Han Xing

List of Publications by Year
in descending order

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33 papers	831 citations	471509 17 h-index	526287 27 g-index
33 all docs	33 docs citations	33 times ranked	937 citing authors

#	Article	IF	Citations
1	Genome-Wide Identification of the AP2/ERF Gene Family and Functional Analysis of GmAP2/ERF144 for Drought Tolerance in Soybean. Frontiers in Plant Science, 2022, 13, 848766.	3.6	14
2	Genome-Wide Association Studies of Plant Architecture-Related Traits in the Chinese Soybean Mini Core Collection. Agronomy, 2022, 12, 817.	3.0	0
3	Key Soybean Seedlings Drought-Responsive Genes and Pathways Revealed by Comparative Transcriptome Analyses of Two Cultivars. International Journal of Molecular Sciences, 2022, 23, 2893.	4.1	13
4	Genome-wide association studies of plant architecture-related traits and 100-seed weight in soybean landraces. BMC Genomic Data, 2021, 22, 10.	1.7	6
5	Genome-wide association analysis for yield-related traits at the R6 stage in a Chinese soybean mini core collection. Genes and Genomics, 2021, 43, 897-912.	1.4	8
6	GmNAC8 acts as a positive regulator in soybean drought stress. Plant Science, 2020, 293, 110442.	3.6	35
7	Comparative Proteomics Analysis Reveals That Lignin Biosynthesis Contributes to Brassinosteroid-Mediated Response to Phytophthora sojae in Soybeans. Journal of Agricultural and Food Chemistry, 2020, 68, 5496-5506.	5.2	8
8	Genome-Wide Analysis Reveals the Role of Mediator Complex in the Soybeanâ€"Phytophthora sojae Interaction. International Journal of Molecular Sciences, 2019, 20, 4570.	4.1	6
9	GmHsp90A2 is involved in soybean heat stress as a positive regulator. Plant Science, 2019, 285, 26-33.	3.6	47
10	Genome-wide association study of four yield-related traits at the R6 stage in soybean. BMC Genetics, 2019, 20, 39.	2.7	22
11	GmWRKY40, a member of the WRKY transcription factor genes identified from Glycine max L., enhanced the resistance to Phytophthora sojae. BMC Plant Biology, 2019, 19, 598.	3.6	42
12	Combining QTL-seq and linkage mapping to fine map a wild soybean allele characteristic of greater plant height. BMC Genomics, 2018, 19, 226.	2.8	57
13	Resistance to Phytophthora pathogens is dependent on gene silencing pathways in plants. Journal of Phytopathology, 2018, 166, 379-385.	1.0	5
14	Metabolomics Analysis of Soybean Hypocotyls in Response to Phytophthora sojae Infection. Frontiers in Plant Science, 2018, 9, 1530.	3.6	38
15	Conditional and unconditional QTL analyses of seed hardness in vegetable soybean (Glycine max L.) Tj ETQq1 1 0.784314 rgBT /Overl	1.2	4
16	Overexpression of Chalcone Isomerase (CHI) Increases Resistance Against Phytophthora sojae in Soybean. Journal of Plant Biology, 2018, 61, 309-319.	2.1	24
17	Genome-wide SNP-based association mapping of resistance to Phytophthora sojae in soybean (Glycine) Tj ETQq1 1 0.784314 rgBT /O	1.2	9
18	Genome-Wide Association Studies of Soybean Seed Hardness in the Chinese Mini Core Collection. Plant Molecular Biology Reporter, 2018, 36, 605-617.	1.8	10

#	Article	IF	Citations
19	Overexpression of gma-miR1510a/b suppresses the expression of a NB-LRR domain gene and reduces resistance to Phytophthora sojae. Gene, 2017, 621, 32-39.	2.2	32
20	Transcriptomics Analysis of Apple Leaves in Response to Alternaria alternata Apple Pathotype Infection. Frontiers in Plant Science, 2017, 8, 22.	3.6	72
21	Fine Mapping of a Resistance Gene RpsHN that Controls Phytophthora sojae Using Recombinant Inbred Lines and Secondary Populations. Frontiers in Plant Science, 2017, 8, 538.	3.6	47
22	GmCYP82A3, a Soybean Cytochrome P450 Family Gene Involved in the Jasmonic Acid and Ethylene Signaling Pathway, Enhances Plant Resistance to Biotic and Abiotic Stresses. PLoS ONE, 2016, 11, e0162253.	2.5	99
23	Early Abscisic Acid Accumulation Regulates Ascorbate and Glutathione Metabolism in Soybean Leaves Under Progressive Water Stress. Journal of Plant Growth Regulation, 2016, 35, 865-876.	5.1	20
24	Over-expression of GmHAL3 modulates salt stresses tolerance in transgenic arabidopsis. Journal of Plant Biology, 2016, 59, 444-455.	2.1	5
25	Phenotypic evaluation and genetic dissection of resistance to Phytophthora sojae in the Chinese soybean mini core collection. BMC Genetics, 2016, 17, 85.	2.7	43
26	Triadimefon Induced C and N Metabolism and Root Ultra-Structural Changes for Drought Stress Protection in Soybean at Flowering Stage. Journal of Plant Growth Regulation, 2016, 35, 222-231.	5.1	8
27	Loci and candidate gene identification for resistance to Phytophthora sojae via association analysis in soybean [Glycine max (L.) Merr.]. Molecular Genetics and Genomics, 2016, 291, 1095-1103.	2.1	29
28	GmSGT1 is differently required for soybean Rps genes-mediated and basal resistance to Phytophthora sojae. Plant Cell Reports, 2014, 33, 1275-1288.	5.6	17
29	Identification of <scp>QTL</scp>s for growth period traits in soybean using association analysis and linkage mapping. Plant Breeding, 2013, 132, 317-323.	1.9	11
30	Association analysis of vegetable soybean quality traits with SSR markers. Plant Breeding, 2011, 130, 444-449.	1.9	29
31	Proteomics study of changes in soybean lines resistant and sensitive to Phytophthora sojae. Proteome Science, 2011, 9, 52.	1.7	41
32	A survey of soybean germplasm for resistance to Phytophthora sojae. Euphytica, 2010, 176, 261-268.	1.2	8
33	Identification, inheritance and QTL mapping of root traits related to tolerance to rhizo-spheric stresses in soybean (G. max (L.) Merr.). Frontiers of Agriculture in China, 2007, 1, 119-128.	0.2	22