

Emre Ilhan

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

640
citations

759055

12
h-index

839398

18
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21
all docs

21
docs citations

21
times ranked

935
citing authors

#	ARTICLE	IF	CITATIONS
1	Plant growth-promoting bacteria (PGPBs) and copper (II) oxide (CuO) nanoparticle ameliorates DNA damage and DNA Methylation in wheat (<i>Triticum aestivum</i> L.) exposed to NaCl stress. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 751-764.	0.9	17
2	Phylogenetic relationship among taxa in the genus <i>Adonis</i> L. collected from T ¹ / ₄ rkiye based on nrDNA internal transcribed spacer (ITS) markers. <i>Molecular Biology Reports</i> , 2022, 49, 7815-7826.	1.0	2
3	Identification and characterization of the Pvul-GASA gene family in the <i>Phaseolus vulgaris</i> and expression patterns under salt stress. <i>Turkish Journal of Botany</i> , 2021, 45, 655-670.	0.5	2
4	Transcriptome wide characterization of water deficit responsive grape mTERF transcription. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 102-113.	0.9	3
5	Genome-wide identification of CAMTA gene family members in <i>Phaseolus vulgaris</i> L. and their expression profiling during salt stress. <i>Molecular Biology Reports</i> , 2019, 46, 2721-2732.	1.0	31
6	Genetic structure and diversity of <i>Adonis</i> L. (<i>Ranunculaceae</i>) populations collected from Turkey by inter-primer binding site (iPBS) retrotransposon markers. <i>Turkish Journal of Botany</i> , 2019, 43, 585-596.	0.5	16
7	Transcriptome Scale characterization of salt responsive bean TCP transcription factors. <i>Gene</i> , 2018, 642, 64-73.	1.0	24
8	GENOME-WIDE CHARACTERIZATION AND ANALYSIS OF SBP TRANSCRIPTION FACTOR FAMILY IN COMMON BEAN (<i>PHASEOLUS VULGARIS</i> L.). <i>Applied Ecology and Environmental Research</i> , 2018, 16, 5467-5480.	0.2	5
9	<i>Eucalyptus grandis</i> YABBY Transkripsiyon Faktörlerinin Genom Bazında Analizi. T ¹ / ₄ rkiye Tarımsal Araştırmalar Dergisi, 2018, 5, 158-166.	0.5	5
10	Genome of wild olive and the evolution of oil biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9413-E9422.	3.3	233
11	Genome-wide analysis of <i>Phaseolus vulgaris</i> C2C2-YABBY transcription factors under salt stress conditions. <i>3 Biotech</i> , 2017, 7, 302.	1.1	21
12	Genome-wide and expression analysis of <i>Phaseolus vulgaris</i> L. mTERF genes under salt stress. <i>Journal of Biotechnology</i> , 2017, 256, S38.	1.9	0
13	Diversity analysis of genetic, agronomic, and quality characteristics of bread wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Agriculture and Forestry, 2016, 40, 83-94.	0.8	2
14	Molecular and ecological investigations on the wild populations of <i>Glycyrrhiza</i> L. taxa distributed in the East Mediterranean Area of Turkey. <i>Journal of Plant Research</i> , 2016, 129, 1021-1032.	1.2	36
15	Genome-wide identification of salinity responsive HSP70s in common bean. <i>Molecular Biology Reports</i> , 2016, 43, 1251-1266.	1.0	31
16	Hexaploid wheat (<i>Triticum aestivum</i>) root miRNome analysis in response to salt stress. <i>Annals of Applied Biology</i> , 2015, 167, 208-216.	1.3	35
17	Transcriptome analysis of wheat inoculated with <i>Fusarium graminearum</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 867.	1.7	66
18	Transferability of SSR markers from distantly related legumes to <i>Glycyrrhiza</i> species. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2014, 38, 32-38.	0.8	30

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19	Genome-wide fungal stress responsive miRNA expression in wheat. <i>Planta</i> , 2014, 240, 1287-1298.	1.6	62
20	Waterlogging and nitric oxide induce gene expression and increase antioxidant enzyme activity in wheat (<i>Triticum aestivum</i> L.). <i>Acta Biologica Hungarica</i> , 2014, 65, 47-60.	0.7	19
21	Fasulye bitkisinde phospholipase D gen ailesinin tuz ve kuraklık stresi altında genomun karakterizasyonu. <i>European Journal of Science and Technology</i> , 0, , .	0.5	0