phytologist, 2011, 191, 49-56.	7.3	116
27	An efficient regeneration system and Agrobacterium-mediated transformation of Chinese upland rice cultivar Handao297. Plant Cell, Tissue and Organ Culture, 2011, 106, 475-483.	2.3	30
28	Iron for plants and humans. Plant and Soil, 2009, 325, 1-3.	3.7	19
29	FIT interacts with AtbHLH38 and AtbHLH39 in regulating iron uptake gene expression for iron homeostasis in Arabidopsis. Cell Research, 2008, 18, 385-397.	12.0	524
30	Further Analysis of the Function of AtBHLH29 in Regulating the Iron Uptake Process in Arabidopsis thaliana. Journal of Integrative Plant Biology, 2006, 48, 75-84.	8.5	9
31	Identification and genetic characterization of an Aegilops tauschii ortholog of the wheat leaf rust disease resistance gene Lr1. Theoretical and Applied Genetics, 2004, 109, 1133-1138.	3.6	29
32	The tomato fer gene encoding a bHLH protein controls iron-uptake responses in roots. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13938-13943.	7.1	353
33	Requirement and functional redundancy of two large ribonucleotide reductase subunit genes for cell cycle, chloroplast biogenesis and photosynthesis in tomato. Annals of Botany, 0, , .	2.9	3