Zahra Zinati

List of Publications by Year
in descending order

16 papers	118 citations
1684188 5 h-index	1372567 10 g-index
17 all docs	17 docs citations
17 times ranked	135 citing authors

#	Article	IF	Citations
1	Exploring the transcriptome signature associated with tolerance to *Penicillium expansum* in apple through feature selection algorithms and differential gene expression analysis. New Zealand Journal of Crop and Horticultural Science, 2023, 51, 547-565.	1.3	1
2	Identification of important genes involved in priming induced drought tolerance in barley through transcriptomic data mining. Crop and Pasture Science, 2022, 73, 1011-1025.	1.5	2
3	A comprehensive meta-analysis to identify transcriptional signatures of abiotic stress responses in barley (Hordeum vulgare). Cereal Research Communications, 2021, 49, 385-391.	1.6	4
4	Integrating expression data and genomic sequences to investigate the transcriptional regulation in barley in response to abiotic stress. Biotechnologia, 2021, 102, 21-32.	0.9	1
5	New selection strategies for determining the traits contributing to increased grain yield in wheat (Triticum aestivum L.) under aluminum stress. Genetic Resources and Crop Evolution, 2021, 68, 2061-2073.	1.6	4
6	Mining transcriptome data to identify genes and pathways related to lemon taste using supervised and unsupervised data learning methods. Horticulture Environment and Biotechnology, 2021, 62, 593.	2.1	9
7	Dynamic transcriptomic analysis uncovers key genes and mechanisms involved in seed priming-induced tolerance to drought in barley. Gene Reports, 2020, 21, 100941.	0.8	5
8	Identification of candidate genes related to aroma in rice by analyzing the microarray data of highly aromatic and nonaromatic recombinant inbred line bulks. Biotechnologia, 2019, 100, 227-240.	0.9	1
9	Unveiling the molecular mechanisms of drought stress tolerance in rice (Oryza sativa L.) using computational approaches. Biotechnologia, 2018, 99, 385-400.	0.9	3
10	Identification of novel genes potentially involved in rice (Oryza sativa L.) drought tolerance. Biotechnologia, 2017, 98, 195-208.	0.9	0
11	In silico identification of transcription factors associated with the biosynthesis of carotenoids in corn (Zea mays L.). Biotechnologia, 2017, 1, 41-51.	0.9	3
12	Computational approaches for classification and prediction of P-type ATPase substrate specificity in Arabidopsis. Physiology and Molecular Biology of Plants, 2016, 22, 163-174.	3.1	15
13	In silico identification of miRNAs and their target genes and analysis of gene co-expression network in		