Emre Ilhan

List of Publications by Year
in descending order

21 papers	640 citations	759055 12 h-index	839398 18 g-index
21 all docs	21 docs citations	21 times ranked	935 citing authors

#	Article	IF	Citations
1	Genome of wild olive and the evolution of oil biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9413-E9422.	3.3	233
2	Transcriptome analysis of wheat inoculated with Fusarium graminearum. Frontiers in Plant Science, 2015, 6, 867.	1.7	66
3	Genome-wide fungal stress responsive miRNA expression in wheat. Planta, 2014, 240, 1287-1298.	1.6	62
4	Molecular and ecological investigations on the wild populations of Glycyrrhiza L. taxa distributed in the East Mediterranean Area of Turkey. Journal of Plant Research, 2016, 129, 1021-1032.	1.2	36
5	Hexaploid wheat (Triticum aestivum) root miRNome analysis in response to salt stress. Annals of Applied Biology, 2015, 167, 208-216.	1.3	35
6	Genome-wide identification of salinity responsive HSP70s in common bean. Molecular Biology Reports, 2016, 43, 1251-1266.	1.0	31
7	Genome-wide identification of CAMTA gene family members in Phaseolus vulgaris L. and their expression profiling during salt stress. Molecular Biology Reports, 2019, 46, 2721-2732.	1.0	31
8	Transferability of SSR markers from distantly related legumes to Glycyrrhiza species. Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry, 2014, 38, 32-38.	0.8	30
9	Transcriptome â€“ Scale characterization of salt responsive bean TCP transcription factors. Gene, 2018, 642, 64-73.	1.0	24
10	Genome-wide analysis of Phaseolus vulgaris C2C2-YABBY transcription factors under salt stress conditions. 3 Biotech, 2017, 7, 302.	1.1	21
11	Waterlogging and nitric oxide induce gene expression and increase antioxidant enzyme activity in wheat (Triticum aestivumL.). Acta Biologica Hungarica, 2014, 65, 47-60.	0.7	19
12	Plant growth-promoting bacteria (PGPBs) and copper (II) oxide (CuO) nanoparticle ameliorates DNA damage and DNA Methylation in wheat (Triticum aestivum L.) exposed to NaCl stress. Journal of Plant Biochemistry and Biotechnology, 2022, 31, 751-764.	0.9	17
13	Genetic structure and diversity of Adonis L. (Ranunculaceae) populations collected from Turkey by inter-primer binding site (iPBS) retrotransposon markers. Turkish Journal of Botany, 2019, 43, 585-596.	0.5	16
14	GENOME-WIDE CHARACTERIZATION AND ANALYSIS OF SBP TRANSCRIPTION FACTOR FAMILY IN COMMON BEAN (PHASEOLUS VULGARIS L.). Applied Ecology and Environmental Research, 2018, 16, 5467-5480.	0.2	5
15	Eucalyptus grandis YABBY TranskripsiyonFaktÃ¶rlerinin Genom BazÄ±nda Analizi. TÃ¼rkiye TarÄ±msal AraÅŸtÄ±rmalar Dergisi, 2018, 5, 158-166.	0.5	5
16	Transcriptome wide characterization of water deficit responsive grape mTERF transcription. Journal of Plant Biochemistry and Biotechnology, 2020, 29, 102-113.	0.9	3
17	Diversity analysis of genetic, agronomic, and quality characteristics of bread wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Agriculture and Forestry, 2016, 40, 83-94.	0.8	2
18	Identification and characterization of the Pvul-GASA gene family in the Phaseolus vulgaris and expression patterns under salt stress. Turkish Journal of Botany, 2021, 45, 655-670.	0.5	2

#	Article	IF	Citations
19	Phylogenetic relationship among taxa in the genus Adonis L. collected from TÃ¼rkiye based on nrDNA internal transcribed spacer (ITS) markers. Molecular Biology Reports, 2022, 49, 7815-7826.	1.0	2
20	Genome-wide and expression analysis of Phaseolus vulgaris L. mTERF genes under salt stress. Journal of Biotechnology, 2017, 256, S38.	1.9	0
21	Fasulye bitkisinde phospholipase D gen ailesinin tuz ve kuraklÄ±k stresi altÄ±nda genom Ã§aplÄ± karakterizasyonu. European Journal of Science and Technology, 0, , .	0.5	0