

Ertugrul Filiz

List of Publications by Year in descending order

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76
papers

1,545
citations

394286

19
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345118

36
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docs citations

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times ranked

2022
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#	ARTICLE	IF	CITATIONS
1	Identification and Comparative Analysis of H ₂ O ₂ -Scavenging Enzymes (Ascorbate Peroxidase and) Tj ETQq1 1 0.784314 rgBT /Overlock Science, 2016, 7, 301.	1.7	144
2	Essential and Beneficial Trace Elements in Plants, and Their Transport in Roots: a Review. Applied Biochemistry and Biotechnology, 2017, 181, 464-482.	1.4	114
3	Molecular, morphological, and cytological analysis of diverse <i>Brachypodium distachyon</i> inbred lines. Genome, 2009, 52, 876-890.	0.9	111
4	Genome-wide exploration of metal tolerance protein (MTP) genes in common wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	1.8	101
5	The AP2/ERF Gene Family in <i>Triticum durum</i> : Genome-Wide Identification and Expression Analysis under Drought and Salinity Stresses. Genes, 2020, 11, 1464.	1.0	79
6	Pathogenesis related protein-1 (PR-1) genes in tomato (<i>Solanum lycopersicum</i> L.): Bioinformatics analyses and expression profiles in response to drought stress. Genomics, 2020, 112, 4089-4099.	1.3	67
7	Genome-wide identification and expression analysis of sulfate transporter (SULTR) genes in potato (<i>Solanum tuberosum</i> L.). Planta, 2016, 244, 1167-1183.	1.6	64
8	Genome-wide distribution of superoxide dismutase (SOD) gene families in <i>Sorghum bicolor</i> . Turkish Journal of Biology, 2015, 39, 49-59.	2.1	55
9	Genome-Wide Identification and Expression Profiling of Ascorbate Peroxidase (APX) and Glutathione Peroxidase (GPX) Genes Under Drought Stress in <i>Sorghum</i> (<i>Sorghum bicolor</i> L.). Journal of Plant Growth Regulation, 2018, 37, 925-936.	2.8	41
10	<i>Brachypodium</i> Genomics. International Journal of Plant Genomics, 2008, 2008, 1-7.	2.2	38
11	Genome-wide exploration of silicon (Si) transporter genes, Lsi1 and Lsi2 in plants; insights into Si-accumulation status/capacity of plants. BioMetals, 2017, 30, 185-200.	1.8	37
12	Abiotic stress-induced regulation of antioxidant genes in different <i>Arabidopsis</i> ecotypes: microarray data evaluation. Biotechnology and Biotechnological Equipment, 2019, 33, 128-143.	0.5	37
13	Comparative analyses of phytochelatin synthase (<i>PCS</i>) genes in higher plants. Biotechnology and Biotechnological Equipment, 2019, 33, 178-194.	0.5	36
14	Genome-wide identification and analysis of growth regulating factor genes in <i>Brachypodium distachyon</i> : in silico approaches. Turkish Journal of Biology, 2014, 38, 296-306.	2.1	34
15	Assessment of miRNA expression profile and differential expression pattern of target genes in cold-tolerant and cold-sensitive tomato cultivars. Biotechnology and Biotechnological Equipment, 2015, 29, 851-860.	0.5	32
16	Investigation and Computational Analysis of the Sulfotransferase (SOT) Gene Family in Potato (<i>Solanum tuberosum</i>): Insights into Sulfur Adjustment for Proper Development and Stimuli Responses. Plants, 2021, 10, 2597.	1.6	31
17	Genome-wide and comparative analysis of bHLH38, bHLH39, bHLH100 and bHLH101 genes in <i>Arabidopsis</i> , tomato, rice, soybean and maize: insights into iron (Fe) homeostasis. BioMetals, 2018, 31, 489-504.	1.8	29
18	DREB2 (dehydration-responsive element-binding protein 2) type transcription factor in sorghum (<i>Sorghum bicolor</i>): genome-wide identification, characterization and expression profiles under cadmium and salt stresses. 3 Biotech, 2018, 8, 426.	1.1	28

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19	In silico analysis of Mn transporters (NRAMP1) in various plant species. <i>Molecular Biology Reports</i> , 2016, 43, 151-163.	1.0	25
20	Ammonium transporter 1 (AMT1) gene family in tomato (<i>Solanum lycopersicum</i> L.): Bioinformatics, physiological and expression analyses under drought and salt stresses. <i>Genomics</i> , 2020, 112, 3773-3782.	1.3	21
21	Genome-wide identification of galactinol synthase (GolS) genes in <i>Solanum lycopersicum</i> and <i>Brachypodium distachyon</i> . <i>Computational Biology and Chemistry</i> , 2015, 58, 149-157.	1.1	17
22	Screening of damage induced by lead (Pb) in rye (<i>Secale cereale</i> L.) – a genetic and physiological approach. <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 489-496.	0.5	16
23	Genome-wide identification and cadmium induced expression profiling of sulfate transporter (SULTR) genes in sorghum (<i>Sorghum bicolor</i> L.). <i>BioMetals</i> , 2018, 31, 91-105.	1.8	16
24	Aromatic amino acids biosynthesis genes identification and expression analysis under salt and drought stresses in <i>Solanum lycopersicum</i> L.. <i>Scientia Horticulturae</i> , 2019, 250, 127-137.	1.7	16
25	Genome-wide investigation of proline transporter (ProT) gene family in tomato: Bioinformatics and expression analyses in response to drought stress. <i>Plant Physiology and Biochemistry</i> , 2020, 157, 13-22.	2.8	16
26	The Conservation of VIT1-Dependent Iron Distribution in Seeds. <i>Frontiers in Plant Science</i> , 2019, 10, 907.	1.7	15
27	Comparative and phylogenetic analysis of zinc transporter genes/proteins in plants. <i>Turkish Journal of Biology</i> , 2016, 40, 600-611.	2.1	14
28	Genome-wide identification and expression profiling of EIL gene family in woody plant representative poplar (<i>Populus trichocarpa</i>). <i>Archives of Biochemistry and Biophysics</i> , 2017, 627, 30-45.	1.4	13
29	Genome-wide identification of mildew resistance locus O (MLO) genes in tree model poplar (<i>Populus</i>) Tj ETQq1 1 0.784314 rgBT /Overle 2018, 152, 95-109.	0.8	13
30	Whirly (Why) transcription factors in tomato (<i>Solanum lycopersicum</i> L.): genome-wide identification and transcriptional profiling under drought and salt stresses. <i>Molecular Biology Reports</i> , 2019, 46, 4139-4150.	1.0	13
31	Exploration of two major boron transport genes <i>BOR1</i> and <i>NIP5;1</i> in the genomes of different plants. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 455-468.	0.5	12
32	Comparative Analysis and Modeling of Superoxide Dismutases (SODs) in <i>Brachypodium distachyon</i> L.. <i>Applied Biochemistry and Biotechnology</i> , 2014, 173, 1183-1196.	1.4	11
33	Assessment of genetic variations of silver lime (<i>Tilia tomentosa</i> Moench.) by RAPD markers in urban and forest ecosystems. <i>Biotechnology and Biotechnological Equipment</i> , 2015, 29, 631-636.	0.5	11
34	Comparative analysis of plant lycopene cyclases. <i>Computational Biology and Chemistry</i> , 2015, 58, 81-92.	1.1	11
35	Identification of Differentially Expressed Genes in Chilling-Induced Potato (<i>Solanum tuberosum</i> L.); a Data Analysis Study. <i>Applied Biochemistry and Biotechnology</i> , 2015, 177, 792-811.	1.4	11
36	Isolation of a transcription factor <i>DREB1A</i> gene from <i>Phaseolus vulgaris</i> and computational insights into its characterization: protein modeling, docking and mutagenesis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 3107-3118.	2.0	11

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37	In Silico Analysis of DREB Transcription Factor Genes and Proteins in Grasses. <i>Applied Biochemistry and Biotechnology</i> , 2014, 174, 1272-1285.	1.4	9
38	Identification of O-acetylserine(thiol)lyase (OASTL) genes in sorghum (<i>Sorghum bicolor</i>) and gene expression analysis under cadmium stress. <i>Molecular Biology Reports</i> , 2019, 46, 343-354.	1.0	9
39	Investigation of PIC1 (permease in chloroplasts 1) gene's role in iron homeostasis: bioinformatics and expression analyses in tomato and sorghum. <i>BioMetals</i> , 2020, 33, 29-44.	1.8	9
40	Genome-wide analysis of iron-regulated transporter 1 (IRT1) genes in plants. <i>Horticulture Environment and Biotechnology</i> , 2015, 56, 516-523.	0.7	8
41	Genome-Wide Identification and Comparative Analysis of Copper Transporter Genes in Plants. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2017, 9, 278-291.	2.2	8
42	Genome-wide analyses of ATP sulfurylase (ATPS) genes in higher plants and expression profiles in sorghum (<i>Sorghum bicolor</i>) under cadmium and salinity stresses. <i>Genomics</i> , 2019, 111, 579-589.	1.3	8
43	Diploid <i>Brachypodium distachyon</i> of Turkey: Molecular and Morphologic Analysis. , 2009, , 83-90.		8
44	Application of data analysis in cold stress: a case study of <i>Nicotiana benthamiana</i> . <i>Turkish Journal of Botany</i> , 2015, 39, 1021-1032.	0.5	7
45	Genome-wide analysis of response to low sulfur (LSU) genes in grass species and expression profiling of model grass species <i>Brachypodium distachyon</i> under S deficiency. <i>Turkish Journal of Biology</i> , 2016, 40, 934-943.	2.1	7
46	Insights into a key sulfite scavenger enzyme sulfite oxidase (SOX) gene in plants. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 385-395.	1.4	7
47	A key gene bHLH115 in iron homeostasis: comprehensive bioinformatics analyses in <i>Arabidopsis</i> , tomato, rice, and maize. <i>BioMetals</i> , 2019, 32, 641-656.	1.8	7
48	FIT (Fer-like iron deficiency-induced transcription factor) in plant iron homeostasis: genome-wide identification and bioinformatics analyses. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 143-157.	0.9	7
49	Assessment of the genetic relationship of Turkish olives (<i>Olea europaea</i> subsp. <i>europaea</i>) cultivars based on cpDNA trnL-F regions. <i>Acta Botanica Croatica</i> , 2018, 77, 88-92.	0.3	7
50	Expression and Co-expression Analyses of WRKY, MYB, bHLH and bZIP Transcription Factor Genes in Potato (<i>Solanum tuberosum</i>) Under Abiotic Stress Conditions: RNA-seq Data Analysis. <i>Potato Research</i> , 2021, 64, 721-741.	1.2	6
51	Genome-wide identification of serine acetyltransferase (SAT) gene family in rice (<i>Oryza sativa</i>) and their expressions under salt stress. <i>Molecular Biology Reports</i> , 2021, 48, 6277-6290.	1.0	6
52	Molecular docking of <i>Glycine max</i> and <i>Medicago truncatula</i> ureases with urea; bioinformatics approaches. <i>Molecular Biology Reports</i> , 2016, 43, 129-140.	1.0	5
53	In silico identification and comparative analysis of molybdenum (Mo) transporter genes in plants. <i>Revista Brasileira De Botanica</i> , 2016, 39, 87-99.	0.5	5
54	Genome-wide identification and comparative analysis of EPSPS (aroA) genes in different plant species. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2016, 25, 21-29.	0.9	5

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55	Genome-wide identification and expression analysis of sulphate transporter (SULTR) genes under sulfur deficiency in <i>Brachypodium distachyon</i> . <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 263-273.	0.9	5
56	Antimicrobial peptides Snakin/GASA gene family in sorghum (<i>Sorghum bicolor</i>): Genome-wide identification and bioinformatics analyses. <i>Gene Reports</i> , 2020, 20, 100766.	0.4	5
57	Biological Network Analyses of WRKY Transcription Factor Family in Soybean (<i>Glycine max</i>) under Low Phosphorus Treatment. <i>Journal of Crop Science and Biotechnology</i> , 2020, 23, 127-136.	0.7	5
58	SSRs mining of Brassica species in mitochondrial genomes: Bioinformatic approaches. <i>Horticulture Environment and Biotechnology</i> , 2013, 54, 548-553.	0.7	4
59	Assessment of genetic diversity and phylogenetic relationships of endangered endemic plant <i>Barbarea integrifolia</i> DC. (Brassicaceae) in Turkey. <i>Turkish Journal of Botany</i> , 2014, 38, 1169-1181.	0.5	4
60	Dissecting a co-expression network of basic helix-loop-helix (bHLH) genes from phosphate (Pi)-starved soybean (<i>Glycine max</i>). <i>Plant Gene</i> , 2017, 9, 19-25.	1.4	4
61	Wall associated kinases (WAKs) gene family in tomato (<i>Solanum lycopersicum</i>): Insights into plant immunity. <i>Gene Reports</i> , 2020, 21, 100828.	0.4	4
62	Characterization of wound-induced serine protease inhibitor (wip1) genes and proteins in Turkish maize varieties. <i>Biochemistry (Moscow)</i> , 2014, 79, 836-844.	0.7	3
63	Barley molybdenum cofactor sulfurase (MCSU): sequencing, modeling, and its comparison to other higher plants. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 786-796.	0.8	3
64	STAY-GREEN (SGR) genes in tomato (<i>Solanum lycopersicum</i>): genome-wide identification, and expression analyses reveal their involvements in ripening and salinity stress responses. <i>Horticulture Environment and Biotechnology</i> , 2022, 63, 557-569.	0.7	3
65	Analysis of EST-SSRs in silver birch (<i>Betula pendula</i> Roth.). <i>Journal of Forestry Research</i> , 2016, 27, 639-646.	1.7	2
66	Effects of exogenous nitric oxide on cadmium toxicity in black poplar (<i>Populus nigra</i>): physiological approaches. <i>Acta Botanica Croatica</i> , 2019, 78, 116-124.	0.3	2
67	Genome wide analysis of stress responsive WRKY transcription factors in <i>Arabidopsis thaliana</i> . <i>Turkish Journal of Agriculture: Food Science and Technology</i> , 2016, 4, 279.	0.1	2
68	Genes involved in mRNA surveillance are induced in <i>Brachypodium distachyon</i> under cadmium toxicity. <i>Molecular Biology Reports</i> , 2022, 49, 5303-5313.	1.0	2
69	Comparative analyses of squalene synthase (SQS) proteins in poplar and pine by using bioinformatics tools. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	1
70	Assessment of genetic diversity in natural European hophornbeam (<i>Ostrya carpinifolia</i> Scop.) populations in Turkey. <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 948-955.	0.5	1
71	Comparative analysis of embryo surrounding region (Esr-6) genes in Turkish maize varieties: sequencing and modeling. <i>Revista Brasileira De Botanica</i> , 2016, 39, 287-293.	0.5	1
72	Sulfite Reductase (SiR) Gene in Rice (<i>Oryza sativa</i>): Bioinformatics and Expression Analyses Under Salt and Drought Stresses. <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2246-2260.	2.8	1

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73	Bioinformatics Database Resources for Plant Transcription Factors. , 2017, , 161-177.		0
74	Isolation of quantitative trait loci/gene(s) conferring cadmium tolerance in sorghum.. , 2021, , 463-475.		0
75	Diploid Brachypodium distachyon of Turkey: Molecular and Morphologic Analysis. , 2008, , 1-7.		0
76	Comprehensive analyses of gene expression and identification of metabolites for boron stress tolerance. , 2022, , 187-205.		0