Elahe Tavakol

List of Publications by Year
in descending order

23	646	687363 13	677142 22
papers	citations	h-index	g-index

23	23	23	904
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Barley Uniculme4 Gene Encodes a BLADE-ON-PETIOLE-Like Protein That Controls Tillering and Leaf Patterning. Plant Physiology, 2015, 168, 164-174.	4.8	85
2	Photoperiod-H1 (Ppd-H1) Controls Leaf Size. Plant Physiology, 2016, 172, 405-415.	4.8	77
3	Genetics of Tillering in Rice and Barley. Plant Genome, 2014, 7, plantgenome2013.10.0032.	2.8	75
4	Comprehensive genomic analysis of a plant growth-promoting rhizobacterium Pantoea agglomerans strain P5. Scientific Reports, 2017, 7, 15610.	3.3	69
5	Genome wide screening and comparative genome analysis for Meta-QTLs, ortho-MQTLs and candidate genes controlling yield and yield-related traits in rice. BMC Genomics, 2020, 21, 294.	2.8	44
6	Meta-QTL and ortho-MQTL analyses identified genomic regions controlling rice yield, yield-related traits and root architecture under water deficit conditions. Scientific Reports, 2021, 11, 6942.	3.3	41
7	Detection of genomic regions associated with tiller number in Iranian bread wheat under different water regimes using genome-wide association study. Scientific Reports, 2020, 10, 14034.	3.3	40
8	Novel Aspects on The Interaction Between Grapevine and Plasmopara viticola: Dual-RNA-Seq Analysis Highlights Gene Expression Dynamics in The Pathogen and The Plant During The Battle For Infection. Genes, 2020, 11, 261.	2.4	37
9	Genome-wide meta-analysis on yield and yield-related QTLs in barley (Hordeum vulgare L.). Molecular Breeding, 2019, 39, 1.	2.1	26
10	Isolation, promoter analysis and expression profile of Dreb2 in response to drought stress in wheat ancestors. Gene, 2014, 549, 24-32.	2.2	24
11	OsFD4 promotes the rice floral transition via florigen activation complex formation in the shoot apical meristem. New Phytologist, 2021, 229, 429-443.	7.3	21
12	Detection of consensus genomic regions associated with root architecture of bread wheat on groups 2 and 3 chromosomes using QTL metaâ€“analysis. Australian Journal of Crop Science, 2017, , 777-785.	0.3	19
13	Diversity for AFLP and SSR in Natural Populations of L. from Italy. Crop Science, 2008, 48, 1080.	1.8	14
14	A barley mutant with improved salt tolerance through ion homeostasis and ROS scavenging under salt stress. Acta Physiologiae Plantarum, 2017, 39, 1.	2.1	13
15	Genetic dissection of heading date and yield under Mediterranean dry climate in barley (Hordeum) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	12
16	RNA-seq Transcriptome Profiling of the Halophyte Salicornia persica in Response to Salinity. Journal of Plant Growth Regulation, 2021, 40, 707-721.	5.1	11
17	Virus-Induced Gene Silencing (VIGS) in Aegilops tauschii and Its Use in Functional Analysis of AetDREB2. Molecular Biotechnology, 2018, 60, 41-48.	2.4	10
18	RAPD Markers Associated with Drought Tolerance in Bread Wheat (Triticum aestivum L.). Pakistan Journal of Biological Sciences, 2007, 10, 3237-3239.	0.5	9

#	Article	IF	Citations
19	Phytic acid, iron and zinc content in wheat ploidy levels and amphiploids: the impact of genotype and planting seasons. Archives of Agronomy and Soil Science, 2018, 64, 331-346.	2.6	6
20	Identification and characterization of responsive genes in rice during compatible interactions with pathogenic pathovars of Xanthomonas oryzae. European Journal of Plant Pathology, 2018, 151, 141.	1.7	5
21	Evaluation of agro-morphological traits related to grain yield of Iranian wheat genotypes in drought-stress and normal irrigation conditions. Australian Journal of Crop Science, 2018, 12, 738-748.	0.3	5
22	Microarray analysis of Arabidopsis thaliana exposed to single and mixed infections with Cucumber mosaic virus and turnip viruses. Physiology and Molecular Biology of Plants, 2021, 27, 11-27.	3.1	2
23	Natural Genetic Diversity and Crop Improvement. , 2017, , 185-215.		1