

# PlantCARE, a database of plant cis-acting regulatory elements in silico analysis of promoter sequences

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Different Regulatory Regions Are Required for the Vernalization-Induced Repression of FLOWERING LOCUS C and for the Epigenetic Maintenance of Repression. <i>Plant Cell</i> , 2002, 14, 2527-2537.	3.1	243
2	A Gibbs Sampling Method to Detect Overrepresented Motifs in the Upstream Regions of Coexpressed Genes. <i>Journal of Computational Biology</i> , 2002, 9, 447-464.	0.8	301
3	Functional bioinformatics of microarray data: from expression to regulation. <i>Proceedings of the IEEE</i> , 2002, 90, 1722-1743.	16.4	37
4	The promoter of the nematode resistance gene Hs1pro-1 activates a nematode-responsive and feeding site-specific gene expression in sugar beet ( <i>Beta vulgaris</i> L.) and <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2003, 52, 643-660.	2.0	73
5	Isolation and identification of a super strong plant promoter from cotton leaf curl Multan virus. <i>Plant Molecular Biology</i> , 2003, 53, 1-14.	2.0	32
6	Two cassava promoters related to vascular expression and storage root formation. <i>Planta</i> , 2003, 218, 192-203.	1.6	50
7	AGRIS: Arabidopsis gene regulatory information server, an information resource of Arabidopsis cis-regulatory elements and transcription factors. <i>BMC Bioinformatics</i> , 2003, 4, 25.	1.2	349
8	Glutathione peroxidase genes in Arabidopsis are ubiquitous and regulated by abiotic stresses through diverse signaling pathways. <i>Plant Journal</i> , 2003, 36, 602-615.	2.8	277
9	The Evolution of Transcriptional Regulation in Eukaryotes. <i>Molecular Biology and Evolution</i> , 2003, 20, 1377-1419.	3.5	1,034
10	What drives plant stress genes?. <i>Trends in Plant Science</i> , 2003, 8, 99-102.	4.3	22
11	Bioinformatics: Organisms from Venus, Technology from Jupiter, Algorithms from Mars. <i>European Journal of Control</i> , 2003, 9, 237-278.	1.6	10
12	Genomic Cloning of Ribonucleases in <i>Nicotiana glutinosa</i> Leaves, as Induced in Response to Wounding or to TMV-Infection, and Characterization of Their Promoters. <i>Bioscience, Biotechnology and Biochemistry</i> , 2003, 67, 2574-2583.	0.6	17
13	Microarray analysis of E2Fa-DPa-overexpressing plants uncovers a cross-talking genetic network between DNA replication and nitrogen assimilation. <i>Journal of Cell Science</i> , 2003, 116, 4249-4259.	1.2	75
14	INCLUSive: a web portal and service registry for microarray and regulatory sequence analysis. <i>Nucleic Acids Research</i> , 2003, 31, 3468-3470.	6.5	46
15	Computational Approaches to Identify Promoters and cis-Regulatory Elements in Plant Genomes. <i>Plant Physiology</i> , 2003, 132, 1162-1176.	2.3	158
16	Salicylic Acid and NPR1 Induce the Recruitment of trans-Activating TGA Factors to a Defense Gene Promoter in Arabidopsis. <i>Plant Cell</i> , 2003, 15, 1846-1858.	3.1	295
17	PlantProm: a database of plant promoter sequences. <i>Nucleic Acids Research</i> , 2003, 31, 114-117.	6.5	240
18	Conserved Noncoding Sequences in the Grasses. <i>Genome Research</i> , 2003, 13, 2030-2041.	2.4	107

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20	Conserved Noncoding Sequences among Cultivated Cereal Genomes Identify Candidate Regulatory Sequence Elements and Patterns of Promoter Evolution[W]. <i>Plant Cell</i> , 2003, 15, 1143-1158.	3.1	96
21	Molecular Analysis of the Pathway for the Synthesis of Thiol Tripeptides in the Model Legume Lotus japonicus. <i>Molecular Plant-Microbe Interactions</i> , 2003, 16, 1039-1046.	1.4	41
22	DoOP: Databases of Orthologous Promoters, collections of clusters of orthologous upstream sequences from chordates and plants. <i>Nucleic Acids Research</i> , 2004, 33, D86-D90.	6.5	26
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25	The Fast and Transient Transcriptional Network of Gravity and Mechanical Stimulation in the Arabidopsis Root Apex. <i>Plant Physiology</i> , 2004, 136, 2790-2805.	2.3	162
26	Overexpression of a zinc-finger protein gene from rice confers tolerance to cold, dehydration, and salt stress in transgenic tobacco. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6309-6314.	3.3	427
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74	Cloning and characterization of a pentatricopeptide protein encoding gene (LOJ) that is specifically expressed in lateral organ junctions in <i>Arabidopsis thaliana</i> . <i>Gene</i> , 2005, 353, 67-79.	1.0	36
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414	Native polyubiquitin promoter of rice provides increased constitutive expression in stable transgenic rice plants. <i>Plant Cell Reports</i> , 2012, 31, 271-279.	2.8	28



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422	Abscisic acid regulates pinoresinol and lariciresinol reductase gene expression and secoisolariciresinol accumulation in developing flax ( <i>Linum usitatissimum</i> L.) seeds. <i>Planta</i> , 2012, 235, 85-98.	1.6	35
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424	Functional analysis of light-regulated promoter region of <i>AtPolII</i> gene. <i>Planta</i> , 2012, 235, 411-432.	1.6	18
425	Features of a unique intronless cluster of class I small heat shock protein genes in tandem with box C/D snoRNA genes on chromosome 6 in tomato ( <i>Solanum lycopersicum</i> ). <i>Planta</i> , 2012, 235, 453-471.	1.6	31
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427	Superoxide dismutase multigene family in longan somatic embryos: a comparison of CuZn-SOD, Fe-SOD, and Mn-SOD gene structure, splicing, phylogeny, and expression. <i>Molecular Breeding</i> , 2013, 32, 595-615.	1.0	48
428	Expression patterns and promoter characteristics of the gene encoding <i>Actinidia deliciosa</i> l-galactose-1-phosphate phosphatase involved in the response to light and abiotic stresses. <i>Molecular Biology Reports</i> , 2013, 40, 1473-1485.	1.0	27
429	Developmental and LED Light Source Modulation of Carotenogenic Gene Expression in <i>Oncidium Gower Ramsey</i> Flowers. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 1433-1445.	1.0	3
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443	Computational Identification of MicroRNAs and Their Targets in Cassava ( <i>Manihot esculenta</i> Crantz.). <i>Molecular Biotechnology</i> , 2013, 53, 257-269.	1.3	76
444	Light and abiotic stresses regulate the expression of GDP-l-galactose phosphorylase and levels of ascorbic acid in two kiwifruit genotypes via light-responsive and stress-inducible cis-elements in their promoters. <i>Planta</i> , 2013, 238, 535-547.	1.6	39
445	Characterization and expression analysis of waxy alleles in barley accessions. <i>Genetica</i> , 2013, 141, 227-238.	0.5	19
446	The rice <i>OsLTP6</i> gene promoter directs anther-specific expression by a combination of positive and negative regulatory elements. <i>Planta</i> , 2013, 238, 845-857.	1.6	24
447	Molecular cloning and expression of five glutathione S-transferase (GST) genes from Banana ( <i>Musa</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.8	18
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449	The role of MrbHLH1 and MrMYB1 in regulating anthocyanin biosynthetic genes in tobacco and Chinese bayberry ( <i>Myrica rubra</i> ) during anthocyanin biosynthesis. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 115, 285-298.	1.2	60
450	The promoter of soybean photoreceptor <i>GmPLP1</i> gene enhances gene expression under plant growth regulator and light stresses. <i>Plant Cell, Tissue and Organ Culture</i> , 2013, 114, 109-119.	1.2	17

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452	Molecular characterization of SCARECROW (CsSCR) gene expressed during somatic embryo development and in root of cucumber ( <i>Cucumis sativus</i> L.). <i>Acta Physiologiae Plantarum</i> , 2013, 35, 1483-1495.	1.0	9
453	Molecular analysis of the annexin gene family in soybean. <i>Biologia Plantarum</i> , 2013, 57, 655-662.	1.9	27
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455	Strength comparison between cold-inducible promoters of <i>Arabidopsis</i> cor15a and cor15b genes in potato and tobacco. <i>Plant Physiology and Biochemistry</i> , 2013, 71, 77-86.	2.8	16
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463	CBF gene expression in peach leaf and bark tissues is gated by a circadian clock. <i>Tree Physiology</i> , 2013, 33, 866-877.	1.4	45
464	Transcriptional control of early vein expression of CYCA2; 1 and CYCA2;4 in <i>Arabidopsis</i> leaves. <i>Mechanisms of Development</i> , 2013, 130, 14-24.	1.7	14
465	Altered invertase activities of symptomatic tissues on Beet severe curly top virus (BSCTV) infected <i>Arabidopsis thaliana</i> . <i>Journal of Plant Research</i> , 2013, 126, 743-752.	1.2	11
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470	Designed transcriptional regulators for trait development. <i>Plant Science</i> , 2013, 201-202, 128-136.	1.7	28
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474	Ectopic expression of the ABA-inducible dehydration-responsive chickpea l-myo-inositol 1-phosphate synthase 2 (CaMIPS2) in <i>Arabidopsis</i> enhances tolerance to salinity and dehydration stress. <i>Planta</i> , 2013, 237, 321-335.	1.6	44
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478	Molecular cloning and expression analysis of PDR1-like gene in ginseng subjected to salt and cold stresses or hormonal treatment. <i>Plant Physiology and Biochemistry</i> , 2013, 71, 203-211.	2.8	22
479	Characterization of a T-DNA promoter trap line of <i>Arabidopsis thaliana</i> uncovers a cryptic bi-directional promoter. <i>Gene</i> , 2013, 524, 22-27.	1.0	15
480	MicroRNA Primary Transcripts and Promoter Elements Analysis in Soybean ( <i>Glycine max</i> L. Merrill.). <i>Journal of Integrative Agriculture</i> , 2013, 12, 1522-1529.	1.7	5
481	Isolation and expression profiling of GhNAC transcription factor genes in cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 262	1.0	60
482	Functional analysis and tissue-differential expression of four FAD2 genes in amphidiploid <i>Brassica napus</i> derived from <i>Brassica rapa</i> and <i>Brassica oleracea</i> . <i>Gene</i> , 2013, 531, 253-262.	1.0	36
483	Association genetics of chemical wood properties in black poplar ( <i>Populus nigra</i> ). <i>New Phytologist</i> , 2013, 197, 162-176.	3.5	81
484	The <i>cis</i> -acting CTTC-P1BS module is indicative for gene function of <i>LjVTI12</i> , a SNARE protein gene that is required for arbuscule formation in <i>Ljotus japonicus</i> . <i>Plant Journal</i> , 2013, 74, 280-293.	2.8	67
485	Effects of Deficiency and Excess of Zinc on Morphophysiological Traits and Spatiotemporal Regulation of Zinc-Responsive Genes Reveal Incidence of Cross Talk between Micro- and Macronutrients. <i>Environmental Science &amp; Technology</i> , 2013, 47, 5327-5335.	4.6	80
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501	Characterization of a Maize <i>Wip1</i> Promoter in Transgenic Plants. <i>International Journal of Molecular Sciences</i> , 2013, 14, 23872-23892.	1.8	10
502	Differentially expressed myo-inositol monophosphatase gene ( <i>CaIMP</i> ) in chickpea ( <i>Cicer arietinum</i> L.) encodes a lithium-sensitive phosphatase enzyme with broad substrate specificity and improves seed germination and seedling growth under abiotic stresses. <i>Journal of Experimental Botany</i> , 2013, 64, 5623-5639.	2.4	56
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520	The Rose ( <i>Rosa hybrida</i> ) NAC Transcription Factor 3 Gene, RhNAC3, Involved in ABA Signaling Pathway Both in Rose and Arabidopsis. <i>PLoS ONE</i> , 2014, 9, e109415.	1.1	22
521	Ectopic Expression of CsCTR1, a Cucumber CTR-Like Gene, Attenuates Constitutive Ethylene Signaling in an Arabidopsis <i>ctr1-1</i> Mutant and Expression Pattern Analysis of CsCTR1 in Cucumber ( <i>Cucumis sativus</i> ). <i>International Journal of Molecular Sciences</i> , 2014, 15, 16331-16350.	1.8	11
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528	Isolation, in silico characterization, localization and expression analysis of abiotic stress-responsive rice G-protein $\beta^2$ subunit (RGB1). <i>Plant Signaling and Behavior</i> , 2014, 9, e28890.	1.2	15
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809	Analysis of cis-acting regulatory elements of Respiratory burst oxidase homolog (Rboh) gene families in <i>Arabidopsis</i> and rice provides clues for their diverse functions. <i>Computational Biology and Chemistry</i> , 2016, 62, 104-118.	1.1	65
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929	RING-H2-type E3 gene VpRH2 from <i>Vitis pseudoreticulata</i> improves resistance to powdery mildew by interacting with VpGRP2A. <i>Journal of Experimental Botany</i> , 2017, 68, 1669-1687.	2.4	32
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1056	Genome-wide Identification, Classification and Expression Analysis of the Mildew Resistance Locus O ( <i>O</i> ) Tj ETQq1 1 0.784314 rgBT /Ove 2017, 60, .	0.5	8
1057	Genome-wide identification and characterization of the RIO atypical kinase family in plants. Genes and Genomics, 2018, 40, 669-683.	0.5	6
1058	Genome-wide identification of glutathione peroxidase (GPX) gene family and their response to abiotic stress in cucumber. 3 Biotech, 2018, 8, 159.	1.1	36
1059	Methyl jasmonate as a control factor of the synthase squalene gene promoter and ginsenoside production in American ginseng hairy root cultured in shake flasks and a nutrient sprinkle bioreactor. Industrial Crops and Products, 2018, 115, 182-193.	2.5	28
1060	Genome-wide identification and expression analysis of chitinase gene family in <i>Brassica rapa</i> reveals its role in clubroot resistance. Plant Science, 2018, 270, 257-267.	1.7	46
1061	Gene expression and promoter characterization of heat-shock protein 90B gene (HSP90B) in the model unicellular green alga <i>Chlamydomonas reinhardtii</i> . Plant Science, 2018, 272, 107-116.	1.7	11
1062	Regulation of rice responses to submergence by WRKY transcription factors. Biologia Plantarum, 2018, 62, 551-560.	1.9	10

#	ARTICLE	IF	CITATIONS
1063	Integrated genomic and transcriptomic insights into the two-component high-affinity nitrate transporters in allotetraploid rapeseed. <i>Plant and Soil</i> , 2018, 427, 245-268.	1.8	13
1064	Genome-wide analysis of dirigent gene family in pepper ( <i>Capsicum annuum</i> L.) and characterization of CaDIR7 in biotic and abiotic stresses. <i>Scientific Reports</i> , 2018, 8, 5500.	1.6	51
1065	Ethylene responsive factor ERF110 mediates ethylene-regulated transcription of a sex determination-related orthologous gene in two <i>Cucumis</i> species. <i>Journal of Experimental Botany</i> , 2018, 69, 2953-2965.	2.4	56
1066	Functional Characterization of the Promoter and Second Intron of CUM1 During Flower Development in Cucumber ( <i>Cucumis sativus</i> L.). <i>Horticultural Plant Journal</i> , 2018, 4, 103-110.	2.3	16
1067	Genetic diversity and evolution of reduced sulfur storage during domestication of maize. <i>Plant Journal</i> , 2018, 94, 943-955.	2.8	5
1068	Differentially Expressed Peroxidases from <i>Artemisia annua</i> and Their Responses to Various Abiotic Stresses. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 295-309.	1.0	7
1069	Identification, evolution and expression analyses of Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit gene family in wheat ( <i>Triticum aestivum</i> L.). <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	3
1070	Functional characterization of the gene promoter for an <i>Elaeis guineensis</i> phosphate starvation-inducible, high affinity phosphate transporter in both homologous and heterologous model systems. <i>Plant Physiology and Biochemistry</i> , 2018, 127, 320-335.	2.8	10
1071	AhGLK1 affects chlorophyll biosynthesis and photosynthesis in peanut leaves during recovery from drought. <i>Scientific Reports</i> , 2018, 8, 2250.	1.6	60
1072	Transcriptomic Studies Revealing Enigma of Plant-Pathogen Interaction. , 2018, , 219-238.		3
1073	Transcriptome wide identification and characterization of NO-responsive WRKY transcription factors in <i>Arabidopsis thaliana</i> L.. <i>Environmental and Experimental Botany</i> , 2018, 148, 128-143.	2.0	39
1074	The superoxide dismutase genes might be required for appropriate development of the ovule after fertilization in <i>Xanthoceras sorbifolium</i> . <i>Plant Cell Reports</i> , 2018, 37, 727-739.	2.8	11
1075	Genome-wide in silico analysis of dehydrins in <i>Sorghum bicolor</i> , <i>Setaria italica</i> and <i>Zea mays</i> and quantitative analysis of dehydrin gene expressions under abiotic stresses in <i>Sorghum bicolor</i> . <i>Plant Gene</i> , 2018, 13, 64-75.	1.4	15
1076	Genome-wide identification of barley MCs (metacaspases) and their possible roles in boron-induced programmed cell death. <i>Molecular Biology Reports</i> , 2018, 45, 211-225.	1.0	29
1077	Functional analysis of a type 2C protein phosphatase gene from <i>Ammopiptanthus mongolicus</i> . <i>Gene</i> , 2018, 653, 29-42.	1.0	5
1078	Gene architecture and expression analyses provide insights into the role of glutathione peroxidases (GPXs) in bread wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Plant Physiology</i> , 2018, 223, 19-31.	1.6	39
1079	Salt and drought stress and ABA responses related to bZIP genes from <i>V. radiata</i> and <i>V. angularis</i> . <i>Gene</i> , 2018, 651, 152-160.	1.0	43
1080	Characterization of a sterile dwarf mutant and the cloning of zeaxanthin epoxidase in Asian cotton ( <i>Gossypium arboreum</i> L.). <i>Plant Growth Regulation</i> , 2018, 85, 57-72.	1.8	2

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1081	A profilin gene promoter from switchgrass ( <i>Panicum virgatum</i> L.) directs strong and specific transgene expression to vascular bundles in rice. <i>Plant Cell Reports</i> , 2018, 37, 587-597.	2.8	10
1083	The cinnamyl alcohol dehydrogenase family in flax: Differentiation during plant growth and under stress conditions. <i>Journal of Plant Physiology</i> , 2018, 221, 132-143.	1.6	34
1084	Genome-wide identification and analysis of the evolution and expression patterns of the cellulose synthase gene superfamily in <i>Gossypium</i> species. <i>Gene</i> , 2018, 646, 28-38.	1.0	22
1085	Abscisic acid is involved in aromatic ester biosynthesis related with ethylene in green apples. <i>Journal of Plant Physiology</i> , 2018, 221, 85-93.	1.6	41
1086	Structural characterization of a novel full-length transcript promoter from Horseradish Latent Virus (HRLV) and its transcriptional regulation by multiple stress responsive transcription factors. <i>Plant Molecular Biology</i> , 2018, 96, 179-196.	2.0	12
1087	Genome-wide identification and characterization of SPL transcription factor family and their evolution and expression profiling analysis in cotton. <i>Scientific Reports</i> , 2018, 8, 762.	1.6	56
1088	Genome-wide investigation and expression profiling of APX gene family in <i>Gossypium hirsutum</i> provide new insights in redox homeostasis maintenance during different fiber development stages. <i>Molecular Genetics and Genomics</i> , 2018, 293, 685-697.	1.0	47
1089	Overexpression of the tonoplast sugar transporter CmTST2 in melon fruit increases sugar accumulation. <i>Journal of Experimental Botany</i> , 2018, 69, 511-523.	2.4	77
1090	Molecular Characterization and Expression of PFT, an FHB Resistance Gene at the Fhb1 QTL in Wheat. <i>Phytopathology</i> , 2018, 108, 730-736.	1.1	32
1091	Expression and functional analysis of two <i>PsbS</i> genes in bamboo ( <i>Phyllostachys</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.6	3
1092	TF2Network: predicting transcription factor regulators and gene regulatory networks in Arabidopsis using publicly available binding site information. <i>Nucleic Acids Research</i> , 2018, 46, e31-e31.	6.5	107
1093	Two genetic changes in cis-regulatory elements caused evolution of petal spot position in <i>Clarkia</i> . <i>Nature Plants</i> , 2018, 4, 14-22.	4.7	29
1094	High-efficiency promoter-driven coordinated regulation of multiple metabolic nodes elevates lipid accumulation in the model microalga <i>Phaeodactylum tricornutum</i> . <i>Microbial Cell Factories</i> , 2018, 17, 54.	1.9	53
1095	Genome-wide identification and comparative analysis of the superoxide dismutase gene family in pear and their functions during fruit ripening. <i>Postharvest Biology and Technology</i> , 2018, 143, 68-77.	2.9	27
1096	Three members of <i>Medicago truncatula</i> ST family (MtST4, MtST5 and MtST6) are specifically induced by hormones involved in biotic interactions. <i>Plant Physiology and Biochemistry</i> , 2018, 127, 496-505.	2.8	6
1097	An R2R3-MYB transcription factor, SIMYB28, involved in the regulation of TYLCV infection in tomato. <i>Scientia Horticulturae</i> , 2018, 237, 192-200.	1.7	20
1098	Synergistic effect of abscisic acid and ethylene on color development in tomato ( <i>Solanum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 102 To	1.7	26
1099	<i>Magnaporthe oryzae</i> Induces the Expression of a MicroRNA to Suppress the Immune Response in Rice. <i>Plant Physiology</i> , 2018, 177, 352-368.	2.3	120

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1100	Genome-wide and comparative analysis of bHLH38, bHLH39, bHLH100 and bHLH101 genes in Arabidopsis, tomato, rice, soybean and maize: insights into iron (Fe) homeostasis. <i>BioMetals</i> , 2018, 31, 489-504.	1.8	29
1101	Characterization and expression analysis of circadian clock genes in the diploid woodland strawberry <i>Fragaria vesca</i> . <i>Biologia Plantarum</i> , 2018, 62, 451-461.	1.9	6
1102	Cloning and Analysis of Promoter Regions of Flavonoid Biosynthesis Genes in Safflower. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 239-246.	1.0	4
1103	Metabolic characterization of <i>Hyoscyamus niger</i> root-specific putrescine N-methyltransferase. <i>Plant Physiology and Biochemistry</i> , 2018, 127, 47-54.	2.8	17
1104	Sequence and functional characterization of MIRNA164 promoters from Brassica shows copy number dependent regulatory diversification among homeologs. <i>Functional and Integrative Genomics</i> , 2018, 18, 369-383.	1.4	13
1105	Differential Expression Patterns Within the Grapevine Stilbene Synthase Gene Family Revealed Through Their Regulatory Regions. <i>Plant Molecular Biology Reporter</i> , 2018, 36, 225-238.	1.0	14
1106	Low pH stress responsive transcriptome of seedling roots in wheat ( <i>Triticum aestivum</i> L.). <i>Genes and Genomics</i> , 2018, 40, 1199-1211.	0.5	15
1107	DCEO Biotechnology: Tools To Design, Construct, Evaluate, and Optimize the Metabolic Pathway for Biosynthesis of Chemicals. <i>Chemical Reviews</i> , 2018, 118, 4-72.	23.0	141
1108	Genome-wide analysis identifies chickpea ( <i>Cicer arietinum</i> ) heat stress transcription factors (Hsfs) responsive to heat stress at the pod development stage. <i>Journal of Plant Research</i> , 2018, 131, 525-542.	1.2	32
1109	Subfunctionalization of duplicate MYB genes in <i>Solanum commersonii</i> generated the cold-induced <i>ScAN2</i> and the anthocyanin regulator <i>ScAN1</i> . <i>Plant, Cell and Environment</i> , 2018, 41, 1038-1051.	2.8	45
1110	Genome-wide identification, phylogenetic analysis, and expression profiling of the BBX family genes in pear. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 37-50.	0.9	24
1111	Enhancing auxin accumulation in maize root tips improves root growth and dwarfs plant height. <i>Plant Biotechnology Journal</i> , 2018, 16, 86-99.	4.1	115
1112	Isolation and characterization of <i>Ulva prolifera</i> <i>actin1</i> gene and function verification of the 5â€² flanking region as a strong promoter. <i>Bioengineered</i> , 2018, 9, 124-133.	1.4	10
1113	<i>Muscadinia rotundifolia</i> "Noble" defense response to <i>Plasmopara viticola</i> inoculation by inducing phytohormone-mediated stilbene accumulation. <i>Protoplasma</i> , 2018, 255, 95-107.	1.0	20
1114	Genome-wide identification and characterization of phospholipase C gene family in cotton ( <i>Gossypium</i> ) Tj ETQq0 0.0rgBT /Overlock 10	2.3	26
1115	Fine mapping and candidate gene analysis of the virescent gene v 1 in Upland cotton ( <i>Gossypium</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 12	1.0	12
1116	Characterization of promoter of EgPAL1, a novel PAL gene from the oil palm <i>Elaeis guineensis</i> Jacq.. <i>Plant Cell Reports</i> , 2018, 37, 265-278.	2.8	13
1117	Genome-wide identification and expression analysis of the B-box gene family in the Apple ( <i>Malus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.0	70

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1118	Two members of unassigned type of short-chain dehydrogenase/reductase superfamily (SDR) isolated from <i>Persicaria minor</i> show response towards ABA and drought stress. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2018, 27, 260-271.	0.9	3
1120	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
1121	Gene mapping and transcriptome profiling of a practical photo-thermo-sensitive rice male sterile line with seedling-specific green-reversible albino leaf. <i>Plant Science</i> , 2018, 266, 37-45.	1.7	15
1122	Isolation and characterization of systemic acquired resistance marker gene PR1 and its promoter from <i>Brassica juncea</i> . <i>3 Biotech</i> , 2018, 8, 10.	1.1	34
1123	Evolution of intron-poor clades and expression patterns of the glycosyltransferase family 47. <i>Planta</i> , 2018, 247, 745-760.	1.6	22
1124	The phenotypic and molecular assessment of the non-conserved Arabidopsis MICRORNA163/S-ADENOSYL-METHYLTRANSFERASE regulatory module during biotic stress. <i>Molecular Genetics and Genomics</i> , 2018, 293, 503-523.	1.0	2
1125	Plant Biosynthetic Engineering Through Transcription Regulation: An Insight into Molecular Mechanisms During Environmental Stress. <i>Energy, Environment, and Sustainability</i> , 2018, , 51-72.	0.6	10
1126	Comprehensive analysis and transcript profiling of Arabidopsis thaliana and Oryza sativa catalase gene family suggests their specific roles in development and stress responses. <i>Plant Physiology and Biochemistry</i> , 2018, 123, 54-64.	2.8	49
1127	Identification and characterization of key circadian clock genes of tobacco hairy roots: putative regulatory role in xenobiotic metabolism. <i>Environmental Science and Pollution Research</i> , 2018, 25, 1597-1608.	2.7	11
1128	A transposition-active <i>Phyllostachys edulis</i> long terminal repeat (LTR) retrotransposon. <i>Journal of Plant Research</i> , 2018, 131, 203-210.	1.2	13
1129	Molecular characterization and expression analysis of WRKY family genes in <i>Dendrobium officinale</i> . <i>Genes and Genomics</i> , 2018, 40, 265-279.	0.5	14
1130	Genome-wide identification and expression analysis of beta-galactosidase family members during fruit softening of peach [ <i>Prunus persica</i> (L.) Batsch]. <i>Postharvest Biology and Technology</i> , 2018, 136, 111-123.	2.9	39
1131	Genome-wide identification, molecular evolution, and expression analysis of auxin response factor (ARF) gene family in <i>Brachypodium distachyon</i> L. <i>BMC Plant Biology</i> , 2018, 18, 336.	1.6	31
1132	A new insight into the evolution and functional divergence of <i>FRK</i> genes in <i>Pyrus bretschneideri</i> . <i>Royal Society Open Science</i> , 2018, 5, 171463.	1.1	6
1133	Expansion and Functional Divergence of the <i>SHORT VEGETATIVE PHASE</i> ( <i>SVP</i> ) Genes in Eudicots. <i>Genome Biology and Evolution</i> , 2018, 10, 3026-3037.	1.1	32
1134	GmDRR1, a dirigent protein resistant to <i>Phytophthora sojae</i> in <i>Glycine max</i> (L.) Merr.. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1289-1298.	1.7	8
1135	Isolation and analysis of a multifunctional triterpene synthaseKcMSpromoter region from mangrove plant <i>Kandelia candel</i> . <i>IOP Conference Series: Earth and Environmental Science</i> , 2018, 130, 012013.	0.2	4
1137	Genome-wide analysis of the soybean CRK-family and transcriptional regulation by biotic stress signals triggering plant immunity. <i>PLoS ONE</i> , 2018, 13, e0207438.	1.1	36



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1138	Two MYB transcription factors (CsMYB2 and CsMYB26) are involved in flavonoid biosynthesis in tea plant [ <i>Camellia sinensis</i> (L.) O. Kuntze]. <i>BMC Plant Biology</i> , 2018, 18, 288.	1.6	54
1139	Genome-Wide Identification and Characterization of Pectin Methylesterase Inhibitor Genes in Brassica oleracea. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3338.	1.8	9
1140	Genome-wide Characterization and Expression Analysis of Sugar Transporter Family Genes in Woodland Strawberry. <i>Plant Genome</i> , 2018, 11, 170103.	1.6	39
1141	Comparative genome-wide analysis of WRKY transcription factors in two Asian legume crops: Adzuki bean and Mung bean. <i>Scientific Reports</i> , 2018, 8, 16971.	1.6	35
1142	Genome-wide identification, characterization, and expression analysis of superoxide dismutase (SOD) genes in foxtail millet ( <i>Setaria italica</i> L.). <i>3 Biotech</i> , 2018, 8, 486.	1.1	23
1143	Genome-wide Identification, Classification, and Expression Pattern of Homeobox Gene Family in Brassica rapa under Various Stresses. <i>Scientific Reports</i> , 2018, 8, 16265.	1.6	28
1144	Structural and Functional Analysis of a Bidirectional Promoter from <i>Gossypium hirsutum</i> in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3291.	1.8	11
1146	HyPRP1 performs a role in negatively regulating cotton resistance to <i>V. dahliae</i> via the thickening of cell walls and ROS accumulation. <i>BMC Plant Biology</i> , 2018, 18, 339.	1.6	41
1147	Overexpression of the Wild Soybean R2R3-MYB Transcription Factor GsMYB15 Enhances Resistance to Salt Stress and <i>Helicoverpa Armigera</i> in Transgenic <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3958.	1.8	51
1148	Abundant Small Genetic Alterations after Upland Cotton Domestication. <i>BioMed Research International</i> , 2018, 2018, 1-7.	0.9	2
1149	Genome-wide identification and characterization of gene family for RWP-RK transcription factors in wheat ( <i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2018, 13, e0208409.	1.1	60
1150	The walnut transcription factor JrGRAS2 contributes to high temperature stress tolerance involving in Dof transcriptional regulation and HSP protein expression. <i>BMC Plant Biology</i> , 2018, 18, 367.	1.6	29
1151	Functional characterization of a $\Delta^6$ fatty acid desaturase gene and its 5'-upstream region cloned from the arachidonic acid-rich microalga <i>Myrmecia incisa</i> Reisinger (Chlorophyta). <i>Journal of Oceanology and Limnology</i> , 2018, 36, 2308-2321.	0.6	2
1152	Genome-Wide Identification and Expression Analysis of the CrRLK1L Gene Family in Apple ( <i>Malus</i> ) Tj ETQq1 1 0.784314 rgBT /Overload	1.0	18
1153	Integrated physiologic, genomic and transcriptomic strategies involving the adaptation of allotetraploid rapeseed to nitrogen limitation. <i>BMC Plant Biology</i> , 2018, 18, 322.	1.6	19
1154	Genome-wide characterization and phylogenetic analysis of GSK gene family in three species of cotton: evidence for a role of some GSKs in fiber development and responses to stress. <i>BMC Plant Biology</i> , 2018, 18, 330.	1.6	34
1155	Genome-Wide Analysis of LRR-RLK Gene Family in Four <i>Gossypium</i> Species and Expression Analysis during Cotton Development and Stress Responses. <i>Genes</i> , 2018, 9, 592.	1.0	17
1156	Genome-wide exploration of C2H2 zinc finger family in durum wheat ( <i>Triticum turgidum</i> ssp. Durum): insights into the roles in biological processes especially stress response. <i>BioMetals</i> , 2018, 31, 1019-1042.	1.8	37

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1157	TCP Transcription Factors in Moso Bamboo ( <i>Phyllostachys edulis</i> ): Genome-Wide Identification and Expression Analysis. <i>Frontiers in Plant Science</i> , 2018, 9, 1263.	1.7	60
1158	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. <i>3 Biotech</i> , 2018, 8, 426.	1.1	28
1159	<i>INCREASING NODULE SIZE</i> Expression Is Required for Normal Rhizobial Symbiosis and Nodule Development. <i>Plant Physiology</i> , 2018, 178, 1233-1248.	2.3	30
1160	Genome-Wide Identification of the TCP Transcription Factor Family in Chickpea ( <i>Cicer arietinum</i> L.) and Their Transcriptional Responses to Dehydration and Exogenous Abscisic Acid Treatments. <i>Journal of Plant Growth Regulation</i> , 2018, 37, 1286-1299.	2.8	5
1161	Exploring transcription factors reveals crucial members and regulatory networks involved in different abiotic stresses in <i>Brassica napus</i> L.. <i>BMC Plant Biology</i> , 2018, 18, 202.	1.6	53
1162	Glycinebetaine Biosynthesis in Response to Osmotic Stress Depends on Jasmonate Signaling in Watermelon Suspension Cells. <i>Frontiers in Plant Science</i> , 2018, 9, 1469.	1.7	64
1163	Genome-wide analysis of the rice PPR gene family and their expression profiles under different stress treatments. <i>BMC Genomics</i> , 2018, 19, 720.	1.2	76
1164	Characterization of a strong and constitutive promoter from the <i>Arabidopsis</i> serine carboxypeptidase-like gene <i>AtSCPL30</i> as a potential tool for crop transgenic breeding. <i>BMC Biotechnology</i> , 2018, 18, 59.	1.7	42
1165	Genome-wide identification and characterization of apple long-chain Acyl-CoA synthetases and expression analysis under different stresses. <i>Plant Physiology and Biochemistry</i> , 2018, 132, 320-332.	2.8	41
1166	Genome-Wide Identification and Characterization of wALOG Family Genes Involved in Branch Meristem Development of Branching Head Wheat. <i>Genes</i> , 2018, 9, 510.	1.0	8
1167	Identification, Structural Characterization and Gene Expression Analysis of Members of the Nuclear Factor-Y Family in Chickpea ( <i>Cicer arietinum</i> L.) under Dehydration and Abscisic Acid Treatments. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3290.	1.8	14
1168	NAC transcription factor ONAC066 positively regulates disease resistance by suppressing the ABA signaling pathway in rice. <i>Plant Molecular Biology</i> , 2018, 98, 289-302.	2.0	49
1169	Identification and Expression Analyses of SBP-Box Genes Reveal Their Involvement in Abiotic Stress and Hormone Response in Tea Plant ( <i>Camellia sinensis</i> ). <i>International Journal of Molecular Sciences</i> , 2018, 19, 3404.	1.8	25
1170	Genome-Wide Characterization of the sHsp Gene Family in <i>Salix suchowensis</i> Reveals Its Functions under Different Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3246.	1.8	20
1171	Overexpression of a Novel ROP Gene from the Banana ( <i>MaROP5g</i> ) Confers Increased Salt Stress Tolerance. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3108.	1.8	22
1172	Genome-wide identification of tomato ( <i>Solanum lycopersicum</i> L.) lipoxygenases coupled with expression profiles during plant development and in response to methyl-jasmonate and wounding. <i>Journal of Plant Physiology</i> , 2018, 231, 318-328.	1.6	47
1173	<i>Citrus sinensis</i> MYB transcription factors CsMYB330 and CsMYB308 regulate fruit juice sac lignification through fine-tuning expression of the Cs4CL1 gene. <i>Plant Science</i> , 2018, 277, 334-343.	1.7	37
1174	Genome-wide analysis of the basic Helix-Loop-Helix (bHLH) transcription factor family in maize. <i>BMC Plant Biology</i> , 2018, 18, 235.	1.6	102

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1175	Genome-wide characterization of the NRAMP gene family in <i>Phaseolus vulgaris</i> provides insights into functional implications during common bean development. <i>Genetics and Molecular Biology</i> , 2018, 41, 820-833.	0.6	24
1176	Molecular Cloning and Functional Characterization of the Dehydrin (IpDHN) Gene From <i>Ipomoea pes-caprae</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1454.	1.7	27
1177	Expressional characterization of galacturonosyltransferase-like gene family in <i>Eucalyptus grandis</i> implies a role in abiotic stress responses. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	5
1178	Characterization of cycloartenol synthase KcCAS promoter region from mangrove plant ( <i>Kandelia</i> ) Tj ETQq1 1 0.784314 rgBT <sub>2</sub> /Overlock	0.3	12
1179	Molecular characterization of the genome-wide BOR transporter gene family and genetic analysis of BnaC04.BOR1;1c in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2018, 18, 193.	1.6	22
1180	Genome-Wide Identification of PIFs in Grapes ( <i>Vitis vinifera</i> L.) and Their Transcriptional Analysis under Lighting/Shading Conditions. <i>Genes</i> , 2018, 9, 451.	1.0	19
1181	Genome-wide identification of MADS-box family genes in moso bamboo ( <i>Phyllostachys edulis</i> ) and a functional analysis of PeMADS5 in flowering. <i>BMC Plant Biology</i> , 2018, 18, 176.	1.6	44
1182	Genome-Wide Identification and Expression Profiling of the TCP Family Genes in Spike and Grain Development of Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1282.	1.7	46
1183	<i>Populus trichocarpa</i> PtNF-YA9, A Multifunctional Transcription Factor, Regulates Seed Germination, Abiotic Stress, Plant Growth and Development in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 954.	1.7	38
1184	Profiling of the Differential Abundance of Drought and Salt Stress-Responsive MicroRNAs Across Grass Crop and Genetic Model Plant Species. <i>Agronomy</i> , 2018, 8, 118.	1.3	17
1185	Genome-wide identification, systematic analysis and characterization of SRO family genes in maize ( <i>Zea</i> ) Tj ETQq0 0 0 rgBT <sub>2</sub> /Overlock 10	1.0	12
1186	The type 4 metallothionein from <i>Brassica napus</i> seeds folds in a metal-dependent fashion and favours zinc over other metals. <i>Metallomics</i> , 2018, 10, 1430-1443.	1.0	20
1187	MdMYB58 Modulates Fe Homeostasis by Directly Binding to the MdMATE43 Promoter in Plants. <i>Plant and Cell Physiology</i> , 2018, 59, 2476-2489.	1.5	23
1188	Assessing Field <i>Prunus</i> Genotypes for Drought Responsive Potential by Carbon Isotope Discrimination and Promoter Analysis. <i>Agronomy</i> , 2018, 8, 42.	1.3	4
1189	Identification and characterization of a plastidial $\Delta^3$ fatty acid desaturase EgFAD8 from oil palm ( <i>Elaeis</i> ) Tj ETQq0 0 0 rgBT <sub>2</sub> /Overlock 1	1.1	7
1190	Function of the evolutionarily conserved plant methionine-S-sulfoxide reductase without the catalytic residue. <i>Protoplasma</i> , 2018, 255, 1741-1750.	1.0	7
1191	Molecular cloning and induced expression of the plasma membrane intrinsic protein gene and promoter from mulberry ( <i>Morus multicaulis</i> ). <i>Canadian Journal of Plant Science</i> , 2018, 98, 1245-1253.	0.3	2
1192	Genome-wide Identification and Expression Analyses of RPP13-like Genes in Barley. <i>Biochip Journal</i> , 2018, 12, 102-113.	2.5	18

#	ARTICLE	IF	CITATIONS
1193	RiHSPRO2, a nematode resistance protein-like homolog from a wild crucifer <i>Rorippa indica</i> (L.) Hiern, is a promising candidate to control mustard aphid <i>Lipaphis erysimi</i> . <i>Arthropod-Plant Interactions</i> , 2018, 12, 701-714.	0.5	4
1194	Synthetic Promoters: Designing the cis Regulatory Modules for Controlled Gene Expression. <i>Molecular Biotechnology</i> , 2018, 60, 608-620.	1.3	24
1195	Genome-wide identification and expression analysis of GRF genes regulating apple tree architecture. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	18
1196	Characterization of the glutathione S-transferase (GST) gene family in <i>Pyrus bretschneideri</i> and their expression pattern upon superficial scald development. <i>Plant Growth Regulation</i> , 2018, 86, 211-222.	1.8	36
1197	Characterization of Brassinazole resistant (BZR) gene family and stress induced expression in <i>Eucalyptus grandis</i> . <i>Physiology and Molecular Biology of Plants</i> , 2018, 24, 821-831.	1.4	30
1198	The chromatin remodeler ZmCHB101 impacts expression of osmotic stress-responsive genes in maize. <i>Plant Molecular Biology</i> , 2018, 97, 451-465.	2.0	31
1199	Network Modeling Unravels Mechanisms of Crosstalk between Ethylene and Salicylate Signaling in Potato. <i>Plant Physiology</i> , 2018, 178, 488-499.	2.3	28
1200	Development of endogenous promoters that drive high-level expression of introduced genes in the model diatom <i>Phaeodactylum tricornutum</i> . <i>Marine Genomics</i> , 2018, 42, 41-48.	0.4	12
1201	Genome-wide identification of the AP2/ERF transcription factor family in pepper ( <i>Capsicum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 42	0.9	51
1202	Identification of jumonjiC domain containing gene family among the <i>Oryza</i> species and their expression analysis in FL478, a salt tolerant rice genotype. <i>Plant Physiology and Biochemistry</i> , 2018, 130, 43-53.	2.8	19
1203	Genome-Wide Identification and Functional Analysis of NADPH Oxidase Family Genes in Wheat During Development and Environmental Stress Responses. <i>Frontiers in Plant Science</i> , 2018, 9, 906.	1.7	27
1204	Advances in the Regulation of In Vitro Paclitaxel Production: Methylation of a Y-Patch Promoter Region Alters BAPT Gene Expression in <i>Taxus</i> Cell Cultures. <i>Plant and Cell Physiology</i> , 2018, 59, 2255-2267.	1.5	15
1205	Molecular characterization, modeling, and docking analysis of late phytic acid biosynthesis pathway gene, inositol polyphosphate 6-/3-/5-kinase, a potential candidate for developing low phytate crops. <i>3 Biotech</i> , 2018, 8, 344.	1.1	11
1206	Classification and Genome-Wide Analysis of Chitin-Binding Proteins Gene Family in Pepper ( <i>Capsicum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 42 Applications. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2216.	1.8	35
1207	Functional characterization of two myo-inositol-1-phosphate synthase (MIPS) gene promoters from the halophytic wild rice ( <i>Porteresia coarctata</i> ). <i>Planta</i> , 2018, 248, 1121-1141.	1.6	7
1208	Genome-wide analysis of the potato Hsp20 gene family: identification, genomic organization and expression profiles in response to heat stress. <i>BMC Genomics</i> , 2018, 19, 61.	1.2	183
1209	Molecular characterization and differential expression suggested diverse functions of P-type II Ca <sup>2+</sup> ATPases in <i>Triticum aestivum</i> L. <i>BMC Genomics</i> , 2018, 19, 389.	1.2	39
1210	Genome-wide identification and analysis of the ALTERNATIVE OXIDASE gene family in diploid and hexaploid wheat. <i>PLoS ONE</i> , 2018, 13, e0201439.	1.1	8

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1211	Molecular characterization of the TaWTG1 in bread wheat ( <i>Triticum aestivum</i> L.). <i>Gene</i> , 2018, 678, 23-32.	1.0	5
1212	Genome-Wide Identification of Cyclic Nucleotide-Gated Ion Channel Gene Family in Wheat and Functional Analyses of TaCNGC14 and TaCNGC16. <i>Frontiers in Plant Science</i> , 2018, 9, 18.	1.7	44
1213	An APETALA2 Homolog, RcAP2, Regulates the Number of Rose Petals Derived From Stamens and Response to Temperature Fluctuations. <i>Frontiers in Plant Science</i> , 2018, 9, 481.	1.7	14
1214	Analysis of Î²-Galactosidase During Fruit Development and Ripening in Two Different Texture Types of Apple Cultivars. <i>Frontiers in Plant Science</i> , 2018, 9, 539.	1.7	43
1215	Molecular Characterization of SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) Gene Family in <i>Betula luminifera</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 608.	1.7	39
1216	Genotype-Specific Growth and Proteomic Responses of Maize Toward Salt Stress. <i>Frontiers in Plant Science</i> , 2018, 9, 661.	1.7	20
1217	Molecular Characterization of Magnesium Chelatase in Soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Frontiers in Plant Science</i> , 2018, 9, 720.	1.7	31
1218	Identification and transcriptional analysis of dehydrin gene family in cucumber ( <i>Cucumis sativus</i> ). <i>Acta Physiologiae Plantarum</i> , 2018, 40, 1.	1.0	8
1219	Identification of WRKY Gene Family from <i>Dimocarpus longan</i> and Its Expression Analysis during Flower Induction and Abiotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2169.	1.8	38
1220	Genome-wide identification and expression analysis of <i>Gossypium</i> RING-H2 finger E3 ligase genes revealed their roles in fiber development, and phytohormone and abiotic stress responses. <i>Journal of Cotton Research</i> , 2018, 1, .	1.0	50
1221	Molecular characterization of Brassica napus stress related transcription factors, BnMYB44 and BnVIP1, selected based on comparative analysis of <i>Arabidopsis thaliana</i> and <i>Eutrema salsugineum</i> transcriptomes. <i>Molecular Biology Reports</i> , 2018, 45, 1111-1124.	1.0	21
1222	Identification and comparative analysis of the MCU gene family in pear and its functions during fruit ripening. <i>Journal of Plant Physiology</i> , 2018, 229, 53-62.	1.6	6
1223	Comprehensive analysis of NAC transcription factors uncovers their roles during fiber development and stress response in cotton. <i>BMC Plant Biology</i> , 2018, 18, 150.	1.6	61
1224	The R2R3MYB Gene Family in <i>Phyllostachys edulis</i> : Genome-Wide Analysis and Identification of Stress or Development-Related R2R3MYBs. <i>Frontiers in Plant Science</i> , 2018, 9, 738.	1.7	45
1225	Advances in Integrating Genomics and Bioinformatics in the Plant Breeding Pipeline. <i>Agriculture (Switzerland)</i> , 2018, 8, 75.	1.4	55
1226	Genome-Wide Identification and Expression Profiling of Cytokinin Oxidase/Dehydrogenase (CKX) Genes Reveal Likely Roles in Pod Development and Stress Responses in Oilseed Rape ( <i>Brassica napus</i> L.). <i>Genes</i> , 2018, 9, 168.	1.0	41
1227	Genome-Wide Identification of the Alba Gene Family in Plants and Stress-Responsive Expression of the Rice Alba Genes. <i>Genes</i> , 2018, 9, 183.	1.0	29
1228	Dual role of SND1 facilitates efficient communication between abiotic stress signalling and normal growth in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2018, 8, 10114.	1.6	17

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1229	Contribution of abscisic acid to aromatic volatiles in cherry tomato ( <i>Solanum lycopersicum</i> L.) fruit during postharvest ripening. <i>Plant Physiology and Biochemistry</i> , 2018, 130, 205-214.	2.8	49
1230	Cloning and Functional Analysis of Phosphoethanolamine Methyltransferase Promoter from Maize ( <i>Zea mays</i> L.). <i>International Journal of Molecular Sciences</i> , 2018, 19, 191.	1.8	19
1231	AOX1-Subfamily Gene Members in <i>Olea europaea</i> cv. "Galega Vulgaris" Gene Characterization and Expression of Transcripts during IBA-Induced in Vitro Adventitious Rooting. <i>International Journal of Molecular Sciences</i> , 2018, 19, 597.	1.8	23
1232	Evolution and Stress Responses of <i>Gossypium hirsutum</i> SWEET Genes. <i>International Journal of Molecular Sciences</i> , 2018, 19, 769.	1.8	40
1233	Genome-Wide Analyses of the NAC Transcription Factor Gene Family in Pepper ( <i>Capsicum annum</i> L.): Chromosome Location, Phylogeny, Structure, Expression Patterns, Cis-Elements in the Promoter, and Interaction Network. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1028.	1.8	65
1234	Molecular Evolution and Expression Divergence of HMT Gene Family in Plants. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1248.	1.8	8
1235	Expression of AhDREB1, an AP2/ERF Transcription Factor Gene from Peanut, Is Affected by Histone Acetylation and Increases Abscisic Acid Sensitivity and Tolerance to Osmotic Stress in Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1441.	1.8	39
1236	Genome-Wide Identification and Expression Analysis of the UGlcAE Gene Family in Tomato. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1583.	1.8	27
1237	The Sucrose Synthase Gene Family in Chinese Pear ( <i>Pyrus bretschneideri</i> Rehd.): Structure, Expression, and Evolution. <i>Molecules</i> , 2018, 23, 1144.	1.7	47
1238	Comparative in Silico Analysis of Ferric Reduction Oxidase (FRO) Genes Expression Patterns in Response to Abiotic Stresses, Metal and Hormone Applications. <i>Molecules</i> , 2018, 23, 1163.	1.7	21
1239	Application of a JA-Ile Biosynthesis Inhibitor to Methyl Jasmonate-Treated Strawberry Fruit Induces Upregulation of Specific MBW Complex-Related Genes and Accumulation of Proanthocyanidins. <i>Molecules</i> , 2018, 23, 1433.	1.7	34
1240	Cloning and characterization of BES1/BZR1 transcription factor genes in maize. <i>Plant Growth Regulation</i> , 2018, 86, 235-249.	1.8	62
1241	Isolation and Comparative Analysis of Two Na <sup>+</sup> /H <sup>+</sup> Antiporter NHX2 Genes from <i>Pyrus betulaefolia</i> . <i>Plant Molecular Biology Reporter</i> , 2018, 36, 439-450.	1.0	10
1242	Molecular cloning and functional analysis of the promoter of $\delta^3$ -Tocopherol Methyl Transferase ( $\delta^3$ -TMT) gene of soybean ( <i>Glycine max</i> ). <i>3 Biotech</i> , 2018, 8, 325.	1.1	3
1243	Identification and characterization of the bZIP transcription factor family and its expression in response to abiotic stresses in sesame. <i>PLoS ONE</i> , 2018, 13, e0200850.	1.1	57
1244	Isolation and Characterization of a Green-Tissue Promoter from Common Wild Rice ( <i>Oryza rufipogon</i> ) Tj ETQq1 1 0,784314 rgBT /Overle	1.8	20
1245	Genome-Wide Identification and Analysis of Arabidopsis Sodium Proton Antiporter (NHX) and Human Sodium Proton Exchanger (NHE) Homologs in <i>Sorghum bicolor</i> . <i>Genes</i> , 2018, 9, 236.	1.0	37
1246	Fruits of Rosaceae Family as a Source of Anticancer Compounds and Molecular Innovations. , 2018, , 319-336.		0

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1247	Genetic Transformation of Millets: The Way Ahead. , 2018, , 249-286.		3
1248	Characterization of a ripening-related transcription factor FcNAC1 from <i>Fragaria chiloensis</i> fruit. <i>Scientific Reports</i> , 2018, 8, 10524.	1.6	44
1249	Natural variation in <i>Gm</i> <i>GBP1</i> promoter affects photoperiod control of flowering time and maturity in soybean. <i>Plant Journal</i> , 2018, 96, 147-162.	2.8	45
1250	A Zinc Finger Transcriptional Repressor Confers Pleiotropic Effects on Rice Growth and Drought Tolerance by Down-Regulating Stress-Responsive Genes. <i>Plant and Cell Physiology</i> , 2018, 59, 2129-2142.	1.5	42
1251	Characterization of the <i>Populus</i> Rab family genes and the function of <i>PtRabE1b</i> in salt tolerance. <i>BMC Plant Biology</i> , 2018, 18, 124.	1.6	27
1252	Genome-Wide Identification and Characterization of Four Gene Families Putatively Involved in Cadmium Uptake, Translocation and Sequestration in Mulberry. <i>Frontiers in Plant Science</i> , 2018, 9, 879.	1.7	45
1253	A malectin-like/leucine-rich repeat receptor protein kinase gene, <i>RLK1</i> , regulates powdery mildew resistance in wheat. <i>Molecular Plant Pathology</i> , 2018, 19, 2561-2574.	2.0	30
1254	Genome-wide identification, phylogeny, evolution, and expression patterns of <i>MtN3/saliva/SWEET</i> genes and functional analysis of <i>BcNS</i> in <i>Brassica rapa</i> . <i>BMC Genomics</i> , 2018, 19, 174.	1.2	19
1255	The walnut <i>JrVHAG1</i> gene is involved in cadmium stress response through ABA-signal pathway and MYB transcription regulation. <i>BMC Plant Biology</i> , 2018, 18, 19.	1.6	49
1256	Heterologous expression of rice 9-cis-epoxycarotenoid dioxygenase 4 ( <i>OsNCED4</i> ) in <i>Arabidopsis</i> confers sugar oversensitivity and drought tolerance. , 2018, 59, 2.		41
1257	Genome-wide analysis of the SPL/miR156 module and its interaction with the AP2/miR172 unit in barley. <i>Scientific Reports</i> , 2018, 8, 7085.	1.6	52
1258	Genome-wide analysis of poplar SAUR gene family and expression profiles under cold, polyethylene glycol and indole-3-acetic acid treatments. <i>Plant Physiology and Biochemistry</i> , 2018, 128, 50-65.	2.8	31
1259	Chilling-induced DNA Demethylation is associated with the cold tolerance of <i>Hevea brasiliensis</i> . <i>BMC Plant Biology</i> , 2018, 18, 70.	1.6	34
1260	Genome-wide identification and characterization of ALTERNATIVE OXIDASE genes and their response under abiotic stresses in <i>Camellia sinensis</i> (L.) O. Kuntze. <i>Planta</i> , 2018, 248, 1231-1247.	1.6	9
1261	Genome-Wide Identification, Molecular Evolution, and Expression Profiling Analysis of Pectin Methylesterase Inhibitor Genes in <i>Brassica campestris</i> ssp. <i>chinensis</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1338.	1.8	14
1262	Tomato MYB49 enhances resistance to <i>Phytophthora infestans</i> and tolerance to water deficit and salt stress. <i>Planta</i> , 2018, 248, 1487-1503.	1.6	80
1263	Enhanced vascular activity of a new chimeric promoter containing the full CaMV 35S promoter and the plant XYLOGEN PROTEIN 1 promoter. <i>3 Biotech</i> , 2018, 8, 380.	1.1	5
1264	Genome-wide identification of the auxin/indole-3-acetic acid (Aux/IAA) gene family in pepper, its characterisation, and comprehensive expression profiling under environmental and phytohormones stress. <i>Scientific Reports</i> , 2018, 8, 12008.	1.6	17

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1265	Genome-Wide Identification and Analysis of Polygalacturonase Genes in <i>Solanum lycopersicum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 2290.	1.8	41
1266	Dissecting promoter of <i>MYB1</i> gene showing petal-specific expression. <i>Plant Biotechnology</i> , 2018, 35, 243-248.	0.5	5
1267	Investigation of benzylisoquinoline alkaloid biosynthetic pathway and its transcriptional regulation in lotus. <i>Horticulture Research</i> , 2018, 5, 29.	2.9	50
1268	<i>LOL2</i> and <i>LOL5</i> loci control latex production by laticifer cells in <i>Euphorbia lathyris</i> . <i>New Phytologist</i> , 2018, 219, 1467-1479.	3.5	13
1269	DIACYLGLYCEROL ACYLTRANSFERASE1 Contributes to Freezing Tolerance. <i>Plant Physiology</i> , 2018, 177, 1410-1424.	2.3	77
1270	Identification of a seed maturation protein gene from <i>Coffea arabica</i> (CaSMP) and analysis of its promoter activity in tomato. <i>Plant Cell Reports</i> , 2018, 37, 1257-1268.	2.8	3
1271	Genome-wide analysis and expression profiles of glyoxalase gene families in Chinese cabbage ( <i>Brassica</i> ) Tj ETQq0 0,0rgBT /Oyerlock 10	1.1	18
1272	Genome-wide identification of wheat ( <i>Triticum aestivum</i> ) expansins and expansin expression analysis in cold-tolerant and cold-sensitive wheat cultivars. <i>PLoS ONE</i> , 2018, 13, e0195138.	1.1	30
1273	Transcriptome-wide identification and characterization of the copper and cadmium stress-responsive small RNAs and their targets in <i>Arabidopsis thaliana</i> . <i>Plant and Soil</i> , 2018, 429, 391-405.	1.8	7
1274	Evolutionary variation and expression profiling of Isopentenyl transferase gene family in <i>Arabidopsis thaliana</i> L. and <i>Oryza sativa</i> L.. <i>Plant Gene</i> , 2018, 15, 15-27.	1.4	26
1275	Dicer-like and RNA-dependent RNA polymerase gene family identification and annotation in the cultivated <i>Solanum tuberosum</i> and its wild relative <i>S. commersonii</i> . <i>Planta</i> , 2018, 248, 729-743.	1.6	24
1276	Tomato CYCLOPS/IPD3 is required for mycorrhizal symbiosis but not tolerance to <i>Fusarium</i> wilt in mycorrhiza-deficient tomato mutant <i>rmc</i> . <i>Mycorrhiza</i> , 2018, 28, 495-507.	1.3	7
1277	Promoter of the <i>TmHKT1;4-A1</i> gene of <i>Triticum monococcum</i> directs stress inducible, developmental regulated and organ specific gene expression in transgenic <i>Arabidopsis thaliana</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2018, 34, 99.	1.7	7
1278	Genome-wide analysis of the auxin response factors (ARF) gene family in barley ( <i>Hordeum vulgare</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 14-24.	0.9	39
1279	Isolation and identification of a vegetative organ-specific promoter from maize. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 277-287.	1.4	14
1280	Molecular Features and mRNA Expression of the Receptor for Activated C Kinase 1 from <i>Symbiodinium microadriaticum</i> ssp. <i>microadriaticum</i> During Growth and the Light/Dark cycle. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 254-266.	0.8	2
1281	GhKLCR1, a kinesin light chain-related gene, induces drought-stress sensitivity in <i>Arabidopsis</i> . <i>Science China Life Sciences</i> , 2019, 62, 63-75.	2.3	26
1282	Genome-wide exploration and characterization of miR172/euAP2 genes in <i>Brassica napus</i> L. for likely role in flower organ development. <i>BMC Plant Biology</i> , 2019, 19, 336.	1.6	25



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1283	HVA22 from citrus: A small gene family whose some members are involved in plant response to abiotic stress. <i>Plant Physiology and Biochemistry</i> , 2019, 142, 395-404.	2.8	16
1284	The Roles of GmERF135 in Improving Salt Tolerance and Decreasing ABA Sensitivity in Soybean. <i>Frontiers in Plant Science</i> , 2019, 10, 940.	1.7	28
1285	Cassava AGPase genes and their encoded proteins are different from those of other plants. <i>Planta</i> , 2019, 250, 1621-1635.	1.6	8
1286	Infrastructures of systems biology that facilitate functional genomic study in rice. <i>Rice</i> , 2019, 12, 15.	1.7	21
1287	Characteristics and Expression Pattern of MYC Genes in <i>Triticum aestivum</i> , <i>Oryza sativa</i> , and <i>Brachypodium distachyon</i> . <i>Plants</i> , 2019, 8, 274.	1.6	25
1288	Identification, expression, and putative target gene analysis of nuclear factor-Y (NF-Y) transcription factors in tea plant ( <i>Camellia sinensis</i> ). <i>Planta</i> , 2019, 250, 1671-1686.	1.6	26
1289	Identification and expression analysis of the GDSL esterase/lipase family genes, and the characterization of <i>SaGLIP8</i> in <i>Sedum alfredii</i> Hance under cadmium stress. <i>PeerJ</i> , 2019, 7, e6741.	0.9	18
1290	Genetic determinants controlling maize rubisco activase gene expression and a comparison with rice counterparts. <i>BMC Plant Biology</i> , 2019, 19, 351.	1.6	9
1291	The overexpression of rice <i>ACYL</i> $\alpha$ <i>CoA</i> $\beta$ <i>BINDING PROTEIN</i> 2 increases grain size and bran oil content in transgenic rice. <i>Plant Journal</i> , 2019, 100, 1132-1147.	2.8	28
1292	Highlight on the expression and the function of a novel MnSOD from diploid wheat ( <i>T. monococcum</i> ) in response to abiotic stress and heavy metal toxicity. <i>Plant Physiology and Biochemistry</i> , 2019, 142, 384-394.	2.8	17
1293	The R2R3 MYB transcription factor MdMYB30 modulates plant resistance against pathogens by regulating cuticular wax biosynthesis. <i>BMC Plant Biology</i> , 2019, 19, 362.	1.6	105
1295	Genome-wide analysis of cyclophilin gene family in wheat and identification of heat stress responsive members. <i>Plant Gene</i> , 2019, 19, 100197.	1.4	8
1296	Genome-Wide Analysis and Expression Profiling of the Heat Shock Factor Gene Family in <i>Phyllostachys edulis</i> during Development and in Response to Abiotic Stresses. <i>Forests</i> , 2019, 10, 100.	0.9	15
1297	Genome-Wide Identification and Expression Analysis of the Metacaspase Gene Family in <i>Gossypium</i> Species. <i>Genes</i> , 2019, 10, 527.	1.0	9
1298	Perspectives on the Application of Genome-Editing Technologies in Crop Breeding. <i>Molecular Plant</i> , 2019, 12, 1047-1059.	3.9	118
1299	<i>Trichoderma erinaceum</i> Bio-Priming Modulates the WRKYs Defense Programming in Tomato Against the <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i> (Fol) Challenged Condition. <i>Frontiers in Plant Science</i> , 2019, 10, 911.	1.7	48
1300	Identification and characterisation of the novel endogenous promoter HASP1 and its signal peptide from <i>Phaeodactylum tricornutum</i> . <i>Scientific Reports</i> , 2019, 9, 9941.	1.6	28
1301	Genome-wide identification and expression analysis of the BURP domain-containing genes in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2019, 20, 558.	1.2	17

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1302	Potential of concurrent expression of lipogenic genes by novel strong promoters in the oleaginous microalga <i>Phaeodactylum tricornutum</i> . <i>Biotechnology and Bioengineering</i> , 2019, 116, 3006-3015.	1.7	17
1303	Retrotransposon promoter of <i>Ruby1</i> controls both light- and cold-induced accumulation of anthocyanins in blood orange. <i>Plant, Cell and Environment</i> , 2019, 42, 3092-3104.	2.8	47
1304	Artificial selection on GmOLEO1 contributes to the increase in seed oil during soybean domestication. <i>PLoS Genetics</i> , 2019, 15, e1008267.	1.5	75
1305	Identification of a 119-bp Promoter of the Maize Sulfite Oxidase Gene (ZmSO) That Confers High-Level Gene Expression and ABA or Drought Inducibility in Transgenic Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3326.	1.8	42
1306	Functional Analysis of the Marigold ( <i>Tagetes erecta</i> ) Lycopene $\mu$ -cyclase (TeLCYe) Promoter in Transgenic Tobacco. <i>Molecular Biotechnology</i> , 2019, 61, 703-713.	1.3	7
1307	A bidirectional promoter from Papaya leaf crumple virus functions in both monocot and dicot plants. <i>Physiological and Molecular Plant Pathology</i> , 2019, 108, 101423.	1.3	6
1308	Characterization of the western white pine TIR-NBS-LRR ( <i>PmTNL2</i> ) gene by transcript profiling and promoter analysis. <i>Genome</i> , 2019, 62, 477-488.	0.9	5
1309	Expression and Functional Analysis of the Propamocarb-Related Gene CsMCF in Cucumber. <i>Frontiers in Plant Science</i> , 2019, 10, 871.	1.7	8
1310	RcAPI1, a Homolog of APETALA1, is Associated with Flower Bud Differentiation and Floral Organ Morphogenesis in <i>Rosa chinensis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 3557.	1.8	10
1311	Transcriptional Regulation of Carotenoid Biosynthesis in Plants: So Many Regulators, So Little Consensus. <i>Frontiers in Plant Science</i> , 2019, 10, 1017.	1.7	150
1312	Genome-wide analysis of the NF-Y gene family in peach ( <i>Prunus persica</i> L.). <i>BMC Genomics</i> , 2019, 20, 612.	1.2	36
1313	Different Roles of Heat Shock Proteins (70 kDa) During Abiotic Stresses in Barley ( <i>Hordeum vulgare</i> ) Genotypes. <i>Plants</i> , 2019, 8, 248.	1.6	27
1314	Genome-wide identification of glutathione S-transferase gene family in pepper, its classification, and expression profiling under different anatomical and environmental conditions. <i>Scientific Reports</i> , 2019, 9, 9101.	1.6	74
1315	6-SFT, a Protein from <i>Leymus mollis</i> , Positively Regulates Salinity Tolerance and Enhances Fructan Levels in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2691.	1.8	6
1316	Genome-Wide Analysis of ROS Antioxidant Genes in Resurrection Species Suggest an Involvement of Distinct ROS Detoxification Systems during Desiccation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3101.	1.8	34
1317	Functional characterization of a strong promoter of the early light-inducible protein gene from tomato. <i>Planta</i> , 2019, 250, 1307-1323.	1.6	13
1318	Genome-Wide Identification and Expression Profiling of the Polygalacturonase (PG) and Pectin Methylesterase (PME) Genes in Grapevine ( <i>Vitis vinifera</i> L.). <i>International Journal of Molecular Sciences</i> , 2019, 20, 3180.	1.8	37
1319	Expression Analysis and Regulation Network Identification of the CONSTANS-Like Gene Family in Moso Bamboo ( <i>Phyllostachys edulis</i> ) Under Photoperiod Treatments. <i>DNA and Cell Biology</i> , 2019, 38, 607-626.	0.9	5

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1321	Genome-wide identification and characterization of <i>Gretchen Hagen3</i> ( <i>GH3</i> ) family genes in <i>Brassica napus</i> . <i>Genome</i> , 2019, 62, 597-608.	0.9	7
1322	Isolation and characterization of an atypical LEA gene ( <i>IpLEA</i> ) from <i>Ipomoea pes-caprae</i> conferring salt/drought and oxidative stress tolerance. <i>Scientific Reports</i> , 2019, 9, 14838.	1.6	26
1323	Genome-wide identification, expression profiles and regulatory network of MAPK cascade gene family in barley. <i>BMC Genomics</i> , 2019, 20, 750.	1.2	45
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1326	A Fruitful Decade Using Synthetic Promoters in the Improvement of Transgenic Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 1433.	1.7	81
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1328	Identification of CBF Transcription Factors in Tea Plants and a Survey of Potential CBF Target Genes under Low Temperature. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5137.	1.8	34
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1330	Knockdown of CaHSP60-6 confers enhanced sensitivity to heat stress in pepper ( <i>Capsicum annuum</i> L.). <i>Planta</i> , 2019, 250, 2127-2145.	1.6	29
1331	Identification of an Embryonic Cell-Specific Region within the Pineapple SERK1 Promoter. <i>Genes</i> , 2019, 10, 883.	1.0	8
1332	Differential regulation of the banana stress NAC family by individual and combined stresses of drought and heat in susceptible and resistant genotypes. <i>Plant Physiology and Biochemistry</i> , 2019, 145, 184-194.	2.8	9
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1335	Function analysis of ZmNAC33, a positive regulator in drought stress response in Arabidopsis. <i>Plant Physiology and Biochemistry</i> , 2019, 145, 174-183.	2.8	19
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1349	Genome-Wide Analysis of NAC Gene Family in <i>Betula pendula</i> . Forests, 2019, 10, 741.	0.9	44
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1357	GhVTC1, the Key Gene for Ascorbate Biosynthesis in <i>Gossypium hirsutum</i> , Involves in Cell Elongation Under Control of Ethylene. <i>Cells</i> , 2019, 8, 1039.	1.8	14
1358	Genome-Wide Identification and Expression Analysis of GA2ox, GA3ox, and GA20ox Are Related to Gibberellin Oxidase Genes in Grape ( <i>Vitis Vinifera</i> L.). <i>Genes</i> , 2019, 10, 680.	1.0	44
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1364	Genome-wide identification of and functional insights into the late embryogenesis abundant (LEA) gene family in bread wheat ( <i>Triticum aestivum</i> ). <i>Scientific Reports</i> , 2019, 9, 13375.	1.6	42
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1366	Genome-wide identification and expression profile analysis of nuclear factor Y family genes in <i>Sorghum bicolor</i> L. (Moench). <i>PLoS ONE</i> , 2019, 14, e0222203.	1.1	28
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1382	Calcium-Dependent Protein Kinase Genes in <i>Glycyrrhiza Uralensis</i> Appear to be Involved in Promoting the Biosynthesis of Glycyrrhizic Acid and Flavonoids under Salt Stress. <i>Molecules</i> , 2019, 24, 1837.	1.7	16
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1393	Structural Organization and Functional Activity of the Orthologous TaGLW7 Genes in Bread Wheat ( <i>Triticum aestivum</i> L.). <i>Russian Journal of Genetics</i> , 2019, 55, 571-579.	0.2	1
1394	Genome-wide characterization of the WRKY gene family in cultivated strawberry ( <i>Fragaria ananassa</i> ). <i>Journal of Horticultural Science and Biotechnology</i> , 2019, 9, 8423.	1.6	19
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1398	Molecular cloning and functional characterization of a seed-specific Vv <sup>2</sup> VPE gene promoter from <i>Vitis vinifera</i> . <i>Planta</i> , 2019, 250, 657-665.	1.6	8
1399	Comparative analysis of B-BOX genes and their expression pattern analysis under various treatments in <i>Dendrobium officinale</i> . <i>BMC Plant Biology</i> , 2019, 19, 245.	1.6	31
1400	Isolation and Characterization of CsWRKY7, a Subgroup IId WRKY Transcription Factor from <i>Camellia sinensis</i> , Linked to Development in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2815.	1.8	14
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1407	Genome-Wide Identification and Expression Analyses of the bZIP Transcription Factor Genes in moso bamboo ( <i>Phyllostachys edulis</i> ). <i>International Journal of Molecular Sciences</i> , 2019, 20, 2203.	1.8	26
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1409	Expansion and Evolutionary Patterns of Glycosyltransferase Family 8 in Gramineae Crop Genomes and Their Expression under Salt and Cold Stresses in <i>Oryza sativa</i> ssp. <i>japonica</i> . <i>Biomolecules</i> , 2019, 9, 188.	1.8	30

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1411	Genome-Wide Identification, Evolution, and Transcriptional Profiling of <i>PP2C</i> Gene Family in <i>Brassica rapa</i> . <i>BioMed Research International</i> , 2019, 2019, 1-15.	0.9	30
1412	Effects of Brassinosteroid Associated with Auxin and Gibberellin on Apple Tree Growth and Gene Expression Patterns. <i>Horticultural Plant Journal</i> , 2019, 5, 93-108.	2.3	23
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1414	PgMYB2, a MeJA-Responsive Transcription Factor, Positively Regulates the Dammarenediol Synthase Gene Expression in <i>Panax Ginseng</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2219.	1.8	51
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1416	Identification of Histone H3 (HH3) Genes in <i>Gossypium hirsutum</i> Revealed Diverse Expression During Ovule Development and Stress Responses. <i>Genes</i> , 2019, 10, 355.	1.0	29
1417	Genome-Wide Identification of WRKY Transcription Factors in Chinese jujube ( <i>Ziziphus jujuba</i> Mill.) and Their Involvement in Fruit Developing, Ripening, and Abiotic Stress. <i>Genes</i> , 2019, 10, 360.	1.0	26
1418	The <i>MYB</i> transcription factor Emission of Methyl Anthranilate 1 stimulates emission of methyl anthranilate from <i>Medicago truncatula</i> hairy roots. <i>Plant Journal</i> , 2019, 99, 637-654.	2.8	10
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1425	Functional analysis of citrus AP2 transcription factors identified CsAP2-09 involved in citrus canker disease response and tolerance. <i>Gene</i> , 2019, 707, 178-188.	1.0	33
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1427	Organization and evolution of the chalcone synthase gene family in bread wheat and relative species. <i>BMC Genetics</i> , 2019, 20, 30.	2.7	16



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1429	Genome-wide identification and analysis of the EIN3/EIL gene family in allotetraploid <i>Brassica napus</i> reveal its potential advantages during polyploidization. <i>BMC Plant Biology</i> , 2019, 19, 110.	1.6	21
1430	Comprehensive Analyses of Nitric Oxide-Induced Plant Stem Cell-Related Genes in <i>Arabidopsis thaliana</i> . <i>Genes</i> , 2019, 10, 190.	1.0	13
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1432	Two grapevine metacaspase genes mediate ETI-like cell death in grapevine defence against infection of <i>Plasmopara viticola</i> . <i>Protoplasma</i> , 2019, 256, 951-969.	1.0	34
1433	The DOF Transcription Factor SIDOF10 Regulates Vascular Tissue Formation During Ovary Development in Tomato. <i>Frontiers in Plant Science</i> , 2019, 10, 216.	1.7	21
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1438	Genome-wide identification and characterization of abiotic-stress responsive SOD (superoxide) Tj ETQq0 0 0 rgBT /Oyerlock 10 Tf 50 34	1.2	94
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1440	Synergistic effects of <sc>HSE</sc> and <sc>LTR</sc> elements from <i>hsp70</i> gene promoter of <i>Ulva prolifera</i> (Ulvophyceae, Chlorophyta) upon temperature induction<sup>1</sup>. <i>Journal of Phycology</i> , 2019, 55, 738-743.	1.0	19
1441	A basic Helix-Loop-Helix (SIARANCIO), identified from a <i>Solanum pennellii</i> introgression line, affects carotenoid accumulation in tomato fruits. <i>Scientific Reports</i> , 2019, 9, 3699.	1.6	13
1442	Peach ethylene response factor PpeERF2 represses the expression of ABA biosynthesis and cell wall degradation genes during fruit ripening. <i>Plant Science</i> , 2019, 283, 116-126.	1.7	59
1443	Identification and characterization of core abscisic acid (ABA) signaling components and their gene expression profile in response to abiotic stresses in <i>Setaria viridis</i> . <i>Scientific Reports</i> , 2019, 9, 4028.	1.6	30
1444	Genome-wide identification, evolution, and molecular characterization of the PP2C gene family in woodland strawberry. <i>Gene</i> , 2019, 702, 27-35.	1.0	23
1445	Genome-Wide Analysis of LIM Family Genes in Foxtail Millet ( <i>Setaria italica</i> L.) and Characterization of the Role of SiWLM2b in Drought Tolerance. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1303.	1.8	39

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1447	OsRhoGAP2 promoter drives inflorescence-preferential expression and confers responses to abiotic stresses in transgenic <i>Arabidopsis</i> . <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	1.0	2
1448	Genome-wide identification of WOX genes and their expression patterns under different hormone and abiotic stress treatments in tea plant ( <i>Camellia sinensis</i> ). <i>Trees - Structure and Function</i> , 2019, 33, 1129-1142.	0.9	22
1449	Genome-wide identification, classification and expression analysis of the JmjC domain-containing histone demethylase gene family in maize. <i>BMC Genomics</i> , 2019, 20, 256.	1.2	31
1450	Genomic insights into HSFs as candidate genes for high-temperature stress adaptation and gene editing with minimal off-target effects in flax. <i>Scientific Reports</i> , 2019, 9, 5581.	1.6	18
1451	Circadian Regulation of Alternative Splicing of Drought-Associated CIPK Genes in <i>Dendrobium catenatum</i> (Orchidaceae). <i>International Journal of Molecular Sciences</i> , 2019, 20, 688.	1.8	14
1452	Characterization, expression, and functional analysis of polyamine oxidases and their role in selenium-induced hydrogen peroxide production in <i>Brassica rapa</i> . <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 4082-4093.	1.7	16
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1454	Cloning and functional analysis of the promoter of a stress-inducible gene ( <i>Zmap</i> ) in maize. <i>PLoS ONE</i> , 2019, 14, e0211941.	1.1	16
1455	Genome-wide identification, characterization, interaction network and expression profile of GRAS gene family in sweet orange ( <i>Citrus sinensis</i> ). <i>Scientific Reports</i> , 2019, 9, 2156.	1.6	24
1456	Phylogenomic analysis of cytochrome P450 multigene family and their differential expression analysis in <i>Solanum lycopersicum</i> L. suggested tissue specific promoters. <i>BMC Genomics</i> , 2019, 20, 116.	1.2	40
1457	Comparison of Trihelix transcription factors between wheat and <i>Brachypodium distachyon</i> at genome-wide. <i>BMC Genomics</i> , 2019, 20, 142.	1.2	19
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1460	Genome-wide characterization, molecular evolution and expression profiling of the metacaspases in potato ( <i>Solanum tuberosum</i> L.). <i>Heliyon</i> , 2019, 5, e01162.	1.4	11
1461	Comparative analyses of phytochelatin synthase ( <i>PCS</i> ) genes in higher plants. <i>Biotechnology and Biotechnological Equipment</i> , 2019, 33, 178-194.	0.5	36
1462	The genetic basis of drought tolerance in the high oil crop <i>Sesamum indicum</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 1788-1803.	4.1	63
1463	The Ethylene Signaling Pathway Negatively Impacts CBF/DREB-Regulated Cold Response in Soybean ( <i>Glycine max</i> ). <i>Frontiers in Plant Science</i> , 2019, 10, 121.	1.7	43

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1465	PpERF3 positively regulates ABA biosynthesis by activating PpNCED2/3 transcription during fruit ripening in peach. <i>Horticulture Research</i> , 2019, 6, 19.	2.9	51
1466	A systematic in silico prediction of gibberellic acid stimulated GASA family members: A novel small peptide contributes to floral architecture and transcriptomic changes induced by external stimuli in rice. <i>Journal of Plant Physiology</i> , 2019, 234-235, 117-132.	1.6	37
1467	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
1468	Genome-wide analysis of fatty acid desaturase genes in rice ( <i>Oryza sativa</i> L.). <i>Scientific Reports</i> , 2019, 9, 19445.	1.6	27
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1471	Transcriptional induction of capsidiol synthesis genes by wounding can promote pathogen signal-induced capsidiol synthesis. <i>BMC Plant Biology</i> , 2019, 19, 576.	1.6	5
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1473	Comparative Genome-wide Analysis and Expression Profiling of Histone Acetyltransferase (HAT) Gene Family in Response to Hormonal Applications, Metal and Abiotic Stresses in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5311.	1.8	26
1474	SiMYB3 in Foxtail Millet ( <i>Setaria italica</i> ) Confers Tolerance to Low-Nitrogen Stress by Regulating Root Growth in Transgenic Plants. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5741.	1.8	32
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1477	Functional Differentiation of Duplicated Flavonoid 3-O-Glycosyltransferases in the Flavonol and Anthocyanin Biosynthesis of <i>Freesia hybrida</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1330.	1.7	23
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1479	Identification and Expression Analysis of Gretchen Hagen 3 (GH3) in Kiwifruit ( <i>Actinidia chinensis</i> ) During Postharvest Process. <i>Plants</i> , 2019, 8, 473.	1.6	18
1480	Overexpression of native <i>Musa</i> -miR397 enhances plant biomass without compromising abiotic stress tolerance in banana. <i>Scientific Reports</i> , 2019, 9, 16434.	1.6	28
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1483	Identification and expression analysis of GRAS transcription factors in the wild relative of sweet potato <i>Ipomoea trifida</i> . <i>BMC Genomics</i> , 2019, 20, 911.	1.2	31
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1485	Identification, Evolution, and Expression Profiling of Histone Lysine Methylation Moderators in <i>Brassica rapa</i> . <i>Plants</i> , 2019, 8, 526.	1.6	8
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1497	An inducible expression system in the alga <i>Nannochloropsis gaditana</i> controlled by the nitrate reductase promoter. <i>Journal of Applied Phycology</i> , 2019, 31, 269-279.	1.5	14
1498	GhTCP19 Transcription Factor Regulates Corm Dormancy Release by Repressing <i>GhNCED</i> Expression in <i>Gladiolus</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 52-62.	1.5	26
1499	Multiple transcriptional regulation of walnut <i>JrGSTTau1</i> gene in response to osmotic stress. <i>Physiologia Plantarum</i> , 2019, 166, 748-761.	2.6	10

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1502	Genome-wide annotation and expression responses to biotic stresses of the WALL-ASSOCIATED KINASE - RECEPTOR-LIKE KINASE (WAK-RLK) gene family in Apple ( <i>Malus domestica</i> ). <i>European Journal of Plant Pathology</i> , 2019, 153, 771-785.	0.8	20
1503	Changes to the core and flanking sequences of G-box elements lead to increases and decreases in gene expression in both native and synthetic soybean promoters. <i>Plant Biotechnology Journal</i> , 2019, 17, 724-735.	4.1	19
1504	<i>NFYB12bHLH144</i> complex directly activates <i>Wx</i> to regulate grain quality in rice ( <i>Oryza sativa</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 1222-1235.	4.1	103
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1506	Completion of the cytosolic post-chorismate phenylalanine biosynthetic pathway in plants. <i>Nature Communications</i> , 2019, 10, 15.	5.8	103
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1508	Analysis of Brassica napus dehydrins and their Co-Expression regulatory networks in relation to cold stress. <i>Gene Expression Patterns</i> , 2019, 31, 7-17.	0.3	19
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1510	Genome-wide identification, characterization, and expression analysis of the expansin gene family in Chinese jujube ( <i>Ziziphus jujuba</i> Mill.). <i>Planta</i> , 2019, 249, 815-829.	1.6	32
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1512	Genome-wide analysis reveals the evolution and structural features of WRINKLED1 in plants. <i>Molecular Genetics and Genomics</i> , 2019, 294, 329-341.	1.0	16
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1514	Regulation of $\beta$ -expansins genes in <i>Arabidopsis thaliana</i> seeds during post-osmopriming germination. <i>Physiology and Molecular Biology of Plants</i> , 2019, 25, 511-522.	1.4	10
1515	Genome-wide identification and expression analysis of glycine-rich RNA-binding protein family in sweet potato wild relative <i>Ipomoea trifida</i> . <i>Gene</i> , 2019, 686, 177-186.	1.0	42
1516	Genome-wide identification and expression analysis of StTCP transcription factors of potato ( <i>Solanum tuberosum</i> L.). <i>Computational Biology and Chemistry</i> , 2019, 78, 53-63.	1.1	19
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1519	Systematic analysis of NAC transcription factors gene family and identification of post-flowering drought stress responsive members in sorghum. <i>Plant Cell Reports</i> , 2019, 38, 361-376.	2.8	38
1520	DRMY1, a Myb-Like Protein, Regulates Cell Expansion and Seed Production in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 285-302.	1.5	15
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1523	Cloning and functional characterization of the Na <sup>+</sup> /H <sup>+</sup> antiporter (NHX1) gene promoter from an extreme halophyte <i>Salicornia brachiata</i> . <i>Gene</i> , 2019, 683, 233-242.	1.0	34
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1526	The Dual Effect of the Brassinosteroid Pathway on Rice Black-Streaked Dwarf Virus Infection by Modulating the Peroxidase-Mediated Oxidative Burst and Plant Defense. <i>Molecular Plant-Microbe Interactions</i> , 2019, 32, 685-696.	1.4	21
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1532	H3K4/K9 acetylation and Lr28-mediated expression of six leaf rust responsive genes in wheat ( <i>Triticum aestivum</i> ) cv. Overlock 10. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 320-335.	1.0	16
1533	Expression and function analysis of a rice <i>OsHSP40</i> gene under salt stress. <i>Genes and Genomics</i> , 2019, 41, 175-182.	0.5	22
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1538	Transcription factorsâ€™DNA interactions in rice: identification and verification. <i>Briefings in Bioinformatics</i> , 2020, 21, 946-956.	3.2	19
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1540	Genome-Wide Identification of NAC Transcription Factor Family and Functional Analysis of the Abiotic Stress-Responsive Genes in <i>Medicago sativa</i> L.. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 324-337.	2.8	23
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1543	Genome-wide identification, expression profiling, and network analysis of AT-hook gene family in maize. <i>Genomics</i> , 2020, 112, 1233-1244.	1.3	27
1544	Genome-wide identification and transcriptional profiling of small heat shock protein gene family under diverse abiotic stress conditions in <i>Sorghum bicolor</i> (L.). <i>International Journal of Biological Macromolecules</i> , 2020, 142, 822-834.	3.6	36
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1548	Genome-wide characterisation of superoxide dismutase genes in grape and their expression analyses during berry development process. <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 53-64.	0.9	9
1549	Genome-Wide Analysis of LAZ1 Gene Family from Maize. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 656-668.	2.8	4
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1553	SICAND1, encoding cullin-associated Nedd8-dissociated protein 1, regulates plant height, flowering time, seed germination, and root architecture in tomato. <i>Plant Molecular Biology</i> , 2020, 102, 537-551.	2.0	12
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1557	Insight into the relationship between S-lignin and fiber quality based on multiple research methods. <i>Plant Physiology and Biochemistry</i> , 2020, 147, 251-261.	2.8	6
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1562	Genome-wide identification, characterization, and expression analysis of GDSL-type esterases/lipases gene family in relation to grape berry ripening. <i>Scientia Horticulturae</i> , 2020, 264, 109162.	1.7	26
1563	Genome Wide Identification of C2H2-Type Zinc Finger Proteins of Tomato and Expression Analysis Under Different Abiotic Stresses. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 75-94.	1.0	15
1564	SlMYB102, an R2R3-type MYB gene, confers salt tolerance in transgenic tomato. <i>Plant Science</i> , 2020, 291, 110356.	1.7	66
1565	Isolation of the 9-cis-epoxycarotenoid dioxygenase (NCED) gene from kiwifruit and its effects on postharvest softening and ripening. <i>Scientia Horticulturae</i> , 2020, 261, 109020.	1.7	25
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1568	Cloning and characterization of a gene encoding MIZ1, a domain of unknown function protein and its role in salt and drought stress in rice. <i>Protoplasma</i> , 2020, 257, 475-487.	1.0	18
1569	Endoplasmic reticulum retention signaling and transmembrane channel proteins predicted for oilseed $\omega$ -3 fatty acid desaturase 3 (FAD3) genes. <i>Functional and Integrative Genomics</i> , 2020, 20, 433-458.	1.4	4
1570	Genome-Wide Characterization and Gene Expression Analyses of GATA Transcription Factors in Moso Bamboo ( <i>Phyllostachys edulis</i> ). <i>International Journal of Molecular Sciences</i> , 2020, 21, 14.	1.8	33
1571	Comparative Analysis and Expression Patterns of the PLP_deC Genes in <i>Dendrobium officinale</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 54.	1.8	6
1572	Genome-Wide Identification and Characterization of the bHLH Transcription Factor Family in Pepper ( <i>Capsicum annuum</i> L.). <i>Frontiers in Genetics</i> , 2020, 11, 570156.	1.1	32



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1573	Cloning and functional characterization of two cinnamate 4-hydroxylase genes from <i>Pyrus bretschneideri</i> . <i>Plant Physiology and Biochemistry</i> , 2020, 156, 135-145.	2.8	19
1574	Chromosome-level genome assembly of a parent species of widely cultivated azaleas. <i>Nature Communications</i> , 2020, 11, 5269.	5.8	90
1575	The glutathione peroxidase family of <i>Theobroma cacao</i> : Involvement in the oxidative stress during witches' broom disease. <i>International Journal of Biological Macromolecules</i> , 2020, 164, 3698-3708.	3.6	12
1576	Genome-wide identification and characterization of Respiratory Burst Oxidase Homolog genes in six Rosaceae species and an analysis of their effects on adventitious rooting in apple. <i>PLoS ONE</i> , 2020, 15, e0239705.	1.1	10
1577	A Fragment Substitution in Promoter of MS92/PTC1 Causes Male Sterility in Rice. <i>Rice Science</i> , 2020, 27, 396-404.	1.7	4
1578	Characterization and Comparative Analysis of RWP-RK Proteins from <i>Arachis duranensis</i> , <i>Arachis ipaensis</i> , and <i>Arachis hypogaea</i> . <i>International Journal of Genomics</i> , 2020, 2020, 1-19.	0.8	3
1579	Genome-wide characterization and expression analysis of the heat shock transcription factor family in pumpkin ( <i>Cucurbita moschata</i> ). <i>BMC Plant Biology</i> , 2020, 20, 471.	1.6	9
1580	Comprehensive Genome-Wide Analysis of Thaumatin-Like Gene Family in Four Cotton Species and Functional Identification of GhTLP19 Involved in Regulating Tolerance to Verticillium dahlia and Drought. <i>Frontiers in Plant Science</i> , 2020, 11, 575015.	1.7	20
1581	Genome-Wide Identification, Classification, Characterization, and Expression Analysis of the Wall-Associated Kinase Family during Fruit Development and under Wound Stress in Tomato ( <i>Solanum</i> ) Tj ETQq0 0.0rgBT /Overlock 10	1.0	6
1582	Comprehensive analysis of AGPase genes uncovers their potential roles in starch biosynthesis in lotus seed. <i>BMC Plant Biology</i> , 2020, 20, 457.	1.6	11
1583	Genome-Wide Identification and Expression Analysis of the <i>Dof</i> Gene Family in <i>Medicago sativa</i> L. Under Various Abiotic Stresses. <i>DNA and Cell Biology</i> , 2020, 39, 1976-1989.	0.9	9
1584	Discovery and validation of candidate genes for grain iron and zinc metabolism in pearl millet [ <i>Pennisetum glaucum</i> (L.) R. Br.]. <i>Scientific Reports</i> , 2020, 10, 16562.	1.6	18
1585	Identification and analysis of key genes involved in methyl salicylate biosynthesis in different birch species. <i>PLoS ONE</i> , 2020, 15, e0240246.	1.1	6
1586	Expression of <i>Pinellia ternata</i> leaf agglutinin under rolC promoter confers resistance against a phytophagous sap sucking aphid, <i>Myzus persicae</i> . <i>Electronic Journal of Biotechnology</i> , 2020, 47, 72-82.	1.2	2
1587	Genome-wide identification and analysis of high-affinity nitrate transporter 2 (NRT2) family genes in rapeseed ( <i>Brassica napus</i> L.) and their responses to various stresses. <i>BMC Plant Biology</i> , 2020, 20, 464.	1.6	35
1588	Genome-wide identification and characterization of the bZIP gene family in potato ( <i>Solanum</i> ) Tj ETQq1 1 0.784314rgBT /Overlock 10	1.4	7
1589	Functional <i>Allium fistulosum</i> Centromeres Comprise Arrays of a Long Satellite Repeat, Insertions of Retrotransposons and Chloroplast DNA. <i>Frontiers in Plant Science</i> , 2020, 11, 562001.	1.7	5
1590	Genome-wide identification and expression profiling of cytosine-5 DNA methyltransferases during drought and heat stress in wheat ( <i>Triticum aestivum</i> ). <i>Genomics</i> , 2020, 112, 4796-4807.	1.3	17

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1591	Chitinase Gene Positively Regulates Hypersensitive and Defense Responses of Pepper to <i>Colletotrichum acutatum</i> Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6624.	1.8	20
1592	Calmodulin-Like (CML) Gene Family in <i>Medicago truncatula</i> : Genome-Wide Identification, Characterization and Expression Analysis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7142.	1.8	22
1593	Genome-wide identification of fasciclin-like arabinogalactan proteins in jute and their expression pattern during fiber formation. <i>Molecular Biology Reports</i> , 2020, 47, 7815-7829.	1.0	9
1594	Genome-wide identification and characterization of SRO gene family in wheat: Molecular evolution and expression profiles during different stresses. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 590-611.	2.8	27
1595	Transcriptome wide identification and characterization of regulatory genes involved in EAA metabolism and validation through expression analysis in different developmental stages of finger millet spikes. <i>3 Biotech</i> , 2020, 10, 347.	1.1	6
1596	Genome-Wide Identification and Expression Profile Analysis of the PHT1 Gene Family in <i>Gossypium hirsutum</i> and Its Two Close Relatives of Subgenome Donor Species. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4905.	1.8	5
1597	Molecular characterization of ascorbate peroxidase (APX) and APX-related (APX-R) genes in <i>Triticum aestivum</i> L.. <i>Genomics</i> , 2020, 112, 4208-4223.	1.3	56
1598	EMBRYONIC FLOWER2B, coming from a stable QTL, represses the floral transition in cotton. <i>International Journal of Biological Macromolecules</i> , 2020, 163, 1087-1096.	3.6	11
1599	Heterologous activation of the Hevea PEP16 promoter in the rubber-producing laticiferous tissues of <i>Taraxacum kok-saghyz</i> . <i>Scientific Reports</i> , 2020, 10, 10844.	1.6	4
1600	Evolution of <i>SHORT VEGETATIVE PHASE</i> ( <i>SVP</i> ) genes in Rosaceae: Implications of lineage-specific gene duplication events and function diversifications with respect to their roles in processes other than bud dormancy. <i>Plant Genome</i> , 2020, 13, e20053.	1.6	9
1601	Genome-wide analysis of HSP90 gene family in the Mediterranean olive ( <i>Olea europaea</i> subsp. <i>europaea</i> ) provides insight into structural patterns, evolution and functional diversity. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 2301-2318.	1.4	3
1602	Genome-Wide Identification and Analysis of GHMP Kinase Gene Superfamily in Bread Wheat ( <i>Triticum</i> ) Tj ETQq1 1 Q.784314 rgBT /Over	1.0	4
1603	Identification and Characterization of PLATZ Transcription Factors in Wheat. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8934.	1.8	21
1604	Mutational study of radish leaf curl betasatellite to understand the role of the non-coding region in begomovirus pathogenesis. <i>Physiological and Molecular Plant Pathology</i> , 2020, 112, 101549.	1.3	7
1605	A Synthetic Strong and Constitutive Promoter Derived from the <i>Stellaria media</i> pro-SmAMP1 and pro-SmAMP2 Promoters for Effective Transgene Expression in Plants. <i>Genes</i> , 2020, 11, 1407.	1.0	6
1606	Characterization and Stress Response of the JmjC Domain-Containing Histone Demethylase Gene Family in the Allotetraploid Cotton Species <i>Gossypium hirsutum</i> . <i>Plants</i> , 2020, 9, 1617.	1.6	5
1607	Characterization of two predicted DASH-related proteins from the green alga <i>Volvox carteri</i> provides new insights into their light-mediated transcript regulation and DNA repair activity. <i>Algal Research</i> , 2020, 52, 102116.	2.4	3
1608	A CCAAT-binding factor, SINFYA10, negatively regulates ascorbate accumulation by modulating the d-mannose/l-galactose pathway in tomato. <i>Horticulture Research</i> , 2020, 7, 200.	2.9	19

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1610	Salt-responsive transcriptome analysis of triticale reveals candidate genes involved in the key metabolic pathway in response to salt stress. <i>Scientific Reports</i> , 2020, 10, 20669.	1.6	16
1611	A class III WRKY transcription factor in sugarcane was involved in biotic and abiotic stress responses. <i>Scientific Reports</i> , 2020, 10, 20964.	1.6	46
1612	Optimized combination methods for exploring and verifying disease-resistant transcription factors in melon. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	0
1613	The soybean gene GmHsp22.4 is involved in the resistance response to <i>Meloidogyne javanica</i> in <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2020, 20, 535.	1.6	6
1614	Genome-wide characterization, expression analyses, and functional prediction of the NPF family in <i>Brassica napus</i> . <i>BMC Genomics</i> , 2020, 21, 871.	1.2	17
1615	Identification, evolution, expression, and docking studies of fatty acid desaturase genes in wheat ( <i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2020, 21, 778.	1.2	31
1616	A comprehensive analysis of cotton VQ gene superfamily reveals their potential and extensive roles in regulating cotton abiotic stress. <i>BMC Genomics</i> , 2020, 21, 795.	1.2	17
1617	S-adenosylmethionine synthetase 1 confers drought and salt tolerance in transgenic tomato. <i>Environmental and Experimental Botany</i> , 2020, 179, 104226.	2.0	23
1618	Genome-wide survey of the amino acid transporter gene family in wheat ( <i>Triticum aestivum</i> L.): Identification, expression analysis and response to abiotic stress. <i>International Journal of Biological Macromolecules</i> , 2020, 162, 1372-1387.	3.6	42
1619	The chromosome-level wintersweet ( <i>Chimonanthus praecox</i> ) genome provides insights into floral scent biosynthesis and flowering in winter. <i>Genome Biology</i> , 2020, 21, 200.	3.8	69
1620	Genome-wide identification and expression analysis of SABATH methyltransferases in tea plant ( <i>Camellia sinensis</i> ): insights into their roles in plant defense responses. <i>Plant Signaling and Behavior</i> , 2020, 15, 1804684.	1.2	9
1621	Molecular Characterization, Expression Pattern and Function Analysis of Glycine-Rich Protein Genes Under Stresses in Chinese Cabbage ( <i>Brassica rapa</i> L. ssp. <i>pekinensis</i> ). <i>Frontiers in Genetics</i> , 2020, 11, 774.	1.1	5
1622	Genome-Wide Identification and Functional Characterization of the Heat Shock Factor Family in Eggplant ( <i>Solanum melongena</i> L.) under Abiotic Stress Conditions. <i>Plants</i> , 2020, 9, 915.	1.6	12
1623	In-silico analysis of cucumber ( <i>Cucumis sativus</i> L.) Genome for WRKY transcription factors and cis-acting elements. <i>Computational Biology and Chemistry</i> , 2020, 85, 107212.	1.1	11
1624	Comprehensive genomic analysis of the RNase T2 gene family in Rosaceae and expression analysis in <i>Pyrus bretschneideri</i> . <i>Plant Systematics and Evolution</i> , 2020, 306, 1.	0.3	7
1625	New insight into comprehensive analysis of INDETERMINATE DOMAIN (IDD) gene family in rice. <i>Plant Physiology and Biochemistry</i> , 2020, 154, 547-556.	2.8	6
1626	Calmodulin-binding transcription activator (CAMTA) genes family: Genome-wide survey and phylogenetic analysis in flax ( <i>Linum usitatissimum</i> ). <i>PLoS ONE</i> , 2020, 15, e0236454.	1.1	20

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1627	Ethylene and RIPENING INHIBITOR Modulate Expression of SHSP17.7A, B Class I Small Heat Shock Protein Genes During Tomato Fruit Ripening. <i>Frontiers in Plant Science</i> , 2020, 11, 975.	1.7	20
1628	Genomic identification and expression analysis of the BBX transcription factor gene family in <i>Petunia hybrida</i> . <i>Molecular Biology Reports</i> , 2020, 47, 6027-6041.	1.0	12
1629	Genome-wide characterization of the C2H2 zinc-finger genes in <i>Cucumis sativus</i> and functional analyses of four CsZFPs in response to stresses. <i>BMC Plant Biology</i> , 2020, 20, 359.	1.6	30
1630	Integrated metabolomics and transcriptome analysis on flavonoid biosynthesis in safflower ( <i>Carthamus tinctorius</i> L.) under MeJA treatment. <i>BMC Plant Biology</i> , 2020, 20, 353.	1.6	51
1631	Genome-Wide Identification and Expression Analysis of MAPK and MAPKK Gene Family in Pomegranate ( <i>Punica Granatum</i> L.). <i>Agronomy</i> , 2020, 10, 1015.	1.3	0
1632	Genome-Wide Characterization and Expression Analysis of NHX Gene Family under Salinity Stress in <i>Gossypium barbadense</i> and Its Comparison with <i>Gossypium hirsutum</i> . <i>Genes</i> , 2020, 11, 803.	1.0	22
1633	Gene structure, evolution and expression analysis of the P-ATPase gene family in Chinese pear ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.9	21
1634	Genome-wide evolutionary characterization and expression analysis of SIAMESE-RELATED family genes in maize. <i>BMC Evolutionary Biology</i> , 2020, 20, 91.	3.2	8
1635	Characterization of a novel LmSAP gene promoter from <i>Lobularia maritima</i> : Tissue specificity and environmental stress responsiveness. <i>PLoS ONE</i> , 2020, 15, e0236943.	1.1	15
1636	Early nodulin 93 protein gene: essential for induction of somatic embryogenesis in oil palm. <i>Plant Cell Reports</i> , 2020, 39, 1395-1413.	2.8	8
1637	Pea G $\beta$ subunit of G proteins has a role in nitric oxide-induced stomatal closure in response to heat and drought stress. <i>Protoplasma</i> , 2020, 257, 1639-1654.	1.0	10
1638	Comprehensive analysis of polygalacturonase gene family highlights candidate genes related to pollen development and male fertility in wheat ( <i>Triticum aestivum</i> L.). <i>Planta</i> , 2020, 252, 31.	1.6	7
1639	The SnRK2 family in pepper ( <i>Capsicum annuum</i> L.): genome-wide identification and expression analyses during fruit development and under abiotic stress. <i>Genes and Genomics</i> , 2020, 42, 1117-1130.	0.5	12
1640	Evolution and Expression of the Membrane Attack Complex and Perforin Gene Family in the Poaceae. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5736.	1.8	14
1641	Unravelling Cotton Nonexpressor of Pathogenesis-Related 1(NPR1)-Like Genes Family: Evolutionary Analysis and Putative Role in Fiber Development and Defense Pathway. <i>Plants</i> , 2020, 9, 999.	1.6	9
1642	Identification of MTP gene family in tea plant ( <i>Camellia sinensis</i> L.) and characterization of CsMTP8.2 in manganese toxicity. <i>Ecotoxicology and Environmental Safety</i> , 2020, 202, 110904.	2.9	30
1643	Genome-wide identification and characterization of bHLH family genes from <i>Ginkgo biloba</i> . <i>Scientific Reports</i> , 2020, 10, 13723.	1.6	34
1644	Ginsenosides regulate adventitious root formation in <i>Panax ginseng</i> via a CLE45 $\beta$ WOX11 regulatory module. <i>Journal of Experimental Botany</i> , 2020, 71, 6396-6407.	2.4	10

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1645	Genome-wide analysis of evolution and expression profiles of NAC transcription factor gene family in <i>Juglans regia</i> L.. <i>Annals of Forest Science</i> , 2020, 77, 1.	0.8	6
1646	The combination of blue and red LED light improves growth and phenolic acid contents in <i>Salvia miltiorrhiza</i> Bunge. <i>Industrial Crops and Products</i> , 2020, 158, 112959.	2.5	37
1647	Identification and Analysis of NBS-LRR Genes in <i>Actinidia chinensis</i> Genome. <i>Plants</i> , 2020, 9, 1350.	1.6	20
1648	New insights into the evolution of the SBP-box family and expression analysis of genes in the growth and development of <i>Brassica juncea</i> . <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 810-824.	0.5	4
1649	Phosphatidylinositol pathway-associated genes adjust the rice growth and stress signaling: A global assay of the 5PTase family in the <i>Oryza sativa</i> genome. <i>Plant Gene</i> , 2020, 23, 100244.	1.4	3
1650	Genome-Wide Characterization and Expression of Two-Component System Genes in Cytokinin-Regulated Gall Formation in <i>Zizania latifolia</i> . <i>Plants</i> , 2020, 9, 1409.	1.6	14
1651	Characterization and identification of OsFTL8 gene in rice. <i>Plant Biotechnology Reports</i> , 2020, 14, 683-694.	0.9	7
1652	Genome-Wide Identification and Expression Analysis of the Barrel Medic ( <i>Medicago truncatula</i> ) and Alfalfa ( <i>Medicago sativa</i> L.) Basic Helix-Loop-Helix Transcription Factor Family Under Salt and Drought Stresses. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 2058-2078.	2.8	4
1653	Genome-wide Characterization of cis-acting Elements in the Promoters of Key Carotenoid Pathway Genes from the Main Species of Genus <i>Citrus</i> . <i>Horticultural Plant Journal</i> , 2020, 6, 385-395.	2.3	13
1654	In Silico Analyses of Autophagy-Related Genes in Rapeseed ( <i>Brassica napus</i> L.) under Different Abiotic Stresses and in Various Tissues. <i>Plants</i> , 2020, 9, 1393.	1.6	5
1655	Identification and Expression of the Multidrug and Toxic Compound Extrusion (MATE) Gene Family in <i>Capsicum annuum</i> and <i>Solanum tuberosum</i> . <i>Plants</i> , 2020, 9, 1448.	1.6	12
1656	Genome-wide characterization and expression analysis suggested diverse functions of the mechanosensitive channel of small conductance-like (MSL) genes in cereal crops. <i>Scientific Reports</i> , 2020, 10, 16583.	1.6	24
1657	Cloning and activity analysis of the promoter of nucleotide exchange factor gene <i>ZjFes1</i> from the seagrasses <i>Zostera japonica</i> . <i>Scientific Reports</i> , 2020, 10, 17291.	1.6	11
1658	DoRWA3 from <i>Dendrobium officinale</i> Plays an Essential Role in Acetylation of Polysaccharides. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6250.	1.8	10
1659	Genome-Wide Analysis of the PIN Auxin Efflux Carrier Gene Family in Coffee. <i>Plants</i> , 2020, 9, 1061.	1.6	10
1660	DnaJs, the critical drivers of Hsp70s: genome-wide screening, characterization and expression of DnaJ family genes in <i>Sorghum bicolor</i> . <i>Molecular Biology Reports</i> , 2020, 47, 7379-7390.	1.0	9
1661	The GATA Gene Family in Chickpea: Structure Analysis and Transcriptional Responses to Abscisic Acid and Dehydration Treatments Revealed Potential Genes Involved in Drought Adaptation. <i>Journal of Plant Growth Regulation</i> , 2020, 39, 1647-1660.	2.8	15
1662	Identification of quantitative trait nucleotides and candidate genes for soybean seed weight by multiple models of genome-wide association study. <i>BMC Plant Biology</i> , 2020, 20, 404.	1.6	28

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1664	Mining and evolution analysis of lateral organ boundaries domain (LBD) genes in Chinese white pear ( <i>Pyrus bretschneideri</i> ). <i>BMC Genomics</i> , 2020, 21, 644.	1.2	18
1665	Genome-Wide Identification and Analysis of SRO Gene Family in Chinese Cabbage ( <i>Brassica rapa</i> L.). <i>Plants</i> , 2020, 9, 1235.	1.6	9
1666	Comparative sequence analysis across Brassicaceae, regulatory diversity in KCS5 and KCS6 homologs from <i>Arabidopsis thaliana</i> and <i>Brassica juncea</i> , and intronic fragment as a negative transcriptional regulator. <i>Gene Expression Patterns</i> , 2020, 38, 119146.	0.3	6
1667	Genome-wide identification and classification of resistance genes predicted several decoy domains in <i>Gossypium</i> sp.. <i>Plant Gene</i> , 2020, 24, 100250.	1.4	7
1668	Molecular Cloning and Functional Analysis of the NPR1 Homolog in Kiwifruit ( <i>Actinidia eriantha</i> ). <i>Frontiers in Plant Science</i> , 2020, 11, 551201.	1.7	6
1669	Identification and characterization of SET domain family genes in bread wheat ( <i>Triticum aestivum</i> L.). <i>Scientific Reports</i> , 2020, 10, 14624.	1.6	17
1670	Dissecting the Molecular Function of <i>Triticum aestivum</i> STI Family Members Under Heat Stress. <i>Frontiers in Genetics</i> , 2020, 11, 873.	1.1	11
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1672	Structure and Expression of Bud Dormancy-Associated MADS-Box Genes (DAM) in European Plum. <i>Frontiers in Plant Science</i> , 2020, 11, 1288.	1.7	26
1673	Functional Characterization and in Silico Analysis of Phytoene Synthase Family Genes Responsible for Carotenoid Biosynthesis in Watermelon ( <i>Citrullus lanatus</i> L.). <i>Agronomy</i> , 2020, 10, 1077.	1.3	4
1674	Functional characterization of the Glyoxalase-I (PdGLX1) gene family in date palm under abiotic stresses. <i>Plant Signaling and Behavior</i> , 2020, 15, 1811527.	1.2	10
1675	Genome-Wide Identification of DNA Methylases and Demethylases in Kiwifruit ( <i>Actinidia chinensis</i> ). <i>Frontiers in Plant Science</i> , 2020, 11, 514993.	1.7	7
1676	A GATA Transcription Factor from Soybean ( <i>Glycine max</i> ) Regulates Chlorophyll Biosynthesis and Suppresses Growth in the Transgenic <i>Arabidopsis thaliana</i> . <i>Plants</i> , 2020, 9, 1036.	1.6	25
1677	Genome-Wide Identification, Characterization and Expression Analysis of TCP Transcription Factors in <i>Petunia</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 6594.	1.8	11
1678	PuMYB21/PuMYB54 coordinate to activate PuPLD <sup>21</sup> transcription during peel browning of cold-stored 'Nanguo' pears. <i>Horticulture Research</i> , 2020, 7, 136.	2.9	19
1679	Data-mining bioinformatics: suggesting <i>Arabidopsis thaliana</i> L-type lectin receptor kinase IX.2 (<i>LecRK-IX.2</i>) modulate metabolites and abiotic stress responses. <i>Plant Signaling and Behavior</i> , 2020, 15, 1818031.	1.2	7
1680	Dual-Localized WHIRLY1 Affects Salicylic Acid Biosynthesis via Coordination of ISOCHORISMATE SYNTHASE1, PHENYLALANINE AMMONIA LYASE1, and S-ADENOSYL-L-METHIONINE-DEPENDENT METHYLTRANSFERASE1. <i>Plant Physiology</i> , 2020, 184, 1884-1899.	2.3	24

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1681	NAC transcription factor involves in regulating bacterial wilt resistance in potato. <i>Functional Plant Biology</i> , 2020, 47, 925.	1.1	14
1682	Triple-localized WHIRLY2 Influences Leaf Senescence and Silique Development via Carbon Allocation. <i>Plant Physiology</i> , 2020, 184, 1348-1362.	2.3	23
1683	Genome-Wide Characterization, Evolution, and Expression Analysis of the Leucine-Rich Repeat Receptor-Like Protein Kinase (LRR-RLK) Gene Family in <i>Medicago truncatula</i> . <i>Life</i> , 2020, 10, 176.	1.1	9
1684	The overexpression of OsACBP5 protects transgenic rice against necrotrophic, hemibiotrophic and biotrophic pathogens. <i>Scientific Reports</i> , 2020, 10, 14918.	1.6	20
1685	Genome-Wide Analysis Reveals Transcription Factors Regulated by Spider-Mite Feeding in Cucumber ( <i>Cucumis sativus</i> ). <i>Plants</i> , 2020, 9, 1014.	1.6	2
1686	Systematic characterization of the branch point binding protein, splicing factor 1, gene family in plant development and stress responses. <i>BMC Plant Biology</i> , 2020, 20, 379.	1.6	5
1687	Isolation of novel citrus and plum fruit promoters and their functional characterization for fruit biotechnology. <i>BMC Biotechnology</i> , 2020, 20, 43.	1.7	4
1688	Color Intensity of the Red-Fleshed Berry Phenotype of <i>Vitis vinifera</i> Teinturier Grapes Varies Due to a 408 bp Duplication in the Promoter of <i>VvmybA1</i> . <i>Genes</i> , 2020, 11, 891.	1.0	22
1689	Genome-Wide Identification and Expression Analysis of the NHX (Sodium/Hydrogen Antiporter) Gene Family in Cotton. <i>Frontiers in Genetics</i> , 2020, 11, 964.	1.1	19
1690	Identification and Expression Analysis of the CsMYB Gene Family in Root Knot Nematode-Resistant and Susceptible Cucumbers. <i>Frontiers in Genetics</i> , 2020, 11, 550677.	1.1	9
1691	Isolation and characterization of maize <i>ZmPP2C26</i> gene promoter in drought-response. <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 2189-2197.	1.4	9
1692	Prediction of putative regulatory elements in the subgenomic promoters of cucumber green mottle mosaic virus and their interactions with the RNA dependent RNA polymerase domain. <i>VirusDisease</i> , 2020, 31, 503-516.	1.0	1
1693	Genome-Wide Analysis of the Cyclin Gene Family and Their Expression Profile in <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 9430.	1.8	13
1694	Genome-Wide Analysis of the GRAS Gene Family and Functional Identification of <i>GmGRAS37</i> in Drought and Salt Tolerance. <i>Frontiers in Plant Science</i> , 2020, 11, 604690.	1.7	52
1695	Targeted Transgene Expression in Rice Using a Callus Strong Promoter for Selectable Marker Gene Control. <i>Frontiers in Plant Science</i> , 2020, 11, 602680.	1.7	5
1696	Genome-Wide Identification and Molecular Characterization of the Growth-Regulating Factors-Interacting Factor Gene Family in Tomato. <i>Genes</i> , 2020, 11, 1435.	1.0	10
1697	Glutathione S-transferases GhGSTF1 and GhGSTF2 involved in the anthocyanin accumulation in <i>Gossypium hirsutum</i> L.. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 2565-2575.	3.6	4
1698	Identification of Phytochrome-Interacting Factor Family Members and Functional Analysis of <i>MdPIF4</i> in <i>Malus domestica</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 7350.	1.8	17

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1699	Genome-Wide Characterization of the HSP20 Gene Family Identifies Potential Members Involved in Temperature Stress Response in Apple. <i>Frontiers in Genetics</i> , 2020, 11, 609184.	1.1	27
1700	WRKY Transcription Factors in <i>Medicago sativa</i> L.: Genome-Wide Identification and Expression Analysis Under Abiotic Stress. <i>DNA and Cell Biology</i> , 2020, 39, 2212-2225.	0.9	22
1701	Genome-Wide Characterization of OFP Family Genes in Wheat ( <i>Triticum aestivum</i> L.) Reveals That TaOPF29a-A Promotes Drought Tolerance. <i>BioMed Research International</i> , 2020, 2020, 1-17.	0.9	7
1702	Insights into the Superoxide Dismutase Gene Family and Its Roles in <i>Dendrobium catenatum</i> under Abiotic Stresses. <i>Plants</i> , 2020, 9, 1452.	1.6	11
1703	Comparative Leaf Proteomics of <i>Brassica napus</i> Genotypes with Distinctive Levels of Early Cold Acclimation. <i>Plant Molecular Biology Reporter</i> , 2020, 39, 317.	1.0	3
1704	Genome-wide identification, characterization analysis and expression profiling of auxin-responsive GH3 family genes in wheat ( <i>Triticum aestivum</i> L.). <i>Molecular Biology Reports</i> , 2020, 47, 3885-3907.	1.0	23
1705	A little membrane protein with 54 amino acids confers salt tolerance in rice ( <i>Oryza sativa</i> L.). <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	2
1706	Identification, characterization and expression analysis of calmodulin and calmodulin-like proteins in <i>Solanum pennellii</i> . <i>Scientific Reports</i> , 2020, 10, 7474.	1.6	38
1707	Dynamics of Global Gene Expression and Regulatory Elements in Growing <i>Brachypodium</i> Root System. <i>Scientific Reports</i> , 2020, 10, 7071.	1.6	2
1708	Casparian strip membrane domain proteins in <i>Gossypium arboreum</i> : genome-wide identification and negative regulation of lateral root growth. <i>BMC Genomics</i> , 2020, 21, 340.	1.2	4
1709	Isolation and characterization of a 295-bp strong promoter of maize high-affinity phosphate transporter gene <i>ZmPht1; 5</i> in transgenic <i>Nicotiana benthamiana</i> and <i>Zea mays</i> . <i>Planta</i> , 2020, 251, 106.	1.6	5
1710	Genome-wide identification of the expansin gene family reveals that expansin genes are involved in fibre cell growth in cotton. <i>BMC Plant Biology</i> , 2020, 20, 223.	1.6	32
1711	The Biosynthesis of Main Taste Compounds Is Coordinately Regulated by miRNAs and Phytohormones in Tea Plant ( <i>Camellia sinensis</i> ). <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 6221-6236.	2.4	26
1712	Genome-wide characterization of tea plant ( <i>Camellia sinensis</i> ) Hsf transcription factor family and role of CsHsfA2 in heat tolerance. <i>BMC Plant Biology</i> , 2020, 20, 244.	1.6	26
1713	Identification of Alternative Mitochondrial Electron Transport Pathway Components in Chickpea Indicates a Differential Response to Salinity Stress between Cultivars. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3844.	1.8	9
1714	Genome-wide analysis of the abiotic stress-related bZIP family in switchgrass. <i>Molecular Biology Reports</i> , 2020, 47, 4439-4454.	1.0	16
1715	Gibberellin mediates spermidine-induced salt tolerance and the expression of GT-3b in cucumber. <i>Plant Physiology and Biochemistry</i> , 2020, 152, 147-156.	2.8	16
1716	LncRNA improves cold resistance of winter wheat by interacting with miR398. <i>Functional Plant Biology</i> , 2020, 47, 544.	1.1	48



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1717	First report for availability of HRT-like genes in <i>Eragrostis tef</i> and in silico analysis for elucidating their potential functions. <i>Plant Gene</i> , 2020, 23, 100230.	1.4	8
1718	Genome-wide identification, phylogeny and expression analysis of HSF gene family in barley during abiotic stress response and reproductive development. <i>Plant Gene</i> , 2020, 23, 100231.	1.4	11
1719	Characterization and function of banana DORN1s during fruit ripening and cold storage. <i>Postharvest Biology and Technology</i> , 2020, 167, 111236.	2.9	14
1720	Function analysis and stress-mediated cis-element identification in the promoter region of <i>VqMYB15</i> . <i>Plant Signaling and Behavior</i> , 2020, 15, 1773664.	1.2	30
1721	Genome-wide analysis of polymorphisms identified domestication-associated long low-diversity region carrying important rice grain size/weight quantitative trait loci. <i>Plant Journal</i> , 2020, 103, 1525-1547.	2.8	9
1722	Genome-wide identification and characterization of cucumber bHLH family genes and the functional characterization of <i>CsbHLH041</i> in NaCl and ABA tolerance in <i>Arabidopsis</i> and cucumber. <i>BMC Plant Biology</i> , 2020, 20, 272.	1.6	51
1723	Identification and characterization of the CONSTANS-like gene family and its expression profiling under light treatment in <i>Populus</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 161, 999-1010.	3.6	20
1724	Genome-wide analysis and transcript profiling identify several abiotic and biotic stress-responsive Glutathione S-transferase genes in soybean. <i>Plant Gene</i> , 2020, 23, 100239.	1.4	8
1725	Genome-wide identification and functional characterization of glutathione peroxidase genes in date palm ( <i>Phoenix dactylifera</i> L.) under stress conditions. <i>Plant Gene</i> , 2020, 23, 100237.	1.4	9
1726	Reciprocal regulation between nicotinamide adenine dinucleotide metabolism and abscisic acid and stress response pathways in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2020, 16, e1008892.	1.5	22
1727	Disequilibrium evolution of the Fructose-1,6-bisphosphatase gene family leads to their functional biodiversity in <i>Gossypium</i> species. <i>BMC Genomics</i> , 2020, 21, 379.	1.2	13
1728	Root isoprene formation alters lateral root development. <i>Plant, Cell and Environment</i> , 2020, 43, 2207-2223.	2.8	21
1729	RGPDB: database of root-associated genes and promoters in maize, soybean, and sorghum. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	8
1730	Dark response genes: a group of endogenous pendulum/timing players in maize?. <i>Planta</i> , 2020, 252, 1.	1.6	64
1731	Genome-wide analysis of proline-rich extension-like receptor protein kinase (PERK) in <i>Brassica rapa</i> and its association with the pollen development. <i>BMC Genomics</i> , 2020, 21, 401.	1.2	16
1732	Effect of Arsenic Stress on Expression Pattern of a Rice Specific miR156j at Various Developmental Stages and Their Allied Co-expression Target Networks. <i>Frontiers in Plant Science</i> , 2020, 11, 752.	1.7	31
1733	Bioinformatics analysis of BBX family genes and its response to UV-B in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2020, 15, 1782647.	1.2	18
1734	Structural and Functional Annotation of Transposable Elements Revealed a Potential Regulation of Genes Involved in Rubber Biosynthesis by TE-Derived siRNA Interference in <i>Hevea brasiliensis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 4220.	1.8	6

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1736	Functional Characterization of VvSK Gene Family in Grapevine Revealing Their Role in Berry Ripening. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4336.	1.8	7
1737	Micro-Evolution Analysis Reveals Diverged Patterns of Polyol Transporters in Seven Gramineae Crops. <i>Frontiers in Genetics</i> , 2020, 11, 565.	1.1	13
1738	Genome-wide analysis of the U-box E3 ubiquitin ligase enzyme gene family in tomato. <i>Scientific Reports</i> , 2020, 10, 9581.	1.6	40
1739	MYB44 competitively inhibits the formation of the MYB340-bHLH2-NAC56 complex to regulate anthocyanin biosynthesis in purple-fleshed sweet potato. <i>BMC Plant Biology</i> , 2020, 20, 258.	1.6	44
1740	Genome-wide analysis of NDR1/HIN1-like genes in pepper ( <i>Capsicum annuum</i> L.) and functional characterization of CaNHL4 under biotic and abiotic stresses. <i>Horticulture Research</i> , 2020, 7, 93.	2.9	32
1741	LuluDBâ€”The Database Created Based on Small RNA, Transcriptome, and Degradome Sequencing Shows the Wide Landscape of Non-coding and Coding RNA in Yellow Lupine ( <i>Lupinus luteus</i> L.) Flowers and Pods. <i>Frontiers in Genetics</i> , 2020, 11, 455.	1.1	3
1742	Systematic identification and functional analysis of potato ( <i>Solanum tuberosum</i> L.) bZIP transcription factors and overexpression of potato bZIP transcription factor StbZIP-65 enhances salt tolerance. <i>International Journal of Biological Macromolecules</i> , 2020, 161, 155-167.	3.6	28
1743	Genome-wide analysis of AP2/ERF transcription factors family in <i>Brassica napus</i> . <i>Physiology and Molecular Biology of Plants</i> , 2020, 26, 1463-1476.	1.4	23
1744	Genome-wide identification and expression analysis of WRKY transcription factors in pearl millet ( <i>Pennisetum glaucum</i> ) under dehydration and salinity stress. <i>BMC Genomics</i> , 2020, 21, 231.	1.2	56
1745	The CaChiVI2 Gene of <i>Capsicum annuum</i> L. Confers Resistance Against Heat Stress and Infection of <i>Phytophthora capsici</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 219.	1.7	18
1746	Comprehensive characterization and gene expression patterns of LBD gene family in <i>Gossypium</i> . <i>Planta</i> , 2020, 251, 81.	1.6	21
1747	Perspectives of CRISPR/Cas-mediated cis-engineering in horticulture: unlocking the neglected potential for crop improvement. <i>Horticulture Research</i> , 2020, 7, 36.	2.9	52
1748	Molecular characterization of the gibberellin-stimulated transcript of GASA4 in Citrus. <i>Plant Growth Regulation</i> , 2020, 91, 89-99.	1.8	18
1749	Genome-wide analysis of laccase genes in moso bamboo highlights PeLAC10 involved in lignin biosynthesis and in response to abiotic stresses. <i>Plant Cell Reports</i> , 2020, 39, 751-763.	2.8	34
1750	Genome-wide identification and characterization of the BES1 gene family in apple ( <i>Malus</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.8	24
1751	Exogenous Application of Sucrose Promotes Postharvest Ripening of Kiwifruit. <i>Agronomy</i> , 2020, 10, 245.	1.3	10
1752	Subfunctionalization of phytochrome B1/B2 leads to differential auxin and photosynthetic responses. <i>Plant Direct</i> , 2020, 4, e00205.	0.8	6

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1753	Genome-wide identification and phylogenetic analysis of rice FTIP gene family. <i>Genomics</i> , 2020, 112, 3803-3814.	1.3	11
1754	Genome-wide analysis of glutathione S-transferase gene family in <i>G. max</i> . <i>Biologia (Poland)</i> , 2020, 75, 1691-1705.	0.8	9
1755	BpTCP7 gene from <i>Betula platyphylla</i> regulates tolerance to salt and drought stress through multiple hormone pathways. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 141, 17-30.	1.2	7
1756	Exogenous Abscisic Acid Supplementation at Early Stationary Growth Phase Triggers Changes in the Regulation of Fatty Acid Biosynthesis in <i>Chlorella vulgaris</i> UMT-M1. <i>Applied Biochemistry and Biotechnology</i> , 2020, 191, 1653-1669.	1.4	8
1757	Identification analysis of Plantacyanin ( <i>PLC</i> ) genes in <i>Camellia sinensis</i> and functional identification of <i>CsPLC-3</i> in yeast. <i>Journal of Horticultural Science and Biotechnology</i> , 2020, 95, 578-589.	0.9	1
1758	Identification and Characterization of Tonoplast Sugar Transporter (TST) Gene Family in Cucumber. <i>Horticultural Plant Journal</i> , 2020, 6, 145-157.	2.3	16
1759	Characterization of the Gh4CL gene family reveals a role of Gh4CL7 in drought tolerance. <i>BMC Plant Biology</i> , 2020, 20, 125.	1.6	40
1760	Genome-wide identification and expression analysis of the superoxide dismutase (SOD) gene family in <i>Salvia miltiorrhiza</i> . <i>Gene</i> , 2020, 742, 144603.	1.0	26
1761	Comprehensive Analysis of the TIFY Gene Family and Its Expression Profiles under Phytohormone Treatment and Abiotic Stresses in Roots of <i>Populus trichocarpa</i> . <i>Forests</i> , 2020, 11, 315.	0.9	12
1762	Genome-Wide Identification and Evolutionary Analysis of the Fruit-Weight 2.2-Like Gene Family in Polyploid Oilseed Rape ( <i>Brassica napus</i> L.). <i>DNA and Cell Biology</i> , 2020, 39, 766-782.	0.9	3
1763	Genome-Wide Identification of the VQ Protein Gene Family of Tobacco ( <i>Nicotiana tabacum</i> L.) and Analysis of Its Expression in Response to Phytohormones and Abiotic and Biotic Stresses. <i>Genes</i> , 2020, 11, 284.	1.0	21
1764	Characterization of the Auxin Efflux Transporter PIN Proteins in Pear. <i>Plants</i> , 2020, 9, 349.	1.6	19
1765	Expression profiling of Cordyceps DnaJ protein family in <i>Tolypocladium guangdongense</i> during developmental and temperature stress processes. <i>Gene</i> , 2020, 743, 144563.	1.0	4
1766	Changes in the promoter of a defender against apoptotic cell death gene affect its expression in upland cotton. <i>Journal of Systematics and Evolution</i> , 2020, 59, 1018.	1.6	1
1767	Genome-Wide Analysis of the DREB Subfamily in <i>Saccharum spontaneum</i> Reveals Their Functional Divergence During Cold and Drought Stresses. <i>Frontiers in Genetics</i> , 2019, 10, 1326.	1.1	28
1768	Soybean Stem Canker Caused by <i>Diaporthe caulivora</i> ; Pathogen Diversity, Colonization Process, and Plant Defense Activation. <i>Frontiers in Plant Science</i> , 2019, 10, 1733.	1.7	24
1769	A Comprehensive Transcriptomics Analysis Reveals Long Non-Coding RNA to Be Involved in the Key Metabolic Pathway in Response to Waterlogging Stress in Maize. <i>Genes</i> , 2020, 11, 267.	1.0	27
1770	WOOLLY, interacting with MYB transcription factor MYB31, regulates cuticular wax biosynthesis by modulating <i>CER6</i> expression in tomato. <i>Plant Journal</i> , 2020, 103, 323-337.	2.8	44

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1772	The Cytochrome P450 Monooxygenase Inventory of Grapevine ( <i>Vitis vinifera</i> L.): Genome-Wide Identification, Evolutionary Characterization and Expression Analysis. <i>Frontiers in Genetics</i> , 2020, 11, 44.	1.1	35
1773	WvUCC1 Nucleotide Diversity, Linkage Disequilibrium and Association with Rachis Architecture Traits in Grapevine. <i>Genes</i> , 2020, 11, 598.	1.0	7
1774	Genomic Analysis of the SUMO-Conjugating Enzyme and Genes under Abiotic Stress in Potato ( <i>Solanum tuberosum</i> L.). <i>International Journal of Genomics</i> , 2020, 2020, 1-13.	0.8	8
1775	Genome-wide identification of the class III POD gene family and their expression profiling in grapevine ( <i>Vitis vinifera</i> L.). <i>BMC Genomics</i> , 2020, 21, 444.	1.2	19
1776	A Chloroplast COR413 Protein From <i>Physcomitrella patens</i> Is Required for Growth Regulation Under High Light and ABA Responses. <i>Frontiers in Plant Science</i> , 2020, 11, 845.	1.7	5
1777	Genome-Wide Analysis of Serine Carboxypeptidase-Like Acyltransferase Gene Family for Evolution and Characterization of Enzymes Involved in the Biosynthesis of Galloylated Catechins in the Tea Plant ( <i>Camellia sinensis</i> ). <i>Frontiers in Plant Science</i> , 2020, 11, 848.	1.7	33
1778	Genome-wide Identification and Expression Analysis of TALE Gene Family in Pomegranate ( <i>Punica</i> ) Tj ETQq1 1 0.784314 rgBT/Overlo 1.3	1.3	13
1779	Fasciclin-like arabinogalactan gene family in <i>Nicotiana benthamiana</i> : genome-wide identification, classification and expression in response to pathogens. <i>BMC Plant Biology</i> , 2020, 20, 305.	1.6	29
1780	Autophagy-Related 2 Regulates Chlorophyll Degradation under Abiotic Stress Conditions in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 4515.	1.8	20
1781	How Crisp is CRISPR? CRISPR-Cas-mediated crop improvement with special focus on nutritional traits. , 2020, , 159-197.		5
1782	Genome-wide identification and characterization of SnRK family genes in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2020, 20, 287.	1.6	14
1783	Abscisic acid promotes jasmonic acid biosynthesis via a <i>SAPK10â€bZIP72</i> <i>AOC</i> pathway to synergistically inhibit seed germination in rice ( <i>Oryza sativa</i> ). <i>New Phytologist</i> , 2020, 228, 1336-1353.	3.5	93
1784	PuHox52â€mediated hierarchical multilayered gene regulatory network promotes adventitious root formation in <i>Populus ussuriensis</i> . <i>New Phytologist</i> , 2020, 228, 1369-1385.	3.5	33
1785	Light-regulated expression of terpene synthase gene, <i>AtTPS03</i> , is controlled by the bZIP transcription factor, <i>HY5</i> , in <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 529, 437-443.	1.0	32
1786	Genome-wide investigation of the NAC transcript factor family in perennial ryegrass ( <i>Lolium perenne</i> ) Tj ETQq1 1 0.784314 rgBT/Overlo 1.3	1.3	13
1787	Comprehensive Profiling of Tubby-Like Protein Expression Uncovers Ripening-Related TLP Genes in Tomato ( <i>Solanum lycopersicum</i> ). <i>International Journal of Molecular Sciences</i> , 2020, 21, 1000.	1.8	15
1788	Comparative transcriptomics reveals candidate transcription factors involved in costunolide biosynthesis in medicinal plant- <i>Saussurea lappa</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 150, 52-67.	3.6	13

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1790	Tinkering Cis Motifs Jigsaw Puzzle Led to Root-Specific Drought-Inducible Novel Synthetic Promoters. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1357.	1.8	13
1791	Genome-Wide Identification of the Auxin Response Factor (ARF) Gene Family and Their Expression Analysis during Flower Development of <i>Osmanthus fragrans</i> . <i>Forests</i> , 2020, 11, 245.	0.9	10
1792	Comparative and evolutionary analyses of the divergence of plant oligosaccharyltransferase STT3 isoforms. <i>FEBS Open Bio</i> , 2020, 10, 468-483.	1.0	4
1793	Two promoter regions confer heat-induced activation of SIDREBA4 in <i>Solanum lycopersicum</i> . <i>Biochemical and Biophysical Research Communications</i> , 2020, 524, 689-695.	1.0	2
1794	Wheat PP2C-a10 regulates seed germination and drought tolerance in transgenic <i>Arabidopsis</i> . <i>Plant Cell Reports</i> , 2020, 39, 635-651.	2.8	35
1795	Functional characterization of an inducible bidirectional promoter from <i>Fusarium oxysporum</i> f. sp. cubense. <i>Scientific Reports</i> , 2020, 10, 2323.	1.6	3
1796	Genome-wide identification, phylogeny, and expression analysis of the <i>CA</i> gene family in tomato. <i>Biotechnology and Biotechnological Equipment</i> , 2020, 34, 70-83.	0.5	5
1797	Genome-Wide Profiling and Phylogenetic Analysis of the SWEET Sugar Transporter Gene Family in Walnut and Their Lack of Responsiveness to <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> Infection. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1251.	1.8	17
1798	The Floral Repressor GmFLC-like Is Involved in Regulating Flowering Time Mediated by Low Temperature in Soybean. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1322.	1.8	25
1799	AaCOI1, Encoding a CORONATINE INSENSITIVE 1-Like Protein of <i>Artemisia annua</i> L., Is Involved in Development, Defense, and Anthocyanin Synthesis. <i>Genes</i> , 2020, 11, 221.	1.0	4
1800	Genes ScBx1 and ScIglâ€™Competitors or Cooperators?. <i>Genes</i> , 2020, 11, 223.	1.0	6
1801	Phylogenetic analysis and transcriptional profiling of WRKY genes in sunflower ( <i>Helianthus annuus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Products, 2020, 148, 112268.	2.5	27
1802	The specific W-boxes of GAPC5 promoter bound by TaWRKY are involved in drought stress response in wheat. <i>Plant Science</i> , 2020, 296, 110460.	1.7	13
1803	AhHDA1-mediated AhGLK1 promoted chlorophyll synthesis and photosynthesis regulates recovery growth of peanut leaves after water stress. <i>Plant Science</i> , 2020, 294, 110461.	1.7	13
1804	The Genome-Wide Analysis of RALF-Like Genes in Strawberry (Wild and Cultivated) and Five Other Plant Species (Rosaceae). <i>Genes</i> , 2020, 11, 174.	1.0	6
1805	Genome-Wide Identification and Expression Analysis of Auxin Response Factor (ARF) Gene Family in Longan ( <i>Dimocarpus longan</i> L.). <i>Plants</i> , 2020, 9, 221.	1.6	18
1806	Identification of eukaryotic translation initiation factors and the temperature-dependent nature of Turnip mosaic virus epidemics in allopolyploid <i>Brassica juncea</i> . <i>3 Biotech</i> , 2020, 10, 75.	1.1	5

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1808	B-box Proteins in <i>Arachis duranensis</i> : Genome-Wide Characterization and Expression Profiles Analysis. <i>Agronomy</i> , 2020, 10, 23.	1.3	18
1809	Allele specific expression of Dof genes responding to hormones and abiotic stresses in sugarcane. <i>PLoS ONE</i> , 2020, 15, e0227716.	1.1	14
1810	Role of an Amur grape CBL-interacting protein kinase VaCIPK02 in drought tolerance by modulating ABA signaling and ROS production. <i>Environmental and Experimental Botany</i> , 2020, 172, 103999.	2.0	15
1811	DNA methylation of LDOX gene contributes to the floral colour variegation in peach. <i>Journal of Plant Physiology</i> , 2020, 246-247, 153116.	1.6	17
1812	Differential expression of IDA (INFLORESCENCE DEFICIENT IN ABSCISSION)-like genes in <i>Nicotiana benthamiana</i> during corolla abscission, stem growth and water stress. <i>BMC Plant Biology</i> , 2020, 20, 34.	1.6	10
1813	CsHT11 encodes a pollen-specific hexose transporter and is induced under high level sucrose in pollen tubes of cucumber ( <i>Cucumis sativus</i> ). <i>Plant Growth Regulation</i> , 2020, 90, 237-248.	1.8	6
1814	Analysis of Aldo-keto Reductase Gene Family and Their Responses to Salt, Drought, and Abscisic Acid Stresses in <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 754.	1.8	15
1815	Molecular characterization of teosinte branched1 gene governing branching architecture in cultivated maize and wild relatives. <i>3 Biotech</i> , 2020, 10, 77.	1.1	6
1816	Histone Deacetylase (HDAC) Gene Family in Allotetraploid Cotton and Its Diploid Progenitors: In Silico Identification, Molecular Characterization, and Gene Expression Analysis under Multiple Abiotic Stresses, DNA Damage and Phytohormone Treatments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 321.	1.8	26
1817	Calcium-dependent changes in physicochemical properties and the proteome dynamics influence dehydration responses in rice. <i>Environmental and Experimental Botany</i> , 2020, 172, 103965.	2.0	3
1818	Genome-Wide Identification and Characterization of the NAC Transcription Factor Family in <i>Musa Acuminata</i> and Expression Analysis during Fruit Ripening. <i>International Journal of Molecular Sciences</i> , 2020, 21, 634.	1.8	34
1819	Effect of Transgenesis on mRNA and miRNA Profiles in Cucumber Fruits Expressing Thaumatin II. <i>Genes</i> , 2020, 11, 334.	1.0	7
1820	Genome wide characterization revealed MnMLO2 and MnMLO6A as candidate genes involved in powdery mildew susceptibility in mulberry. <i>Molecular Biology Reports</i> , 2020, 47, 2889-2900.	1.0	7
1821	Isolation and structural analysis of the Bx6 and Bx7 genes controlling the biosynthesis of benzoxazinoids in rye ( <i>Secale cereale</i> L.). <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	6
1822	Genome-wide identification, characterization and expression analysis of the amino acid permease gene family in tea plants ( <i>Camellia sinensis</i> ). <i>Genomics</i> , 2020, 112, 2866-2874.	1.3	17
1823	Genome-wide analysis of CsWOX transcription factor gene family in cucumber ( <i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2020, 10, 6216.	1.6	16
1824	Molecular and biochemical analyses of a novel lectin with MATH domains from <i>Brassica oleracea</i> . <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	1.0	0

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1825	Bioinformatic identification and analyses of the non-specific lipid transfer proteins in wheat. <i>Journal of Integrative Agriculture</i> , 2020, 19, 1170-1185.	1.7	27
1826	Characterization of <i>Rosa chinensis</i> CBF Genes and the Function of RcCBF6 in Cold Tolerance. <i>Journal of Plant Biology</i> , 2020, 63, 267-278.	0.9	2
1827	Cloning and functional identification of a <i>Chilo suppressalis</i> $\epsilon$ -inducible promoter of rice gene, OsHPL2. <i>Pest Management Science</i> , 2020, 76, 3177-3187.	1.7	7
1828	CcMYB6-1 and CcbHLH1, two novel transcription factors synergistically involved in regulating anthocyanin biosynthesis in cornflower. <i>Plant Physiology and Biochemistry</i> , 2020, 151, 271-283.	2.8	20
1829	Genome-wide identification and functional analysis of ARF transcription factors in <i>Brassica juncea</i> var. <i>tumida</i> . <i>PLoS ONE</i> , 2020, 15, e0232039.	1.1	9
1830	Genome-Wide Identification, Phylogeny, and Expressional Profiles of the Mitogen-Activated Protein Kinase Kinase Kinase (MAPKKK) Gene Family in <i>Pyropia yezoensis</i> . <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	6
1831	GUS-reporter based analysis of the promoter activity of <i>Gossypium hirsutum</i> NAC transcription factor, GhNAC4 that is induced by phytohormones and environmental stresses. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 141, 643-654.	1.2	9
1832	Genome-wide mining and comparative analysis of fatty acid elongase gene family in <i>Brassica napus</i> and its progenitors. <i>Gene</i> , 2020, 747, 144674.	1.0	19
1833	Functional characterization of the promoter of pearl millet heat shock protein 10 (PgHsp10) in response to abiotic stresses in transgenic tobacco plants. <i>International Journal of Biological Macromolecules</i> , 2020, 156, 103-110.	3.6	8
1834	Genome-wide identification of expansin genes in <i>Brachypodium distachyon</i> and functional characterization of BdEXPA27. <i>Plant Science</i> , 2020, 296, 110490.	1.7	16
1835	Ectopic expression of the persimmon $\beta$ -galactosidase gene DkGAL2 promotes leaf growth, delays dark-induced senescence and enhances tolerance to abiotic stress in <i>Arabidopsis</i> . <i>Scientia Horticulturae</i> , 2020, 265, 109232.	1.7	5
1836	<i>MADS78</i> and <i>MADS79</i> Are Essential Regulators of Early Seed Development in Rice. <i>Plant Physiology</i> , 2020, 182, 933-948.	2.3	49
1837	Chalcone synthase (CHS) family members analysis from eggplant ( <i>Solanum melongena</i> L.) in the flavonoid biosynthetic pathway and expression patterns in response to heat stress. <i>PLoS ONE</i> , 2020, 15, e0226537.	1.1	36
1838	Genome-wide analysis of wheat DNA-binding with one finger (Dof) transcription factor genes: evolutionary characteristics and diverse abiotic stress responses. <i>BMC Genomics</i> , 2020, 21, 276.	1.2	28
1839	Identification and expression analysis of WRKY gene family under drought stress in peanut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.1	38
1840	Expression Analyses of Soybean VOZ Transcription Factors and the Role of GmVOZ1G in Drought and Salt Stress Tolerance. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2177.	1.8	21
1841	Transcriptomic Response to Water Deficit Reveals a Crucial Role of Phosphate Acquisition in a Drought-Tolerant Common Bean Landrace. <i>Plants</i> , 2020, 9, 445.	1.6	8
1842	Identification and in silico evaluation of bHLH genes in the <i>Sesamum indicum</i> genome: Growth regulation and stress dealing specially through the metal ions homeostasis and flavonoid biosynthesis. <i>Gene Reports</i> , 2020, 19, 100639.	0.4	2

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1843	Genome-wide identification and expression analysis of detoxification efflux carriers (DTX) genes family under abiotic stresses in flax. <i>Physiologia Plantarum</i> , 2021, 171, 483-501.	2.6	21
1844	Genome-Wide Identification and Expression Analysis of the BvSnRK2 Genes Family in Sugar Beet (Beta) Tj ETQq1 1 0,784314 <sub>5</sub> rgBT /Over	2.8	5
1845	Genome-wide identification and expression analysis of the NF- $\kappa$ B transcription factor family in <i>Populus</i> . <i>Physiologia Plantarum</i> , 2021, 171, 309-327.	2.6	31
1846	The dynamics of cis-regulatory elements in promoter regions of tomato sucrose transporter genes. <i>International Journal of Vegetable Science</i> , 2021, 27, 167-186.	0.6	3
1847	Identification and characterization of the bZIP transcription factor family in yellowhorn. <i>Journal of Forestry Research</i> , 2021, 32, 273-284.	1.7	5
1848	Identification of yellowhorn ( <i>Xanthoceras sorbifolium</i> ) WRKY transcription factor family and analysis of abiotic stress response model. <i>Journal of Forestry Research</i> , 2021, 32, 987-1004.	1.7	19
1849	Bioinformatics analysis of WRKY transcription factors in grape and their potential roles prediction in sugar and abscisic acid signaling pathway. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 67-80.	0.9	9
1850	Moderate Salinity Stress Reduces Rice Grain Yield by Influencing Expression of Grain Number- and Grain Filling-Associated Genes. <i>Journal of Plant Growth Regulation</i> , 2021, 40, 1111-1120.	2.8	6
1851	Identification and expression analysis of the <i>Hevea brasiliensis</i> phosphate transporter 1 gene family. <i>Trees - Structure and Function</i> , 2021, 35, 407-419.	0.9	0
1852	Genome-wide identification of wheat ( <i>Triticum aestivum</i> L.) expansin genes and functional characterization of TaEXPB1A. <i>Environmental and Experimental Botany</i> , 2021, 182, 104307.	2.0	10
1853	Identification and characterization of a natural SNP variant in ALTERNATIVE OXIDASE gene associated with cold stress tolerance in watermelon. <i>Plant Science</i> , 2021, 304, 110735.	1.7	7
1854	Molecular characterization revealed the role of catalases under abiotic and arsenic stress in bread wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Hazardous Materials</i> , 2021, 403, 123585.	6.5	56
1855	GhTULP34, a member of tubby-like proteins, interacts with GhSKP1A to negatively regulate plant osmotic stress. <i>Genomics</i> , 2021, 113, 462-474.	1.3	19
1856	Functional characterization and expression profiling of glyoxalase <i>scp</i> genes in date palm grown under abiotic stresses. <i>Physiologia Plantarum</i> , 2021, 172, 780-794.	2.6	9
1857	Glutaredoxin like protein (RtGRL1) regulates H <sub>2</sub> O <sub>2</sub> and Na <sup>+</sup> accumulation by maintaining the glutathione pool during abiotic stress. <i>Plant Physiology and Biochemistry</i> , 2021, 159, 135-147.	2.8	13
1858	Comprehensive identification and characterization of abiotic stress and hormone responsive glycosyl hydrolase family 1 genes in <i>Medicago truncatula</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 158, 21-33.	2.8	26
1859	MdKNOX19, a class II knotted-like transcription factor of apple, plays roles in ABA signalling/sensitivity by targeting ABI5 during organ development. <i>Plant Science</i> , 2021, 302, 110701.	1.7	15
1860	SLMYB14 promotes flavonoids accumulation and confers higher tolerance to 2,4,6-trichlorophenol in tomato. <i>Plant Science</i> , 2021, 303, 110796.	1.7	18



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1862	PAP90, a novel rice protein plays a critical role in regulation of D1 protein stability of PSII. <i>Journal of Advanced Research</i> , 2021, 30, 197-211.	4.4	6
1863	Nitrogen starvation-inducible promoter of microalga <i>Neochloris oleoabundans</i> lipogenic gene encoding diacylglycerol acyltransferase 2. <i>Journal of Applied Phycology</i> , 2021, 33, 331-341.	1.5	2
1864	Effects of shading on lignin biosynthesis in the leaf of tea plant ( <i>Camellia sinensis</i> (L.) O. Kuntze). <i>Molecular Genetics and Genomics</i> , 2021, 296, 165-177.	1.0	21
1865	Unusual DNA-binding properties of the <i>Arabidopsis thaliana</i> WRKY50 transcription factor at target gene promoters. <i>Plant Cell Reports</i> , 2021, 40, 69-83.	2.8	5
1866	Overexpression of miR1861h increases tolerance to salt stress in rice ( <i>Oryza sativa</i> L.). <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 87-92.	0.8	14
1867	Maize bHLH55 functions positively in salt tolerance through modulation of AsA biosynthesis by directly regulating GDP-mannose pathway genes. <i>Plant Science</i> , 2021, 302, 110676.	1.7	26
1868	The JA-responsive MYC2-BADH-like transcriptional regulatory module in <i>Poncirus trifoliata</i> contributes to cold tolerance by modulation of glycine betaine biosynthesis. <i>New Phytologist</i> , 2021, 229, 2730-2750.	3.5	50
1869	CaPSY1 gene plays likely the key role in carotenoid metabolism of pepper ( <i>Capsicum annuum</i> ) at ripening. <i>Functional Plant Biology</i> , 2021, 48, 141.	1.1	14
1870	Comparative in silico analysis of <i>Eragrostis tef</i> (Zucc.) Trotter with other species for elucidating presence of growth regulating factors (GRFs). <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 499-512.	0.8	4
1871	Genome-wide Identification, Expression Profiling and Promoter Analysis of Trehalose-6-Phosphate Phosphatase Gene Family in Rice. <i>Journal of Plant Biology</i> , 2021, 64, 55-71.	0.9	13
1872	Genome-wide identification and expression analysis of Aux/IAA gene family in strawberry ( <i>Fragaria</i> ) Tj ETQq1 1 0.784314 rgBT <sub>1</sub> /Overlook	0.4	1
1873	Increased Wheat Protein Content via Introgression of an HMW Glutenin Selectively Reshapes the Grain Proteome. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100097.	2.5	12
1874	Molecular characterization of miRNA genes and their expression in <i>Dimocarpus longan</i> Lour. <i>Planta</i> , 2021, 253, 41.	1.6	3
1875	Systematic Analysis of the bZIP Family in Tobacco and Functional Characterization of NtbZIP62 Involvement in Salt Stress. <i>Agronomy</i> , 2021, 11, 148.	1.3	13
1876	Genome wide identification and expression pattern analysis of the GRAS family in quinoa. <i>Functional Plant Biology</i> , 2021, 48, 948-962.	1.1	9
1877	Genome-wide analysis and characterization of GRAS family in switchgrass. <i>Bioengineered</i> , 2021, 12, 6096-6114.	1.4	5
1878	Tuning promoter boundaries improves regulatory motif discovery in nonmodel plants: the peach example. <i>Plant Physiology</i> , 2021, 185, 1242-1258.	2.3	25

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1879	Whole-genome characterization of <i>Rosa chinensis</i> AP2/ERF transcription factors and analysis of negative regulator RcdREB2B in <i>Arabidopsis</i> . <i>BMC Genomics</i> , 2021, 22, 90.	1.2	15
1880	Genome-wide identification, evolution, expression, and alternative splicing profiles of peroxiredoxin genes in cotton. <i>PeerJ</i> , 2021, 9, e10685.	0.9	4
1881	Genome-wide analysis of growth-regulating factors (GRFs) in <i>Triticum aestivum</i> . <i>PeerJ</i> , 2021, 9, e10701.	0.9	22
1882	Genome-wide identification of the histone acetyltransferase gene family in <i>Triticum aestivum</i> . <i>BMC Genomics</i> , 2021, 22, 49.	1.2	22
1883	Genome-wide identification and in silico gene expression analysis of the related to ABI3/VP1 (RAV) transcription factor family in barley ( <i>Hordeum vulgare</i> L.). <i>Biocell</i> , 2021, 45, 1673-1685.	0.4	0
1884	A Novel Putative Microtubule-Associated Protein Is Involved in Arbuscule Development during Arbuscular Mycorrhiza Formation. <i>Plant and Cell Physiology</i> , 2021, 62, 306-320.	1.5	9
1885	Genome-Wide Characterization and Expression Analysis of the HD-ZIP Gene Family in Response to Salt Stress in Pepper. <i>International Journal of Genomics</i> , 2021, 2021, 1-14.	0.8	13
1886	Study of JASMONATE ZIM-Domain gene family to waterlogging stress in <i>Cucumis sativus</i> L. <i>Vegetable Research</i> , 2021, 1, 1-12.	0.2	2
1887	A Web Platform to Integrate Bioinformatics Tools. A Case of Study. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 506-515.	0.5	0
1888	Genome-wide characterization and analysis of the CCT motif family genes in soybean ( <i>Glycine max</i> ). <i>Planta</i> , 2021, 253, 15.	1.6	26
1889	Genome-wide mining of wheat B-BOX zinc finger (BBX) gene family provides new insights into light stress responses. <i>Crop and Pasture Science</i> , 2021, 72, 17.	0.7	8
1890	Comparative genomic analysis of superoxide dismutase (SOD) genes in three Rosaceae species and expression analysis in <i>Pyrus bretschneideri</i> . <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 39-52.	1.4	8
1891	Genome-Wide Analysis and the Expression Pattern of the ERF Gene Family in <i>Hypericum perforatum</i> . <i>Plants</i> , 2021, 10, 133.	1.6	3
1893	Genome-wide analysis of haloacid dehalogenase genes reveals their function in phosphate starvation responses in rice. <i>PLoS ONE</i> , 2021, 16, e0245600.	1.1	5
1894	Comparative analysis of transcriptomic profiling to identify genes involved in the bulged surface of pear fruit ( <i>Pyrus bretschneideri</i> Rehd. cv. Yuluxiangli). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 69-80.	1.4	3
1895	Functional analysis of TmHKT1;4-A2 promoter through deletion analysis provides new insight into the regulatory mechanism underlying abiotic stress adaptation. <i>Planta</i> , 2021, 253, 18.	1.6	4
1896	UDP-Glucose Dehydrogenases: Identification, Expression, and Function Analyses in Upland Cotton ( <i>Gossypium hirsutum</i> ). <i>Frontiers in Genetics</i> , 2020, 11, 597890.	1.1	5
1897	Genome-wide identification, characterization and expression analysis of the expansin gene family under drought stress in tea ( <i>Camellia sinensis</i> L.). <i>Plant Science Today</i> , 2021, 8, 32-44.	0.4	9

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1898	EasyBio: A Bioinformatics Web Platform to Analyze Families of Genes. <i>Advances in Intelligent Systems and Computing</i> , 2021, , 210-219.	0.5	0
1899	Genome Wide Identification and Analysis of the R2R3-MYB Transcription Factor Gene Family in the Mangrove <i>Avicennia marina</i> . <i>Agronomy</i> , 2021, 11, 123.	1.3	4
1900	Identification, Classification, and Expression Analysis of the Triacylglycerol Lipase (TGL) Gene Family Related to Abiotic Stresses in Tomato. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1387.	1.8	9
1901	Response of phytohormone mediated plant homeodomain (PHD) family to abiotic stress in upland cotton ( <i>Gossypium hirsutum</i> spp.). <i>BMC Plant Biology</i> , 2021, 21, 13.	1.6	22
1902	Identification and Downstream Analyses of Domains Amplified in Plant Genomes: The Case of StAR-Related Lipid Transfer (START) Domains in Rice. <i>Methods in Molecular Biology</i> , 2021, 2238, 325-338.	0.4	1
1904	Functional characterization of soybean ( <i>Glycine max</i> ) DIRIGENT genes reveals an important role of GmDIR27 in the regulation of pod dehiscence. <i>Genomics</i> , 2021, 113, 979-990.	1.3	12
1905	Genome-wide identification and classification of Lipoxygenase gene family and their roles in sorghum-aphid interaction. <i>Plant Molecular Biology</i> , 2021, 105, 527-541.	2.0	18
1906	Digital Gene Expression Analysis of Huanglongbing Affected Mandarins ( <i>Citrus reticulata</i> Blanco) In Response to Thermotherapy. <i>Horticultural Plant Journal</i> , 2021, 7, 1-12.	2.3	5
1907	Genome-Wide Identification of the NHX Gene Family in <i>Punica granatum</i> L. and Their Expressional Patterns under Salt Stress. <i>Agronomy</i> , 2021, 11, 264.	1.3	17
1908	Genome-wide bioinformatics analysis revealed putative substrate specificities of SABATH and MES family members in silver birch ( <i>Betula pendula</i> ). <i>Silvae Genetica</i> , 2021, 70, 57-74.	0.4	3
1909	Villin Family Members Associated with Multiple Stress Responses in Cotton. <i>Phyton</i> , 2021, 90, 1645-1660.	0.4	4
1910	A gene regulatory network for antenna size control in carbon dioxide-deprived <i>Chlamydomonas reinhardtii</i> cells. <i>Plant Cell</i> , 2021, 33, 1303-1318.	3.1	10
1911	Genome-wide identification, characterization and transcriptional profiling of NHX-type (Na <sup>+</sup> /H <sup>+</sup> ) antiporters under salinity stress in soybean. <i>3 Biotech</i> , 2021, 11, 16.	1.1	19
1912	Genome-wide identification and characterization of NBS-encoding genes in <i>Raphanus sativus</i> L. and their roles related to <i>Fusarium oxysporum</i> resistance. <i>BMC Plant Biology</i> , 2021, 21, 47.	1.6	18
1913	Genome wide identification and expression analysis of pepper C2H2 zinc finger transcription factors in response to anthracnose pathogen <i>Colletotrichum truncatum</i> . <i>3 Biotech</i> , 2021, 11, 118.	1.1	9
1914	Genome-Wide Characterization, Evolution, and Expression Profile Analysis of GATA Transcription Factors in <i>Brachypodium distachyon</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2026.	1.8	21
1915	Comprehensive Genome-Wide Exploration of C2H2 Zinc Finger Family in Grapevine ( <i>Vitis vinifera</i> L.): Insights into the Roles in the Pollen Development Regulation. <i>Genes</i> , 2021, 12, 302.	1.0	20
1916	Genome-wide identification and expression profiling of glutathione S-transferase family under multiple abiotic and biotic stresses in <i>Medicago truncatula</i> L.. <i>PLoS ONE</i> , 2021, 16, e0247170.	1.1	23

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1918	The <i>Medicago truncatula</i> Sugar Transport Protein 13 and Its Lr67res-Like Variant Confer Powdery Mildew Resistance in Legumes via Defense Modulation. Plant and Cell Physiology, 2021, 62, 650-667.	1.5	11
1919	Characterization of Mungbean CONSTANS-LIKE Genes and Functional Analysis of CONSTANS-LIKE 2 in the Regulation of Flowering Time in Arabidopsis. Frontiers in Plant Science, 2021, 12, 608603.	1.7	13
1921	Genome-wide characterization of the hyperaccumulator <i>Sedum alfredii</i> F-box family under cadmium stress. Scientific Reports, 2021, 11, 3023.	1.6	3
1922	Evolutionary Divergence and Biased Expression of NAC Transcription Factors in Hexaploid Bread Wheat ( <i>Triticum aestivum</i> L.). Plants, 2021, 10, 382.	1.6	9
1923	Genome-wide identification, characterisation, and evolution of <i>ABF/AREB</i> subfamily in nine Rosaceae species and expression analysis in mei ( <i>Prunus mume</i> ). PeerJ, 2021, 9, e10785.	0.9	8
1924	Genome-Wide Characterization of HSP90 Gene Family in Cucumber and Their Potential Roles in Response to Abiotic and Biotic Stresses. Frontiers in Genetics, 2021, 12, 584886.	1.1	9
1925	Genome-wide identification of chitinase genes in <i>Thalassiosira pseudonana</i> and analysis of their expression under abiotic stresses. BMC Plant Biology, 2021, 21, 87.	1.6	12
1926	Genome-wide identification and function characterization of GATA transcription factors during development and in response to abiotic stresses and hormone treatments in pepper. Journal of Applied Genetics, 2021, 62, 265-280.	1.0	18
1927	Genome-Wide Analysis Reveals the Potential Role of MYB Transcription Factors in Floral Scent Formation in <i>Hedychium coronarium</i> . Frontiers in Plant Science, 2021, 12, 623742.	1.7	53
1928	Molecular characterization, expression and functional analysis of acyl-CoA-binding protein gene family in maize ( <i>Zea mays</i> ). BMC Plant Biology, 2021, 21, 94.	1.6	12
1929	Genome-wide identification and characterisation of phenylalanine ammonia-lyase gene family in grapevine. Journal of Horticultural Science and Biotechnology, 2021, 96, 456-468.	0.9	18
1930	Isolation and Functional Characterization of the Promoters of Miltiradiene Synthase Genes, TwTPS27a and TwTPS27b, and Interaction Analysis with the Transcription Factor TwTGA1 from <i>Tripterygium wilfordii</i> . Plants, 2021, 10, 418.	1.6	11
1931	Genome-wide in silico identification and expression analysis of beta-galactosidase family members in sweetpotato [ <i>Ipomoea batatas</i> (L.) Lam.]. BMC Genomics, 2021, 22, 140.	1.2	18
1932	Genome-wide analysis of fluoride exporter genes in plants. 3 Biotech, 2021, 11, 124.	1.1	2
1933	Genome-Wide Characterization of Lectin Receptor Kinases in <i>Saccharum spontaneum</i> L. and Their Responses to <i>Stagonospora tainanensis</i> Infection. Plants, 2021, 10, 322.	1.6	11
1934	Comparative genomic analysis reveals evolutionary and structural attributes of MCM gene family in <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> . Journal of Biotechnology, 2021, 327, 117-132.	1.9	2
1935	Genome-Wide Identification and Comprehensive Analyses of TCP Gene Family in Banana ( <i>Musa</i> L.). Tropical Plant Biology, 2021, 14, 180-202.	1.0	8

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1937	Genome-Wide Identification and Characterization of Wheat 14-3-3 Genes Unravels the Role of TaGRF6-A in Salt Stress Tolerance by Binding MYB Transcription Factor. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1904.	1.8	22
1938	Systematic Investigations of the ZF-HD Gene Family in Tobacco Reveal Their Multiple Roles in Abiotic Stresses. <i>Agronomy</i> , 2021, 11, 406.	1.3	9
1939	Genome-wide identification and expression profiling of chitinase genes in tea ( <i>Camellia sinensis</i> (L.) O.) Tj ETQq1 1 0.784314 rgBT /Over	1.4	16
1940	Genome-wide characterization of PEBP family genes in nine Rosaceae tree species and their expression analysis in <i>P. mume</i> . <i>Bmc Ecology and Evolution</i> , 2021, 21, 32.	0.7	10
1941	Characteristic and evolution of HAT and HDAC genes in Gramineae genomes and their expression analysis under diverse stress in <i>Oryza sativa</i> . <i>Planta</i> , 2021, 253, 72.	1.6	12
1943	Genome-wide identification and functional characterization of the PheE2F/DP gene family in Moso bamboo. <i>BMC Plant Biology</i> , 2021, 21, 158.	1.6	6
1945	Identification and characterization of SlbHLH, SlDof and SlWRKY transcription factors interacting with SlDPD gene involved in costunolide biosynthesis in <i>Saussurea lappa</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 173, 146-159.	3.6	2
1946	Genome-Wide Analysis of the Trihelix Gene Family and Their Response to Cold Stress in <i>Dendrobium officinale</i> . <i>Sustainability</i> , 2021, 13, 2826.	1.6	3
1947	Genomic-Wide Analysis of the PLC Family and Detection of GmPI-PLC7 Responses to Drought and Salt Stresses in Soybean. <i>Frontiers in Plant Science</i> , 2021, 12, 631470.	1.7	15
1948	The Arabidopsis SMALL AUXIN UP RNA32 Protein Regulates ABA-Mediated Responses to Drought Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 625493.	1.7	44
1949	Cytokinin Type-B Response Regulators Promote Bulbil Initiation in <i>Lilium lancifolium</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 3320.	1.8	6
1950	Identification, characterization, and expression profiles of the GASA genes in cotton. <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	13
1951	Roles of the 14-3-3 gene family in cotton flowering. <i>BMC Plant Biology</i> , 2021, 21, 162.	1.6	18
1952	Zinc Finger-Homeodomain Transcriptional Factors (ZF-HDs) in Wheat ( <i>Triticum aestivum</i> L.): Identification, Evolution, Expression Analysis and Response to Abiotic Stresses. <i>Plants</i> , 2021, 10, 593.	1.6	16
1953	Genome-wide identification and expression analysis of dirigent-jacalin genes from plant chimeric lectins in Moso bamboo ( <i>Phyllostachys edulis</i> ). <i>PLoS ONE</i> , 2021, 16, e0248318.	1.1	7
1954	VOZS identification from TEF [ <i>Eragrostis tef</i> (Zucc.) Trotter] using in silico tools decipher their involvement in abiotic stress. <i>Materials Today: Proceedings</i> , 2022, 49, 3357-3364.	0.9	4
1955	Transcriptional Dynamics of Genes Purportedly Involved in the Control of Meiosis, Carbohydrate, and Secondary Metabolism during Sporulation in <i>Ganoderma lucidum</i> . <i>Genes</i> , 2021, 12, 504.	1.0	6

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1957	Genome-Wide Analysis of Dof Genes and Their Response to Abiotic Stress in Rose ( <i>Rosa chinensis</i> ). <i>Frontiers in Genetics</i> , 2021, 12, 538733.	1.1	13
1958	The prohibitins (PHB) gene family in tomato: Bioinformatic identification and expression analysis under abiotic and phytohormone stresses. <i>GM Crops and Food</i> , 2021, 12, 535-550.	2.0	6
1959	Identification of the PP2C gene family in paper mulberry ( <i>Broussonetia papyrifera</i> ) and its roles in the regulation mechanism of the response to cold stress. <i>Biotechnology Letters</i> , 2021, 43, 1089-1102.	1.1	13
1960	Characterization and expression quantitative trait loci analysis of <i>TaABI4</i> , a pre-harvest sprouting related gene in wheat. <i>Seed Science Research</i> , 2021, 31, 188-198.	0.8	2
1961	Genome-wide identification and characterization of the TPS gene family in wheat ( <i>Triticum aestivum</i> L.) and expression analysis in response to aphid damage. <i>Acta Physiologiae Plantarum</i> , 2021, 43, 1.	1.0	8
1962	Genome-wide identification of the GATA gene family in potato ( <i>Solanum tuberosum</i> L.) and expression analysis. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 37-48.	0.9	8
1963	Genome-wide analysis of AP2/ERF transcription factors in pineapple reveals functional divergence during flowering induction mediated by ethylene and floral organ development. <i>Genomics</i> , 2021, 113, 474-489.	1.3	37
1964	Genome-wide identification of superoxide dismutase gene families and their expression patterns under low-temperature, salt and osmotic stresses in watermelon and melon. <i>3 Biotech</i> , 2021, 11, 194.	1.1	8
1965	Arabidopsis lysin motif/FA-box containing protein InLYP1 fine-tunes glycine metabolism by degrading glycine decarboxylase GLDP2. <i>Plant Journal</i> , 2021, 106, 394-408.	2.8	5
1966	Yield and antiyield genes in common bean ( <i>Phaseolus vulgaris</i> L.)., 2021, 3, e91.		3
1967	Molecular characterization of Fe-acquisition genes causing decreased Fe uptake and photosynthetic inefficiency in Fe-deficient sunflower. <i>Scientific Reports</i> , 2021, 11, 5537.	1.6	8
1968	Genome-Wide Investigation of Major Enzyme-Encoding Genes in the Flavonoid Metabolic Pathway in Tartary Buckwheat ( <i>Fagopyrum tataricum</i> ). <i>Journal of Molecular Evolution</i> , 2021, 89, 269-286.	0.8	11
1969	Genome-wide identification and expression analysis of ADP-ribosylation factors associated with biotic and abiotic stress in wheat ( <i>Triticum aestivum</i> L.). <i>PeerJ</i> , 2021, 9, e10963.	0.9	6
1970	Expansion and Molecular Characterization of AP2/ERF Gene Family in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 632155.	1.1	23
1971	Genome-Wide Identification and Characterization of the CsFHY3/FAR1 Gene Family and Expression Analysis under Biotic and Abiotic Stresses in Tea Plants ( <i>Camellia sinensis</i> ). <i>Plants</i> , 2021, 10, 570.	1.6	17
1972	Genome-wide characterization and expression profiling of EIN3/EIL family genes in <i>Zea mays</i> . <i>Plant Gene</i> , 2021, 25, 100270.	1.4	8
1973	Genome-wide identification and expression pattern of SnRK gene family under several hormone treatments and its role in floral scent emission in <i>Hedychium coronarium</i> . <i>PeerJ</i> , 2021, 9, e10883.	0.9	4
1974	<i>St</i> PIP1, a PAMP-induced peptide in potato, elicits plant defenses and is associated with disease symptom severity in a compatible interaction with <i>Potato virus Y</i> . <i>Journal of Experimental Botany</i> , 2021, 72, 4472-4488.	2.4	16

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1975	Genome-Wide Identification and Characterization of TALE Superfamily Genes in Soybean ( <i>Glycine max</i> ) Tj ETQq0 0 0.185 BT /Overlock 10 T	1.8	12
1976	Genome-wide analysis of zinc finger motif-associated homeodomain (ZF-HD) family genes and their expression profiles under abiotic stresses and phytohormones stimuli in tea plants ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 BT /Overlock 10 T	1.7	10
1977	Cloning and characterization of the DIR1 promoter from <i>Eucommia ulmoides</i> Oliv and its response to hormonal and abiotic stress. <i>Plant Cell, Tissue and Organ Culture</i> , 2021, 146, 313-322.	1.2	6
1978	The chromosome-scale reference genome of safflower ( <i>Carthamus tinctorius</i> ) provides insights into linoleic acid and flavonoid biosynthesis. <i>Plant Biotechnology Journal</i> , 2021, 19, 1725-1742.	4.1	60
1979	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
1980	Bioinformatics and Expression Analysis of IDA-Like Genes Reveal Their Potential Functions in Flower Abscission and Stress Response in Tobacco ( <i>Nicotiana tabacum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 670794.	1.1	3
1981	Late embryogenesis abundant (LEA) gene family in <i>Salvia miltiorrhiza</i> : identification, expression analysis, and response to drought stress. <i>Plant Signaling and Behavior</i> , 2021, 16, 1891769.	1.2	13
1982	Genome-wide identification and transcriptional characterization of DNA methyltransferases conferring temperature-sensitive male sterility in wheat. <i>BMC Genomics</i> , 2021, 22, 310.	1.2	3
1983	Genome-wide identification of heat shock factors and heat shock proteins in response to UV and high intensity light stress in lettuce. <i>BMC Plant Biology</i> , 2021, 21, 185.	1.6	29
1984	Genome-Wide Identification and Characterization of Germin and Germin-Like Proteins (GLPs) and Their Response Under Powdery Mildew Stress in Wheat ( <i>Triticum aestivum</i> L.). <i>Plant Molecular Biology Reporter</i> , 2021, 39, 821-832.	1.0	13
1985	Molecular characterization of Leucoanthocyanidin reductase and Flavonol synthase gene in <i>Arachis hypogaea</i> . <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 2301-2315.	1.8	6
1986	Genome-wide identification of sucrose nonfermenting-1-related protein kinase (SnRK) genes in barley and RNA-seq analyses of their expression in response to abscisic acid treatment. <i>BMC Genomics</i> , 2021, 22, 300.	1.2	12
1987	Comprehensive analysis and identification of drought-responsive candidate NAC genes in three semi-arid tropics (SAT) legume crops. <i>BMC Genomics</i> , 2021, 22, 289.	1.2	11
1988	Coordinated and High-Level Expression of Biosynthetic Pathway Genes Is Responsible for the Production of a Major Floral Scent Compound Methyl Benzoate in <i>Hedychium coronarium</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 650582.	1.7	14
1989	Genome-wide identification and expression of the lipoxygenase gene family in jujube ( <i>Ziziphus jujuba</i> ) in response to phytoplasma infection. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2022, 31, 139-153.	0.9	8
1990	Identification, Expression, and Interaction Analysis of Ovate Family Proteins in <i>Populus trichocarpa</i> Reveals a Role of PtOFP1 Regulating Drought Stress Response. <i>Frontiers in Plant Science</i> , 2021, 12, 650109.	1.7	1
1991	Identification and Expression Analysis of SLAC/SLAH Gene Family in <i>Brassica napus</i> L.. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4671.	1.8	4
1992	Genome-wide identification, evolutionary relationship and expression analysis of AGO, DCL and RDR family genes in tea. <i>Scientific Reports</i> , 2021, 11, 8679.	1.6	11

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1993	Genome-Wide In Silico Identification and Comparative Analysis of Dof Gene Family in Brassica napus. <i>Plants</i> , 2021, 10, 709.	1.6	18
1994	Characterization of MYB35 regulated methyl jasmonate and wound responsive Geraniol 10-hydroxylase-1 gene from <i>Bacopa monnieri</i> . <i>Planta</i> , 2021, 253, 89.	1.6	8
1995	Identification of transcription factors controlling cell wall invertase gene expression for reproductive development via bioinformatic and transgenic analyses. <i>Plant Journal</i> , 2021, 106, 1058-1074.	2.8	14
1996	Genome-Wide Identification and Expression of Chitinase Class I Genes in Garlic ( <i>Allium sativum</i> L.) Cultivars Resistant and Susceptible to <i>Fusarium proliferatum</i> . <i>Plants</i> , 2021, 10, 720.	1.6	19
1997	Genome-wide identification, characterization and expression analysis of the LIM transcription factor family in quinoa. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 787-800.	1.4	10
1998	Engineering Resistance to Bacterial Blight and Bacterial Leaf Streak in Rice. <i>Rice</i> , 2021, 14, 38.	1.7	15
1999	Genome-Wide Investigation of the NF-X1 Gene Family in <i>Populus trichocarpa</i> Expression Profiles during Development and Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4664.	1.8	6
2000	Identification and Characterization of Abiotic Stress Responsive CBL-CIPK Family Genes in <i>Medicago</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 4634.	1.8	20
2001	The potential roles of different metacaspases in maize defense response. <i>Plant Signaling and Behavior</i> , 2021, 16, 1906574.	1.2	2
2002	Gain-of-function mutagenesis through activation tagging identifies XPB2 and SEN1 helicase genes as potential targets for drought stress tolerance in rice. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2253-2272.	1.8	4
2003	Genome-wide identification of ABCC gene family and their expression analysis in pigment deposition of fiber in brown cotton ( <i>Gossypium hirsutum</i> ). <i>PLoS ONE</i> , 2021, 16, e0246649.	1.1	9
2004	Exploration of glutathione reductase for abiotic stress response in bread wheat ( <i>Triticum aestivum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	2.8	44
2005	Genome-Wide Identification of Tannase Genes and Their Function of Wound Response and Astringent Substances Accumulation in Juglandaceae. <i>Frontiers in Plant Science</i> , 2021, 12, 664470.	1.7	4
2006	Fine mapping identified the gibberellin 2-oxidase gene CpDw leading to a dwarf phenotype in squash ( <i>Cucurbita pepo</i> L.). <i>Plant Science</i> , 2021, 306, 110857.	1.7	13
2007	In Silico Approach for Unraveling the Structural and Functional Roles of NF-X1-Like Proteins in Underutilized Cereal <i>Eragrostis tef</i> . <i>Biology Bulletin</i> , 2021, 48, 251-262.	0.1	3
2008	Overexpression of <i>PIF4</i> affects plant morphology and accelerates reproductive phase transitions in soybean. <i>Food and Energy Security</i> , 2021, 10, e291.	2.0	12
2009	Genome-Wide Identification and Expression of the PIN Auxin Efflux Carrier Gene Family in Watermelon ( <i>Citrullus lanatus</i> ). <i>Agriculture (Switzerland)</i> , 2021, 11, 447.	1.4	4
2010	Lupeol Accumulation Correlates with Auxin in the Epidermis of Castor. <i>Molecules</i> , 2021, 26, 2978.	1.7	7



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2011	Evolutionary analysis of GRAS gene family for functional and structural insights into hexaploid bread wheat ( <i>Triticum aestivum</i> ). <i>Journal of Biosciences</i> , 2021, 46, 1.	0.5	6
2012	Genome-Wide Identification Reveals That <i>Nicotiana benthamiana</i> Hypersensitive Response (HR)-Like Lesion Inducing Protein 4 (NbHRLI4) Mediates Cell Death and Salicylic Acid-Dependent Defense Responses to Turnip Mosaic Virus. <i>Frontiers in Plant Science</i> , 2021, 12, 627315.	1.7	6
2013	Overexpression of an expansin-like gene, GhEXLB2 enhanced drought tolerance in cotton. <i>Plant Physiology and Biochemistry</i> , 2021, 162, 468-475.	2.8	11
2014	Comprehensive genome-wide identification, characterization, and expression profiling of MATE gene family in <i>Nicotiana tabacum</i> . <i>Gene</i> , 2021, 783, 145554.	1.0	12
2015	Genome-Wide Analysis of the G2-Like Transcription Factor Genes and Their Expression in Different Senescence Stages of Tobacco ( <i>Nicotiana tabacum</i> L.). <i>Frontiers in Genetics</i> , 2021, 12, 626352.	1.1	12
2016	Synthetic Promoters from Strawberry Vein Banding Virus (SVBV) and Dahlia Mosaic Virus (DaMV). <i>Molecular Biotechnology</i> , 2021, 63, 792-806.	1.3	2
2017	Genome-wide identification, evolutionary estimation and functional characterization of two cotton CKI gene types. <i>BMC Plant Biology</i> , 2021, 21, 229.	1.6	1
2018	Genome-wide identification of the DUF668 gene family in cotton and expression profiling analysis of GhDUF668 in <i>Gossypium hirsutum</i> under adverse stress. <i>BMC Genomics</i> , 2021, 22, 395.	1.2	21
2019	Papain-Like Cysteine Protease Gene Family in Fig ( <i>Ficus carica</i> L.): Genome-Wide Analysis and Expression Patterns. <i>Frontiers in Plant Science</i> , 2021, 12, 681801.	1.7	21
2020	Fatty Acid Desaturases: Uncovering Their Involvement in Grapevine Defence against Downy Mildew. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5473.	1.8	16
2021	A salicylic acid inducible mulberry WRKY transcription factor, MiWRKY53 is involved in plant defence response. <i>Plant Cell Reports</i> , 2021, 40, 2151-2171.	2.8	13
2022	Genome-wide identification and characterization of <i>NAC</i> genes in <i>Brassica juncea</i> var. <i>tumida</i> . <i>PeerJ</i> , 2021, 9, e11212.	0.9	11
2023	Early-stage iron deficiency alters physiological processes and iron transporter expression, along with photosynthetic and oxidative damage to sorghum. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 4770-4777.	1.8	12
2024	Comparison and Characterization of a Cell Wall Invertase Promoter from Cu-Tolerant and Non-Tolerant Populations of <i>Elsholtzia haichowensis</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 5299.	1.8	1
2025	Molecular mechanisms of mutualistic and antagonistic interactions in a plant-pollinator association. <i>Nature Ecology and Evolution</i> , 2021, 5, 974-986.	3.4	30
2026	Multiomics reveal pivotal roles of sodium translocation and compartmentation in regulating salinity resistance in allotetraploid rapeseed. <i>Journal of Experimental Botany</i> , 2021, 72, 5687-5708.	2.4	7
2027	Genome-wide identification of auxin response factor (ARF) family in kiwifruit ( <i>Actinidia chinensis</i> ) and analysis of their inducible involvements in abiotic stresses. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1261-1276.	1.4	15
2028	R2R3-MYB transcription factor family in tea plant ( <i>Camellia sinensis</i> ): Genome-wide characterization, phylogeny, chromosome location, structure and expression patterns. <i>Genomics</i> , 2021, 113, 1565-1578.	1.3	45

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2029	OsZIP72 Is Involved in Transcriptional Gene-Regulation Pathway of Abscisic Acid Signal Transduction by Activating Rice High-Affinity Potassium Transporter OsHKT1;1. <i>Rice Science</i> , 2021, 28, 257-267.	1.7	16
2030	The NIP Genes in Sugar Beet: Underlying Roles in Silicon Uptake and Growth Improvement. <i>Silicon</i> , 2022, 14, 3551-3562.	1.8	5
2031	Physiological responses and genome-wide characterization of TaNRAMP1 gene in Mn-deficient wheat. <i>Plant Physiology and Biochemistry</i> , 2021, 162, 280-290.	2.8	5
2032	High promoter sequence variation in subgroup 6 members of R2R3-MYB genes is involved in different floral anthocyanin color patterns in <i>Lilium</i> spp.. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1005-1015.	1.0	6
2033	Identification, evolution, expression analysis of phospholipase D (PLD) gene family in tea ( <i>Camellia</i> ). <i>Trends in Plant Science</i> , 2021, 10, 1010-1015.	1.4	10
2035	Genome-wide analysis of the serine carboxypeptidase-like protein family in <i>Triticum aestivum</i> reveals TaSCPL184-6D is involved in abiotic stress response. <i>BMC Genomics</i> , 2021, 22, 350.	1.2	24
2036	A transcription factor TaTCP20 regulates the expression of Ppd-D1b in common wheat. <i>Plant Biotechnology Reports</i> , 2021, 15, 359-367.	0.9	1
2037	Overexpression of GhMPK3 from Cotton Enhances Cold, Drought, and Salt Stress in <i>Arabidopsis</i> . <i>Agronomy</i> , 2021, 11, 1049.	1.3	15
2038	Identification and expression analysis of the WRKY gene family in <i>Isatis indigotica</i> . <i>Gene</i> , 2021, 783, 145561.	1.0	24
2039	Identification and molecular characterization of rice bran-specific lipases. <i>Plant Cell Reports</i> , 2021, 40, 1215-1228.	2.8	8
2040	A MADS-Box Gene CiMADS43 Is Involved in Citrus Flowering and Leaf Development through Interaction with CiAGL9. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5205.	1.8	19
2041	Genome-wide identification, characterization and expression analysis of the carotenoid cleavage oxygenase (CCO) gene family in <i>Saccharum</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 162, 196-210.	2.8	20
2042	New Insights Into Structure and Function of TIFY Genes in <i>Zea mays</i> and <i>Solanum lycopersicum</i> : A Genome-Wide Comprehensive Analysis. <i>Frontiers in Genetics</i> , 2021, 12, 657970.	1.1	31
2043	Characterization of the pectin methylesterase inhibitor gene family in Rosaceae and role of PbrPMEI23/39/41 in methylesterified pectin distribution in pear pollen tube. <i>Planta</i> , 2021, 253, 118.	1.6	13
2044	Genome-Wide Identification, Classification and Expression Analysis of the MYB Transcription Factor Family in <i>Petunia</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 4838.	1.8	18
2045	Genome-Wide Study of NOT2_3_5 Protein Subfamily in Cotton and Their Necessity in Resistance to <i>Verticillium</i> wilt. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5634.	1.8	2
2046	Genome-wide identification, characterization and expression profiles of the CCD gene family in <i>Gossypium</i> species. <i>3 Biotech</i> , 2021, 11, 249.	1.1	11
2047	When rice gets the chills: comparative transcriptome profiling at germination shows WRKY transcription factor responses. <i>Plant Biology</i> , 2021, 23, 100-112.	1.8	14

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2048	Genome-wide identification of the Tubby-Like Protein (TLPs) family in medicinal model plant <i>Salvia miltiorrhiza</i> . PeerJ, 2021, 9, e11403.	0.9	11
2049	Genome-wide characterization of the <i>PDI</i> gene family in <i>Medicago truncatula</i> and their roles in response to endoplasmic reticulum stress. <i>Genome</i> , 2021, 64, 599-614.	0.9	4
2050	Genome-wide in silico identification and characterization of sodium-proton (Na <sup>+</sup> /H <sup>+</sup> ) antiporters in <i>Indica</i> rice. <i>Plant Gene</i> , 2021, 26, 100280.	1.4	9
2051	Genome wide identification and characterization of light-harvesting Chloro a/b binding (LHC) genes reveals their potential role in enhancing drought tolerance in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	8
2052	A comparative genome-wide analysis of the ABC transporter gene family among three <i>Gossypium</i> species. <i>Crop Science</i> , 2021, 61, 2489-2509.	0.8	1
2053	Genome-wide identification of the <i>Capsicum</i> bHLH transcription factor family: discovery of a candidate regulator involved in the regulation of species-specific bioactive metabolites. <i>BMC Plant Biology</i> , 2021, 21, 262.	1.6	30
2054	CHARACTERISATION OF HORDEUM VULGARE CELLULOSE SYNTHASE-LIKE F6 PROMOTER VIA TRANSGENE EXPRESSION IN RICE. <i>Malaysian Journal of Science</i> , 2021, 40, 61-86.	0.2	0
2055	Genome-wide comparison of the GRAS protein family in eight Rosaceae species and <i>GRAS</i> gene expression analysis in Chinese white pear ( <i>Pyrus bretschneideri</i> Rehder). <i>New Zealand Journal of Crop and Horticultural Science</i> , 2022, 50, 303-325.	0.7	5
2056	Genome-wide identification of WD40 superfamily genes and prediction of WD40 gene of flavonoid-related genes in <i>Ginkgo biloba</i> . <i>Notulae Botanicae Horti Agrobotanici Cluj-Napoca</i> , 2021, 49, 12086.	0.5	7
2057	<i>Pseudocrossidium replicatum</i> (Taylor) R.H. Zander is a fully desiccation-tolerant moss that expresses an inducible molecular mechanism in response to severe abiotic stress. <i>Plant Molecular Biology</i> , 2021, 107, 387-404.	2.0	7
2058	Genome-Wide Investigation of N6-Methyladenosine Regulatory Genes and Their Roles in Tea ( <i>Camellia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10	1.7	18
2059	Identification and expression profiling of proline metabolizing genes in <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i> to reveal their stress-specific transcript alteration. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1469-1485.	1.4	8
2060	Genome-wide analysis and functional characterization of the DELLA gene family associated with stress tolerance in <i>B. napus</i> . <i>BMC Plant Biology</i> , 2021, 21, 286.	1.6	10
2061	A Rapid Pipeline for Pollen- and Anther-Specific Gene Discovery Based on Transcriptome Profiling Analysis of Maize Tissues. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6877.	1.8	6
2062	Genome-Wide Analysis of Myeloblastosis-Related Genes in <i>Brassica napus</i> L. and Positive Modulation of Osmotic Tolerance by BnMRD107. <i>Frontiers in Plant Science</i> , 2021, 12, 678202.	1.7	10
2063	Genome-wide Identification and Abiotic Stress Response Pattern Analysis of NF-Y Gene Family in Peanut ( <i>Arachis Hypogaea</i> L.). <i>Tropical Plant Biology</i> , 2021, 14, 329-344.	1.0	4
2064	Genome-wide characterization of bZIP transcription factors and their expression patterns in response to drought and salinity stress in <i>Jatropha curcas</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 181, 1207-1223.	3.6	18
2065	Comparative Transcriptome-Based Mining of Senescence-Related MADS, NAC, and WRKY Transcription Factors in the Rapid-Senescence Line DLS-91 of <i>Brassica rapa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 6017.	1.8	2

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2066	Molecular Cloning, Transcriptional Profiling, Subcellular Localization, and miRNA-Binding Site Analysis of Six SCL9 Genes in Poplar. <i>Plants</i> , 2021, 10, 1338.	1.6	2
2067	Expression Profile of FaFT1 and Its Ectopic Expression in Arabidopsis Demonstrate Its Function in the Reproductive Development of <i>Fragaria</i> – <i>Ananassa</i> . <i>Journal of Plant Growth Regulation</i> , 0, , 1.	2.8	0
2068	Differential abundance proteins associated with rapid growth of etiolated coleoptiles in maize. <i>Plant Direct</i> , 2021, 5, e00332.	0.8	1
2069	Deciphering the role of helicases and translocases: A multifunctional gene family safeguarding plants from diverse environmental adversities. <i>Current Plant Biology</i> , 2021, 26, 100204.	2.3	9
2070	Identification of the trehalose-6-phosphate synthase gene family in <i>Medicago truncatula</i> and expression analysis under abiotic stresses. <i>Gene</i> , 2021, 787, 145641.	1.0	5
2071	Genome-wide identification and expression analysis of LBD transcription factor genes in Moso bamboo ( <i>Phyllostachys edulis</i> ). <i>BMC Plant Biology</i> , 2021, 21, 296.	1.6	24
2072	Genome-Wide Identification and Transcript Analysis of TCP Gene Family in Banana ( <i>Musa acuminata</i> L.). <i>Biochemical Genetics</i> , 2021, , 1.	0.8	10
2073	Genome-Wide Identification and Characterization of Cysteine-Rich Receptor-Like Protein Kinase Genes in Tomato and Their Expression Profile in Response to Heat Stress. <i>Diversity</i> , 2021, 13, 258.	0.7	12
2074	Identification and Expression Analysis of miR160 and Their Target Genes in Cucumber. <i>Biochemical Genetics</i> , 2022, 60, 127-152.	0.8	6
2075	Pathogenesis-Related Genes of PR1, PR2, PR4, and PR5 Families Are Involved in the Response to Fusarium Infection in Garlic ( <i>Allium sativum</i> L.). <i>International Journal of Molecular Sciences</i> , 2021, 22, 6688.	1.8	49
2076	Genome-Wide Identification, Diversification, and Expression Analysis of Lectin Receptor-Like Kinase (LecRLK) Gene Family in Cucumber under Biotic Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6585.	1.8	12
2077	Characterization of APX and APX-R gene family in <i>Brassica juncea</i> and <i>B. rapa</i> for tolerance against abiotic stresses. <i>Plant Cell Reports</i> , 2022, 41, 571-592.	2.8	18
2078	In silico mining of WRKY TFs through <i>Solanum melongena</i> L. and <i>Solanum incanum</i> L. transcriptomes and identification of SiWRKY53 as a source of resistance to bacterial wilt. <i>Plant Gene</i> , 2021, 26, 100278.	1.4	13
2079	Genome-Wide Identification of the Nramp Gene Family in <i>Spirodela polyrhiza</i> and Expression Analysis under Cadmium Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6414.	1.8	17
2080	Combined gene family characterization and RNA-Seq to study the response of $\beta$ -ketoacyl-CoA synthase to abiotic stress in rice ( <i>Oryza sativa</i> L.). <i>Plant Growth Regulation</i> , 2021, 95, 97-110.	1.8	1
2081	Analysis of expression characteristics of soybean leaf and root tissue-specific promoters in <i>Arabidopsis</i> and soybean. <i>Transgenic Research</i> , 2021, 30, 799-810.	1.3	8
2082	Molecular cloning and characterization of high-affinity potassium transporter (AlHKT2;1) gene promoter from halophyte <i>Aeluropus lagopoides</i> . <i>International Journal of Biological Macromolecules</i> , 2021, 181, 1254-1264.	3.6	7
2083	Identification and characterization of 5 walnut MYB genes in response to drought stress involved in ABA signaling. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1323-1335.	1.4	13

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2084	Natural variations in the non-coding region of ZmNAC080308 contributes maintaining grain yield under drought stress in maize. <i>BMC Plant Biology</i> , 2021, 21, 305.	1.6	12
2085	Functional Exploration of Chaperonin (HSP60/10) Family Genes and their Abiotic Stress-induced Expression Patterns in <i>Sorghum bicolor</i> . <i>Current Genomics</i> , 2021, 22, 137-152.	0.7	10
2086	Genome-wide identification and analysis of the MLO gene family for candidate powdery mildew susceptibility factors in <i>Momordica charantia</i> . <i>Scientia Horticulturae</i> , 2021, 283, 110119.	1.7	5
2087	Genome-wide identification and analysis of the MADS-box gene family and its potential role in fruit ripening in black raspberry ( <i>Rubus occidentalis</i> L.). <i>Journal of Berry Research</i> , 2021, 11, 301-315.	0.7	3
2088	In Silico analysis of CCGAC and CATGTG cis-regulatory elements across genomes reveals their roles in gene regulation under stress. <i>Current Genomics</i> , 2021, 22, 353-362.	0.7	0
2089	Molecular Traits and Functional Analysis of the CLAVATA3/Endosperm Surrounding Region-Related Small Signaling Peptides in Three Species of <i>Gossypium</i> Genus. <i>Frontiers in Plant Science</i> , 2021, 12, 671626.	1.7	0
2090	Molecular characterization of the COPT/Ctr-type copper transporter family under heavy metal stress in alfalfa. <i>International Journal of Biological Macromolecules</i> , 2021, 181, 644-652.	3.6	11
2091	Identification of a 193Åbp promoter region of TaNRX1-D gene from common wheat that contributes to osmotic or ABA stress inducibility in transgenic <i>Arabidopsis</i> . <i>Genes and Genomics</i> , 2021, 43, 1035-1048.	0.5	9
2092	Genome-Wide Identification and Expression Analyses of CONSTANS-Like Family Genes in Cucumber ( <i>Cucumis sativus</i> L.). <i>Journal of Plant Growth Regulation</i> , 2022, 41, 1627-1641.	2.8	4
2093	Comprehensive identification and expression analysis of B-Box genes in cotton. <i>BMC Genomics</i> , 2021, 22, 439.	1.2	12
2094	Identification and analysis of the structure, expression and nucleotide polymorphism of the GPAT gene family in rice. <i>Plant Gene</i> , 2021, 26, 100290.	1.4	7
2095	A tomato receptor-like cytoplasmic kinase, SlZRK1, acts as a negative regulator in wound-induced jasmonic acid accumulation and insect resistance. <i>Journal of Experimental Botany</i> , 2021, 72, 7285-7300.	2.4	6
2096	Characterization of expansin genes and their transcriptional regulation by histone modifications in strawberry. <i>Planta</i> , 2021, 254, 21.	1.6	8
2097	The roles of trichome development genes in stress resistance. <i>Plant Growth Regulation</i> , 2021, 95, 137-148.	1.8	9
2098	Genome-wide characterization and expression profiling of the PDR gene family in tobacco ( <i>Nicotiana glauca</i> ). <i>Plant Growth Regulation</i> , 2021, 95, 149-157.	1.8	7
2099	Mitogen-Activated Protein Kinase Expression Profiling Revealed Its Role in Regulating Stress Responses in Potato ( <i>Solanum tuberosum</i> ). <i>Plants</i> , 2021, 10, 1371.	1.6	16
2100	Genome wide identification, classification and functional characterization of heat shock transcription factors in cultivated and ancestral cottons ( <i>Gossypium</i> spp.). <i>International Journal of Biological Macromolecules</i> , 2021, 182, 1507-1527.	3.6	11
2101	Genome-wide Identification and Characterization of Expansin Genes in Jute. <i>Tropical Plant Biology</i> , 0, , 1.	1.0	3

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2103	SIBBX20 interacts with the COP9 signalosome subunit SICSN5-2 to regulate anthocyanin biosynthesis by activating SIDFR expression in tomato. <i>Horticulture Research</i> , 2021, 8, 163.	2.9	27
2104	The GASA Gene Family in Cacao ( <i>Theobroma cacao</i> , Malvaceae): Genome Wide Identification and Expression Analysis. <i>Agronomy</i> , 2021, 11, 1425.	1.3	40
2105	Genome-wide identification, characterization, and expression analysis of the monovalent cation-proton antiporter superfamily in maize, and functional analysis of its role in salt tolerance. <i>Genomics</i> , 2021, 113, 1940-1951.	1.3	13
2106	Genome-Wide Identification and Evolutionary Analysis of Gossypium Tubby-Like Protein (TLP) Gene Family and Expression Analyses During Salt and Drought Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 667929.	1.7	13
2107	Genome-Wide Analysis and Expression Profile of Superoxide Dismutase (SOD) Gene Family in Rapeseed ( <i>Brassica napus</i> L.) under Different Hormones and Abiotic Stress Conditions. <i>Antioxidants</i> , 2021, 10, 1182.	2.2	47
2108	Comprehensive in silico Characterization of Universal Stress Proteins in Rice ( <i>Oryza sativa</i> L.) With Insight Into Their Stress-Specific Transcriptional Modulation. <i>Frontiers in Plant Science</i> , 2021, 12, 712607.	1.7	11
2109	Characterization of Nucleotide Binding Site-Encoding Genes in Sweetpotato, <i>Ipomoea batatas</i> (L.) Lam., and Their Response to Biotic and Abiotic Stresses. <i>Cytogenetic and Genome Research</i> , 2021, 161, 257-271.	0.6	7
2110	Insertion of Badnaviral DNA in the Late Blight Resistance Gene (R1a) of Brinjal Eggplant ( <i>Solanum</i> )	1.7	11
2111	Genome-Wide Characterization of B-Box Gene Family and Its Roles in Responses to Light Quality and Cold Stress in Tomato. <i>Frontiers in Plant Science</i> , 2021, 12, 698525.	1.7	31
2112	Ferredoxin 1 is downregulated by the accumulation of abscisic acid in an ABI5-dependent manner to facilitate rice stripe virus infection in <i>Nicotiana benthamiana</i> and rice. <i>Plant Journal</i> , 2021, 107, 1183-1197.	2.8	16
2113	Identification and Characterization of SPL Transcription Factor Family Reveals Organization and Chilling-Responsive Patterns in Cabbage ( <i>Brassica oleracea</i> var. <i>capitata</i> L.). <i>Agronomy</i> , 2021, 11, 1445.	1.3	2
2114	The DUB family in <i>Populus</i> : identification, characterization, evolution and expression patterns. <i>BMC Genomics</i> , 2021, 22, 541.	1.2	4
2115	Genome-wide identification and expression analysis of U-box gene family in wild emmer wheat ( <i>Triticum turgidum</i> L. ssp. <i>dicoccoides</i> ). <i>Gene</i> , 2021, 799, 145840.	1.0	6
2116	The Coordinated Upregulated Expression of Genes Involved in MEP, Chlorophyll, Carotenoid and Tocopherol Pathways, Mirrored the Corresponding Metabolite Contents in Rice Leaves during De-Etiolation. <i>Plants</i> , 2021, 10, 1456.	1.6	3
2117	Characterization of Vascular plant One-Zinc finger (VOZ) in soybean ( <i>Glycine max</i> and <i>Glycine soja</i> ) and their expression analyses under drought condition. <i>PLoS ONE</i> , 2021, 16, e0253836.	1.1	12
2118	A Review of Omics Technologies and Bioinformatics to Accelerate Improvement of Papaya Traits. <i>Agronomy</i> , 2021, 11, 1356.	1.3	9
2119	In silico promoter and expression analyses of rice Auxin Binding Protein 57 (ABP57). <i>Plant Science Today</i> , 2021, 8, 741-748.	0.4	0

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2120	Genome-Wide Identification and Expression Analysis of Tomato ADK Gene Family during Development and Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7708.	1.8	8
2122	Analysis of Evolution, Expression and Genetic Transformation of TCP Transcription Factors in Blueberry Reveal That VcTCP18 Negatively Regulates the Release of Flower Bud Dormancy. <i>Frontiers in Plant Science</i> , 2021, 12, 697609.	1.7	11
2123	Genome-wide molecular characterization of Phosphate Transporter 1 and Phosphate Starvation Response gene families in <i>Elaeis guineensis</i> Jacq. and their transcriptional response under different levels of phosphate starvation. <i>Acta Physiologiae Plantarum</i> , 2021, 43, 1.	1.0	1
2124	Based on the whole genome clarified the evolution and expression process of fatty acid desaturase genes in three soybeans. <i>International Journal of Biological Macromolecules</i> , 2021, 182, 1966-1980.	3.6	13
2125	Genome-Wide Identification and Characterization of the Potato IQD Family During Development and Stress. <i>Frontiers in Genetics</i> , 2021, 12, 693936.	1.1	9
2126	Genome-wide identification and analysis of the YABBY gene family in Moso Bamboo ( <i>Phyllostachys Tj ETQq1 1 0.784314 rgBT /Overl</i>	0.9	9
2127	Genome-Wide Analysis and Functional Characterization of the UDP-Glycosyltransferase Family in Grapes. <i>Horticulturae</i> , 2021, 7, 204.	1.2	11
2128	Expression profiling of the Dof gene family under abiotic stresses in spinach. <i>Scientific Reports</i> , 2021, 11, 14429.	1.6	9
2129	Genome-Wide Identification of the Early Flowering 4 (ELF4) Gene Family in Cotton and Silent GhELF4-1 and GhEFL3-6 Decreased Cotton Stress Resistance. <i>Frontiers in Genetics</i> , 2021, 12, 686852.	1.1	1
2130	Genome-wide analysis and expression patterns of lipid phospholipid phospholipase gene family in <i>Brassica napus</i> L. <i>BMC Genomics</i> , 2021, 22, 548.	1.2	13
2131	Cloning and Functional Identification of Phosphoethanolamine Methyltransferase in Soybean ( <i>Glycine max</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 612158.	1.7	2
2132	Evolution and Characterization of Acetyl Coenzyme A: Diacylglycerol Acyltransferase Genes in Cotton Identify the Roles of GhDGAT3D in Oil Biosynthesis and Fatty Acid Composition. <i>Genes</i> , 2021, 12, 1045.	1.0	11
2133	Transcriptome, degradome and physiological analysis provide new insights into the mechanism of inhibition of litchi fruit senescence by melatonin. <i>Plant Science</i> , 2021, 308, 110926.	1.7	23
2135	Genome-Wide Investigation of Spliceosomal SM/LSM Genes in Wheat ( <i>Triticum aestivum</i> L.) and Its Progenitors. <i>Agronomy</i> , 2021, 11, 1429.	1.3	0
2136	Genome-wide identification of the MIOX gene family and their expression profile in cotton development and response to abiotic stress. <i>PLoS ONE</i> , 2021, 16, e0254111.	1.1	9
2137	Genome-wide identification of alcohol dehydrogenase (ADH) gene family under waterlogging stress in wheat ( <i>Triticum aestivum</i> ). <i>PeerJ</i> , 2021, 9, e11861.	0.9	11
2138	Genome-Wide Association Study in Rice Revealed a Novel Gene in Determining Plant Height and Stem Development, by Encoding a WRKY Transcription Factor. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8192.	1.8	16
2140	Genome-wide identification and comparative analysis of the WRKY gene family in aquatic plants and their response to abiotic stresses in giant duckweed ( <i>Spirodela polyrhiza</i> ). <i>Genomics</i> , 2021, 113, 1761-1777.	1.3	19

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2142	Genome-wide identification and expression analysis of Hsf and Hsp gene families in cucumber ( <i>Cucumis Tj ETQq1 1.0.784314 rgBT /Ow</i> )	1.8	18
2143	Functional Characterization of GhACX3 Gene Reveals Its Significant Role in Enhancing Drought and Salt Stress Tolerance in Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 658755.	1.7	15
2144	TPS-b family genes involved in signature aroma terpenes emission in ripe kiwifruit. <i>Plant Signaling and Behavior</i> , 2021, 16, 1962657.	1.2	5
2145	Structure characterization and potential role of soybean phospholipases A multigene family in response to multiple abiotic stress uncovered by CRISPR/Cas9 technology. <i>Environmental and Experimental Botany</i> , 2021, 188, 104521.	2.0	14
2146	Genome-Wide Identification and Analysis of the MADS-Box Gene Family in American Beautyberry ( <i>Callicarpa americana</i> ). <i>Plants</i> , 2021, 10, 1805.	1.6	8
2147	Genome-wide identification, gene cloning, subcellular location and expression analysis of SPL gene family in <i>P. granatum L.</i> <i>BMC Plant Biology</i> , 2021, 21, 400.	1.6	12
2148	Genome-wide identification, characterization and expression analysis of MATE family genes in apple ( <i>Malus A— domestica Borkh</i> ). <i>BMC Genomics</i> , 2021, 22, 632.	1.2	12
2149	The Complexity of Modulating Anthocyanin Biosynthesis Pathway by Deficit Irrigation in Table Grapes. <i>Frontiers in Plant Science</i> , 2021, 12, 713277.	1.7	5
2150	Genome-Wide Identification and Characterization of Short-Chain Dehydrogenase/Reductase (SDR) Gene Family in <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 9498.	1.8	19
2151	Evolution and functional diversity of abiotic stress-responsive NAC transcription factor genes in <i>Linum usitatissimum L.</i> <i>Environmental and Experimental Botany</i> , 2021, 188, 104512.	2.0	12
2152	Stress responsiveness of vindoline accumulation in <i>Catharanthus roseus</i> leaves is mediated through co-expression of allene oxide cyclase with pathway genes. <i>Protoplasma</i> , 2022, 259, 755-773.	1.0	4
2153	Genome-wide investigation and comparative analysis of <scp>MATE</scp> gene family in Rosaceae species and their regulatory role in abiotic stress responses in Chinese pear (<i>Pyrus Tj ETQq0 0 0 rgBT /Overlock 1.0 Tf 50 257 Td (br)	1.6	10
2154	Genome-wide analysis of HECT E3 ubiquitin ligase gene family in <i>Solanum lycopersicum</i> . <i>Scientific Reports</i> , 2021, 11, 15891.	1.6	10
2155	Genome-wide identification and analysis of the heat shock transcription factor family in moso bamboo ( <i>Phyllostachys edulis</i> ). <i>Scientific Reports</i> , 2021, 11, 16492.	1.6	23
2156	Genome-Wide Analysis of Glycoside Hydrolase Family 35 Genes and Their Potential Roles in Cell Wall Development in <i>Medicago truncatula</i> . <i>Plants</i> , 2021, 10, 1639.	1.6	2
2157	Genome wide investigation of MAPKKs from <i>Cicer arietinum</i> and their involvement in plant defense against <i>Helicoverpa armigera</i> . <i>Physiological and Molecular Plant Pathology</i> , 2021, 115, 101685.	1.3	10
2158	AcWRKY40 mediates ethylene biosynthesis during postharvest ripening in kiwifruit. <i>Plant Science</i> , 2021, 309, 110948.	1.7	9



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2159	Evolutionary and Characteristic Analysis of RING-DUF1117 E3 Ubiquitin Ligase Genes in <i>Gossypium</i> Discerning the Role of GhRDUF4D in <i>Verticillium dahliae</i> Resistance. <i>Biomolecules</i> , 2021, 11, 1145.	1.8	13
2160	Genome-wide identification and characterization of <i>WOX</i> genes in <i>Cucumis sativus</i> . <i>Genome</i> , 2021, 64, 761-776.	0.9	18
2161	Molecular Characterization of GS2 and Fd-GOGAT Homeologues and Their Biased Response to Nitrogen Stress in Bread Wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2555-2569.	2.8	6
2162	<i>Carbon Starved Anther</i> modulates sugar and ABA metabolism to protect rice seed germination and seedling fitness. <i>Plant Physiology</i> , 2021, 187, 2405-2418.	2.3	11
2163	Identification and Expression Analysis of LBD Genes in Moso Bamboo ( <i>Phyllostachys edulis</i> ). <i>Journal of Plant Growth Regulation</i> , 2022, 41, 2798-2817.	2.8	5
2164	Genome-Wide Identification, Phylogenetic and Expression Pattern Analysis of GATA Family Genes in Cucumber ( <i>Cucumis sativus</i> L.). <i>Plants</i> , 2021, 10, 1626.	1.6	11
2165	Phylogeny, gene structure and GATA genes expression in different tissues of solanaceae species. <i>Biocatalysis and Agricultural Biotechnology</i> , 2021, 35, 102015.	1.5	12
2166	Magnesium transporter Gene Family: Genome-Wide Identification and Characterization in <i>Theobroma cacao</i> , <i>Corchorus capsularis</i> , and <i>Gossypium hirsutum</i> of Family Malvaceae. <i>Agronomy</i> , 2021, 11, 1651.	1.3	40
2167	A cysteine-rich receptor-like protein kinase CaCKR5 modulates immune response against <i>Ralstonia solanacearum</i> infection in pepper. <i>BMC Plant Biology</i> , 2021, 21, 382.	1.6	17
2168	Genome-wide analysis of <i>BpDof</i> genes and the tolerance to drought stress in birch ( <i>Betula</i> ). <i>Trends in Plant Science</i> , 2021, 16, 107-114.	0.9	8
2169	Light dominates the diurnal emissions of herbivore-induced volatiles in wild tobacco. <i>BMC Plant Biology</i> , 2021, 21, 401.	1.6	15
2170	Genome-wide identification, phylogeny, and expression analysis of the bHLH gene family in tobacco ( <i>Nicotiana tabacum</i> ). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1747-1764.	1.4	15
2171	Genome-wide analysis of R2R3-MYB transcription factors family in the autopolyploid <i>Saccharum spontaneum</i> : an exploration of dominance expression and stress response. <i>BMC Genomics</i> , 2021, 22, 622.	1.2	20
2172	Genome wide analysis of IQD gene family in diploid and tetraploid species of cotton ( <i>Gossypium</i> spp.). <i>International Journal of Biological Macromolecules</i> , 2021, 184, 1035-1061.	3.6	7
2173	Cloning and functional characterization of two GsSnRK1 gene promoters from wild soybean. <i>Plant Biotechnology Reports</i> , 2021, 15, 627-639.	0.9	2
2174	Evolution of pectin synthesis relevant galacturonosyltransferase gene family and its expression during cotton fiber development. <i>Journal of Cotton Research</i> , 2021, 4, .	1.0	3
2175	The DUF221 domain-containing (DDP) genes identification and expression analysis in tomato under abiotic and phytohormone stress. <i>GM Crops and Food</i> , 2021, 12, 586-599.	2.0	5
2176	Identification of Rf Genes in Hexaploid Wheat ( <i>Triticumaestivum</i> L.) by RNA-Seq and Paralog Analyses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9146.	1.8	6

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2177	Identification and Expression Analyses of Invertase Genes in Moso Bamboo Reveal Their Potential Drought Stress Functions. <i>Frontiers in Genetics</i> , 2021, 12, 696300.	1.1	5
2178	Novel structural annotation and functional expression analysis of GTP_EFTU conserved genes in pepper based on the PacBio sequencing data. <i>Horticultural Plant Journal</i> , 2021, 7, 443-456.	2.3	6
2179	Genome-Wide Identification, Expression Profile, and Alternative Splicing Analysis of CAMTA Family Genes in Cucumber ( <i>Cucumis sativus</i> L.). <i>Agronomy</i> , 2021, 11, 1827.	1.3	12
2180	CBF transcription factors involved in the cold response of <i>Camellia japonica</i> (Naidong). <i>PeerJ</i> , 2021, 9, e12155.	0.9	4
2181	Identification and Characterization of Secondary Wall-Associated NAC Genes and Their Involvement in Hormonal Responses in Tobacco ( <i>Nicotiana tabacum</i> ). <i>Frontiers in Plant Science</i> , 2021, 12, 712254.	1.7	5
2182	Genome-Wide Identification and Characterization of the Cystatin Gene Family in Bread Wheat ( <i>Triticum</i> ) Tj ETQq1 1.0.784314 rgBT /Ov	1.8	5
2183	Genome-wide analysis and characterization of R2R3-MYB family in pigeon pea ( <i>Cajanus cajan</i> ) and their functional identification in phenylpropanoids biosynthesis. <i>Planta</i> , 2021, 254, 64.	1.6	13
2184	Genome-wide identification of DCL, AGO and RDR gene families and their associated functional regulatory elements analyses in banana ( <i>Musa acuminata</i> ). <i>PLoS ONE</i> , 2021, 16, e0256873.	1.1	14
2185	Genome-Wide Identification and Expression Analysis of the Aux/IAA and Auxin Response Factor Gene Family in <i>Medicago truncatula</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 10494.	1.8	18
2186	Genome-Wide Identification and Expression Analysis of JAZ Family Involved in Hormone and Abiotic Stress in Sweet Potato and Its Two Diploid Relatives. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9786.	1.8	8
2187	Molecular and in silico characterization of tomato LBD transcription factors reveals their role in fruit development and stress responses. <i>Plant Gene</i> , 2021, 27, 100309.	1.4	4
2188	Genome-Wide Identification and Expression Analysis of Metal Tolerance Protein Gene Family in <i>Medicago truncatula</i> Under a Broad Range of Heavy Metal Stress. <i>Frontiers in Genetics</i> , 2021, 12, 713224.	1.1	20
2189	Transcriptional profiling reveals changes in gene regulation and signaling transduction pathways during temperature stress in wucai ( <i>Brassica campestris</i> L.). <i>BMC Genomics</i> , 2021, 22, 687.	1.2	8
2190	Genome-Wide Identification of WUSCHEL-Related Homeobox Gene Family and their Expression Analysis During Somatic Embryogenesis in Oil Palm ( <i>Elaeis guineensis</i> ). <i>Tropical Plant Biology</i> , 2022, 15, 55-64.	1.0	4
2191	Genome-wide analysis of OSCA gene family members in <i>Vigna radiata</i> and their involvement in the osmotic response. <i>BMC Plant Biology</i> , 2021, 21, 408.	1.6	19
2192	Genome-Wide Investigation of SBT Family Genes in Pineapple and Functional Analysis of AcoSBT1.12 in Floral Transition. <i>Frontiers in Genetics</i> , 2021, 12, 730821.	1.1	6
2193	Identification of C3H2C3-type RING E3 ubiquitin ligase in grapevine and characterization of drought resistance function of VyrCHC114. <i>BMC Plant Biology</i> , 2021, 21, 422.	1.6	2
2194	Functional divergence of <i>Brassica napus</i> BnaABI1 paralogs in the structurally conserved PP2CA gene subfamily of Brassicaceae. <i>Genomics</i> , 2021, 113, 3185-3197.	1.3	3

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2195	Genome-wide identification of ZF-HD gene family in <i>Triticum aestivum</i> : Molecular evolution mechanism and function analysis. <i>PLoS ONE</i> , 2021, 16, e0256579.	1.1	13
2197	Identification of HvLRX, a new dehydration and light responsive gene in Tibetan hulless barley ( <i>Hordeum vulgare</i> var. <i>nudum</i> ). <i>Genes and Genomics</i> , 2021, 43, 1445-1461.	0.5	6
2198	Comprehensive analysis and expression profiles of cassava UDP-glycosyltransferases (UGT) family reveal their involvement in development and stress responses in cassava. <i>Genomics</i> , 2021, 113, 3415-3429.	1.3	13
2199	Genome-Wide Identification and Analysis of the Metallothionein Genes in <i>Oryza</i> Genus. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9651.	1.8	8
2200	All-flesh fruit in tomato is controlled by reduced expression dosage of <i>AFF</i> through a structural variant mutation in the promoter. <i>Journal of Experimental Botany</i> , 2022, 73, 123-138.	2.4	12
2201	Genome-wide identification and analysis of WRKY gene family in maize provide insights into regulatory network in response to abiotic stresses. <i>BMC Plant Biology</i> , 2021, 21, 427.	1.6	42
2202	Genome-Wide Identification and Expression Profiling of the BZR Transcription Factor Gene Family in <i>Nicotiana benthamiana</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 10379.	1.8	9
2203	Genome-Wide Identification, Evolution, and Comparative Analysis of B-Box Genes in <i>Brassica rapa</i> , <i>B. oleracea</i> , and <i>B. napus</i> and Their Expression Profiling in <i>B. rapa</i> in Response to Multiple Hormones and Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10367.	1.8	8
2204	Genome-Wide Characterization of Glutathione Peroxidase (GPX) Gene Family in Rapeseed ( <i>Brassica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 TF 5 2021, 10, 1481.	2.2	25
2205	Genome-wide identification and analysis of <i>Catharanthus roseus</i> RLK1-like kinases in <i>Nicotiana benthamiana</i> . <i>BMC Plant Biology</i> , 2021, 21, 425.	1.6	6
2206	Genome-Wide Identification MIKC-Type MADS-Box Gene Family and Their Roles during Development of Floral Buds in Wheel Wingnut ( <i>Cyclocarya paliurus</i> ). <i>International Journal of Molecular Sciences</i> , 2021, 22, 10128.	1.8	8
2207	Characterization and expression analysis of wall-associated kinase (WAK) and WAK-like family in cotton. <i>International Journal of Biological Macromolecules</i> , 2021, 187, 867-879.	3.6	20
2208	Genome-Wide Identification and Expression Analysis of Thioredoxin (Trx) Genes in Seed Development of <i>Vitis vinifera</i> . <i>Journal of Plant Growth Regulation</i> , 2022, 41, 3030-3045.	2.8	5
2209	Jasmonic Acid-Dependent MYC Transcription Factors Bind to a Tandem G-Box Motif in the YUCCA8 and YUCCA9 Promoters to Regulate Biotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9768.	1.8	12
2210	Genome-Wide Characterization of the MLO Gene Family in <i>Cannabis sativa</i> Reveals Two Genes as Strong Candidates for Powdery Mildew Susceptibility. <i>Frontiers in Plant Science</i> , 2021, 12, 729261.	1.7	14
2211	Genome-Wide Identification and Characterization of the Abiotic-Stress-Responsive GRF Gene Family in Diploid Woodland Strawberry ( <i>Fragaria vesca</i> ). <i>Plants</i> , 2021, 10, 1916.	1.6	13
2212	Genome-wide investigation of SQUAMOSA promoter binding protein-like transcription factor family in pearl millet ( <i>Pennisetum glaucum</i> (L) R. Br.). <i>Plant Gene</i> , 2021, 27, 100313.	1.4	6
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2218	Molecular Characterization and Expression Analysis of the Na <sup>+</sup> /H <sup>+</sup> Exchanger Gene Family in <i>Capsicum annuum</i> L.. <i>Frontiers in Genetics</i> , 2021, 12, 680457.	1.1	2
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2231	Genome-Wide Identification and Transcriptional Expression Profiles of Transcription Factor WRKY in Common Walnut ( <i>Juglans regia</i> L.). <i>Genes</i> , 2021, 12, 1444.	1.0	17
2232	Functional characterization of late embryogenesis abundant genes and promoters in pearl millet ( <i>Pennisetum glaucum</i> L.) Tj ETQq1 1 0.784314 rgBT <sub>6</sub> /Overlook	2.6	26

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2233	Genome-wide identification and expression analysis of the SNARE genes in Foxtail millet ( <i>Setaria</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	1.8	7
2235	Genome-wide identification and molecular evolution analysis of the heat shock transcription factor (HSF) gene family in four diploid and two allopolyploid <i>Gossypium</i> species. <i>Genomics</i> , 2021, 113, 3112-3127.	1.3	13
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2248	In Silico Study of the RSH (RelA/SpoT Homologs) Gene Family and Expression Analysis in Response to PGPR Bacteria and Salinity in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 10666.	1.8	9
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2250	Functional characterization of the chlorophyll b reductase gene NYC1 associated with chlorophyll degradation and photosynthesis in <i>Zoysia japonica</i> . <i>Environmental and Experimental Botany</i> , 2021, 191, 104607.	2.0	19
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2255	Comparative in silico analysis of phosphate transporter gene family, PHT, in <i>Camelina sativa</i> genome. <i>Gene Reports</i> , 2021, 25, 101351.	0.4	2
2256	Genome-wide characterization of homeobox-leucine zipper gene family in tomato ( <i>Solanum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 587 T Environmental and Experimental Botany, 2021, 192, 104652.	2.0	10
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2349	Genome-wide Identification and Characterization of Transcription Factor Binding Motifs of NBS-LRR Genes in Rice and Arabidopsis. <i>Journal of Genomes and Exomes</i> , 0, 3, 7-15.	0.0	6
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2358	Cloning and analysis of plant fatty acid desaturase 7 gene promoter from <i>Brassica napus</i> . <i>African Journal of Biotechnology</i> , 2012, 11, .	0.3	4
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2360	Annotation of gene sequence and protein structure of brinjal EDS1. <i>Bioinformation</i> , 2017, 13, 54-59.	0.2	2
2361	Genome-wide identification of the SPL gene family in <i>Dichanthelium oligosanthes</i> . <i>Bioinformation</i> , 2019, 15, 165-171.	0.2	6
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2363	Genome-wide identification and expression analysis of the ERF transcription factor family in pineapple ( <i>Ananas comosus</i> (L.) Merr.). <i>PeerJ</i> , 2020, 8, e10014.	0.9	10
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2367	Molecular evolution and expression divergence of three key Met biosynthetic genes in plants: <i>CGS</i> , <i>HMT</i> and <i>MMT</i> . PeerJ, 2018, 6, e6023.	0.9	10
2368	Genome-wide identification and expression profile analysis of the <i>Hsp20</i> gene family in Barley ( <i>Hordeum vulgare</i> L.). PeerJ, 2019, 7, e6832.	0.9	23
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2378	Genome-wide identification and characterization of the soybean SOD family during alkaline stress. PeerJ, 2020, 8, e8457.	0.9	16
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2403	Genome-Wide Identification and Characterization of the FAR1/FHY3 Family in <i>Populus trichocarpa</i> Torr. & Gray and Expression Analysis in Light Response. <i>Forests</i> , 2021, 12, 1385.	0.9	5
2404	Genome-Wide Identification and Characterization of Polygalacturonase Gene Family in Maize ( <i>Zea mays</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 7	1.8	14
2405	The CaCIPK3 gene positively regulates drought tolerance in pepper. <i>Horticulture Research</i> , 2021, 8, 216.	2.9	31
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2409	Toward Integrated Multi-Omics Intervention: Rice Trait Improvement and Stress Management. <i>Frontiers in Plant Science</i> , 2021, 12, 741419.	1.7	14
2410	Ion transporters and their exploration for conferring abiotic stress tolerance in plants. <i>Plant Growth Regulation</i> , 2022, 96, 1-23.	1.8	6
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2413	Characterization of endogenous promoters of GapC1 and GS for recombinant protein expression in <i>Phaeodactylum tricornutum</i> . <i>MicrobiologyOpen</i> , 2021, 10, e1239.	1.2	0
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2505	Genome-Wide Investigation of the NAC Transcription Factor Family in <i>Miscanthus sinensis</i> and Expression Analysis Under Various Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2021, 12, 766550.	1.7	10
2506	Genome-wide identification reveals the function of CEP peptide in cucumber root development. <i>Plant Physiology and Biochemistry</i> , 2021, 169, 119-126.	2.8	8
2507	Carrot AOX2a Transcript Profile Responds to Growth and Chilling Exposure. <i>Plants</i> , 2021, 10, 2369.	1.6	7
2508	Identification of Glutathione Peroxidase Gene Family in <i>Ricinus communis</i> and Functional Characterization of RcGPX4 in Cold Tolerance. <i>Frontiers in Plant Science</i> , 2021, 12, 707127.	1.7	6
2509	Review A Short Review of Promoters of Cotton Fibre Genes: Strength and Tissue Specificity. <i>Pakistan Journal of Scientific and Industrial Research Series B: Biological Sciences</i> , 2020, 63, 127-131.	0.1	0
2511	Isolation and functional analysis of 4-coumarate:coenzyme A ligase gene promoters from <i>Salvia miltiorrhiza</i> . <i>Biologia Plantarum</i> , 0, , .	1.9	0
2512	Structure and expression analysis of seven salt-relatedERFgenes of <i>Populus</i> . <i>PeerJ</i> , 2020, 8, e10206.	0.9	5
2516	Expression and Regulation of the <i>Arabidopsis thaliana</i> Cel1 Endo 1,4 beta Glucanase Gene During Compatible Plant-Nematode Interactions. <i>Journal of Nematology</i> , 2006, 38, 354-61.	0.4	10
2517	Bioinformatic and empirical analysis of a gene encoding serine/threonine protein kinase regulated in response to chemical and biological fertilizers in two maize (L.) cultivars. <i>Molecular Biology Research Communications</i> , 2017, 6, 65-75.	0.2	4
2518	Genome-wide characterization of <i>Brassica napus</i> INDETERMINATE DOMAIN genes reveals a negative role for BnA08.IDD7 in plant development. <i>Industrial Crops and Products</i> , 2022, 175, 114263.	2.5	2

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2520	Genome-wide identification, characterization and expression profiles of heavy metal ATPase 3 (HMA3) in plants. <i>Journal of King Saud University - Science</i> , 2022, 34, 101730.	1.6	5
2521	Expression profiling of WRKY transcription factors in Spinach. <i>Euphytica</i> , 2021, 217, 1.	0.6	1
2522	BpTCP3 Transcription Factor Improves Salt Tolerance of <i>Betula platyphylla</i> by Reducing Reactive Oxygen Species Damage. <i>Forests</i> , 2021, 12, 1633.	0.9	2
2523	Molybdenum (Mo) transporter genes in Panicoideae species: a genome-wide evolution study. <i>Journal of Crop Science and Biotechnology</i> , 0, , 1.	0.7	0
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2525	Phylogenetic Analysis of the Plant U2 snRNP Auxiliary Factor Large Subunit A Gene Family in Response to Developmental Cues and Environmental Stimuli. <i>Frontiers in Plant Science</i> , 2021, 12, 739671.	1.7	3
2526	ZmSNAC13, a maize NAC transcription factor conferring enhanced resistance to multiple abiotic stresses in transgenic <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 170, 160-170.	2.8	16
2527	Genome-wide analysis of BURP genes and identification of a BURP-V gene RcbURP4 in <i>Rosa chinensis</i> . <i>Plant Cell Reports</i> , 2022, 41, 395-413.	2.8	4
2528	Genome-wide analysis of autophagy-related genes in <i>Medicago truncatula</i> highlights their roles in seed development and response to drought stress. <i>Scientific Reports</i> , 2021, 11, 22933.	1.6	14
2529	Variation in cis-regulation of a NAC transcription factor contributes to drought tolerance in wheat. <i>Molecular Plant</i> , 2022, 15, 276-292.	3.9	78
2530	Genome-wide analysis of long terminal repeat retrotransposons from the cranberry <i>Vaccinium macrocarpon</i> . <i>Journal of Berry Research</i> , 2022, 12, 165-185.	0.7	2
2531	In silico analysis and expression profiling of S-domain receptor-like kinases (SD-RLKs) under different abiotic stresses in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2021, 22, 817.	1.2	6
2532	Overexpression of cassava RSZ21b enhances drought tolerance in <i>Arabidopsis</i> . <i>Journal of Plant Physiology</i> , 2022, 268, 153574.	1.6	5
2533	Genome-Wide Identification Transcriptional Expression Analysis of E2F-DP Transcription Factor Family in Wheat. <i>Plant Molecular Biology Reporter</i> , 2022, 40, 339-358.	1.0	2
2534	Phylogenetic Analysis of the Membrane Attack Complex/Perforin Domain-Containing Proteins in <i>Gossypium</i> and the Role of GhMACPF26 in Cotton Under Cold Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 684227.	1.7	6
2535	Genome-Wide Identification and Expression Analysis of the Plant U-Box Protein Gene Family in <i>Phyllostachys edulis</i> . <i>Frontiers in Genetics</i> , 2021, 12, 710113.	1.1	11
2536	Genome-Wide Identification and Expression Analysis of the MADS-Box Gene Family in Sweet Potato [ <i>Ipomoea batatas</i> (L.) Lam]. <i>Frontiers in Genetics</i> , 2021, 12, 750137.	1.1	16

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2538	The barley HvSTP13GR mutant triggers resistance against biotrophic fungi. <i>Molecular Plant Pathology</i> , 2022, 23, 278-290.	2.0	10
2539	Genome-wide identification and expression analysis of sucrose nonfermenting-1-related protein kinase (SnRK) genes in <i>Triticum aestivum</i> in response to abiotic stress. <i>Scientific Reports</i> , 2021, 11, 22477.	1.6	9
2540	The kinetochore protein NNF1 has a moonlighting role in the vegetative development of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2021, , .	2.8	4
2541	Genome-Wide Analysis of the Fatty Acid Desaturase Gene Family Reveals the Key Role of PfFAD3 in $\Delta^5$ -Linolenic Acid Biosynthesis in <i>Perilla</i> Seeds. <i>Frontiers in Genetics</i> , 2021, 12, 735862.	1.1	10
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2543	Transcriptome-Wide Identification and Expression Profiling of SPX Domain-Containing Members in Responses to Phosphorus Deprivation of <i>Pinus massoniana</i> . <i>Forests</i> , 2021, 12, 1627.	0.9	2
2544	Genome-wide analysis of the <i>CalS</i> gene family in cotton reveals their potential roles in fiber development and responses to stress. <i>PeerJ</i> , 2021, 9, e12557.	0.9	6
2545	Characterization of a strong constitutive promoter from paper mulberry vein banding virus. <i>Archives of Virology</i> , 2022, 167, 163-170.	0.9	2
2546	Global Characterization of XRN 5 <sup>2</sup> -3 <sup>2</sup> Exoribonucleases and Their Responses to Environmental Stresses in Plants. <i>Diversity</i> , 2021, 13, 612.	0.7	1
2547	Primer Designing for Amplifying an AT-Rich Promoter from <i>Arabidopsis thaliana</i> . <i>Methods in Molecular Biology</i> , 2022, 2392, 115-123.	0.4	0
2548	Genome-wide identification and expression profiling of the COBRA-like genes reveal likely roles in stem strength in rapeseed ( <i>Brassica napus</i> L.). <i>PLoS ONE</i> , 2021, 16, e0260268.	1.1	3
2549	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. <i>Plants</i> , 2021, 10, 2597.	1.6	31
2550	Strawberry WRKY Transcription Factor WRKY50 Is Required for Resistance to Necrotrophic Fungal Pathogen <i>Botrytis cinerea</i> . <i>Agronomy</i> , 2021, 11, 2377.	1.3	7
2551	Different G6PDH isoforms show specific roles in acclimation to cold stress at various growth stages of barley ( <i>Hordeum vulgare</i> ) and <i>Arabidopsis thaliana</i> . <i>Plant Physiology and Biochemistry</i> , 2021, 169, 190-202.	2.8	8
2552	Genome-wide characterization of bZIP gene family identifies potential members involved in flavonoids biosynthesis in <i>Ginkgo biloba</i> L.. <i>Scientific Reports</i> , 2021, 11, 23420.	1.6	14
2553	Crosstalk between the redox signalling and the detoxification: GSTs under redox control?. <i>Plant Physiology and Biochemistry</i> , 2021, 169, 149-159.	2.8	9
2554	Analysis of CcGASA family members in <i>Citrus clementina</i> (Hort. ex Tan.) by a genome-wide approach. <i>BMC Plant Biology</i> , 2021, 21, 565.	1.6	9

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2557	Genome-wide identification and expression analysis of ammonium transporter 1 (AMT1) gene family in cassava ( <i>Manihot esculenta</i> Crantz) and functional analysis of MeAMT1;1 in transgenic <i>Arabidopsis</i> . <i>3 Biotech</i> , 2022, 12, 4.	1.1	4
2558	Genome-Wide Identification and Gene Expression Analysis of Acyl-Activating Enzymes Superfamily in Tomato ( <i>Solanum lycopersicum</i> ) Under Aluminum Stress. <i>Frontiers in Plant Science</i> , 2021, 12, 754147.	1.7	10
2559	Regulation of cytokinin biosynthesis using PtRD26<sub>pro</sub>-PT module improves drought tolerance through PtARR10&P;PtYUC4/5&P;mediated reactive oxygen species removal in<i>Populus</i>. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 771-786.	4.1	14
2560	Genome Wide Identification of Respiratory Burst Oxidase Homolog (Rboh) Genes in <i>Citrus sinensis</i> and Functional Analysis of CsRbohD in Cold Tolerance. <i>International Journal of Molecular Sciences</i> , 2022, 23, 648.	1.8	13
2561	Genome-wide identification and characterization of F-box family proteins in sweet potato and its expression analysis under abiotic stress. <i>Gene</i> , 2022, 817, 146191.	1.0	4
2562	Genome-wide identification and expression profiles of AP2/ERF transcription factor family in mung bean ( <i>Vigna radiata</i> L.). <i>Journal of Applied Genetics</i> , 2022, , 1.	1.0	1
2563	Genome-wide identification and expression analysis of the coronatine-insensitive 1 (COI1) gene family in response to biotic and abiotic stresses in <i>Saccharum</i> . <i>BMC Genomics</i> , 2022, 23, 38.	1.2	4
2564	Genome-Wide Identification and Characterization of the RCI2 Gene Family in Allotetraploid <i>Brassica napus</i> Compared with Its Diploid Progenitors. <i>International Journal of Molecular Sciences</i> , 2022, 23, 614.	1.8	5
2565	Systematic analysis of the non-specific lipid transfer protein gene family in <i>Nicotiana tabacum</i> reveal its potential roles in stress responses. <i>Plant Physiology and Biochemistry</i> , 2022, 172, 33-47.	2.8	15
2566	Characterization of <i>Chaetoceros lorenzianus</i> -infecting DNA virus-derived promoters of genes from open reading frames of unknown function in <i>Phaeodactylum tricornutum</i> . <i>Marine Genomics</i> , 2022, 61, 100921.	0.4	2
2567	Investigation of the interaction of a papain-like cysteine protease (RD19c) with selenium-binding protein 1 (SBP1) in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2022, 315, 111157.	1.7	5
2568	Genome-wide characterization on MT family and their expression in response to environmental cues in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>International Journal of Biological Macromolecules</i> , 2022, 198, 54-67.	3.6	2
2569	Genome wide identification and characterization of small heat shock protein gene family in pigeonpea and their expression profiling during abiotic stress conditions. <i>International Journal of Biological Macromolecules</i> , 2022, 197, 88-102.	3.6	10
2570	Expansion of CONSTANS-like genes in sunflower confers putative neofunctionalization in the adaptation to abiotic stresses. <i>Industrial Crops and Products</i> , 2022, 176, 114400.	2.5	5
2571	Genome-wide identification and expression analysis of GDSL esterase/lipase genes in tomato. <i>Journal of Integrative Agriculture</i> , 2022, 21, 389-406.	1.7	7
2572	Characterization of YABBY genes and the correlation between their transcript levels and histone modifications in strawberry. <i>Scientia Horticulturae</i> , 2022, 295, 110815.	1.7	2
2573	Identification of MdGRF genes and the necessary role of MdGRF02 in apple root growth regulation. <i>Scientia Horticulturae</i> , 2022, 295, 110866.	1.7	1

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2575	Integrative transcriptomic and metabolomic alterations unravel the effect of melatonin on mitigating postharvest chilling injury upon plum (cv.Friar) fruit. <i>Postharvest Biology and Technology</i> , 2022, 186, 111819.	2.9	22
2576	Phylogenetic Analysis of the SQUAMOSA Promoter-Binding Protein-Like Genes in Four Ipomoea Species and Expression Profiling of the IbSPLs During Storage Root Development in Sweet Potato (Ipomoea) Tj ETQq0 0 0 rBT /Overclock 10 Tf 5		
2577	Overexpression of a Cotton Aquaporin Gene GhTIP1;1-like Confers Cold Tolerance in Transgenic Arabidopsis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1361.	1.8	9
2578	Comprehensive In Silico Analysis and Transcriptional Profiles Highlight the Importance of Mitochondrial Dicarboxylate Carriers (DICs) on Hypoxia Response in Both Arabidopsis thaliana and Eucalyptus grandis. <i>Plants</i> , 2022, 11, 181.	1.6	3
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2581	Genome-wide identification and characterization of the CLASP_N gene family in upland cotton (Gossypium hirsutum L.). <i>PeerJ</i> , 2022, 10, e12733.	0.9	2
2582	Genome-wide identification and analysis of the regulation wheat DnaJ family genes following wheat yellow mosaic virus infection. <i>Journal of Integrative Agriculture</i> , 2022, 21, 153-169.	1.7	11
2583	Genome-wide identification and expression analysis of the cucumber <i>PYL</i> gene family. <i>PeerJ</i> , 2022, 10, e12786.	0.9	8
2584	Identification and functional characterization of the CVOMTs and EOMTs genes promoters from Ocimum basilicum L.. <i>Plant Cell, Tissue and Organ Culture</i> , 2022, 148, 387-402.	1.2	1
2585	Evolution and Stress Responses of CLO Genes and Potential Function of the GhCLO06 Gene in Salt Resistance of Cotton. <i>Frontiers in Plant Science</i> , 2021, 12, 801239.	1.7	3
2586	Weak Effect of Gypsy Retrotransposon Bursts on Sonneratia alba Salt Stress Gene Expression. <i>Frontiers in Plant Science</i> , 2021, 12, 830079.	1.7	7
2588	Genome-wide identification and expression analysis of wall-associated kinase (WAK) gene family in potato (Solanum tuberosum L.). <i>Plant Biotechnology Reports</i> , 2022, 16, 317-331.	0.9	12
2589	Genome-Wide Identification of CIPK Genes in Sugar Beet (Beta vulgaris) and Their Expression Under NaCl Stress. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 260-274.	2.8	5
2590	Role of K <sup>+</sup> efflux antiporter (KEA) in plants. , 2022, , 115-128.		0
2591	Molecular Actors Involved in the Softening of Fragaria chiloensis Fruit Accelerated by ABA Treatment. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 433-448.	2.8	7
2592	Genome-wide identification and characterization of the bHLH gene family in an ornamental woody plant Prunus mume. <i>Horticultural Plant Journal</i> , 2022, 8, 531-544.	2.3	19
2593	Phylogenetic and Expression Analysis of CENH3 and APOLLO Genes in Sexual and Apomictic Boechera Species. <i>Plants</i> , 2022, 11, 387.	1.6	2

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2595	Duplication and Specialization of <i>NUDX1</i> in <i>Rosaceae</i> Led to Geraniol Production in Rose Petals. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	13
2596	Heat shock transcription factor (Hsf) gene family in common bean ( <i>Phaseolus vulgaris</i> ): genome-wide identification, phylogeny, evolutionary expansion and expression analyses at the sprout stage under abiotic stress. <i>BMC Plant Biology</i> , 2022, 22, 33.	1.6	33
2597	Analysis of NIA and GSNOR family genes and nitric oxide homeostasis in response to wheat-leaf rust interaction. <i>Scientific Reports</i> , 2022, 12, 803.	1.6	9
2598	Genome-wide survey of the dehydrin genes in bread wheat ( <i>Triticum aestivum</i> L.) and its relatives: identification, evolution and expression profiling under various abiotic stresses. <i>BMC Genomics</i> , 2022, 23, 73.	1.2	13
2599	Exogenous auxin-induced ENHANCER OF SHOOT REGENERATION 2 (ESR2) enhances femaleness of cucumber by activating the <i>CsACS2</i> gene. <i>Horticulture Research</i> , 2022, 9, .	2.9	8
2600	Cation/Proton Antiporter Genes in Tomato: Genomic Characterization, Expression Profiling, and Co-Localization with Salt Stress-Related QTLs. <i>Agronomy</i> , 2022, 12, 245.	1.3	6
2601	Essential Roles of Cupredoxin Family Proteins in Soybean Cyst Nematode Resistance. <i>Phytopathology</i> , 2022, 112, 1545-1558.	1.1	3
2602	RAD gene family analysis in cotton provides some key genes for flowering and stress tolerance in upland cotton <i>G. hirsutum</i> . <i>BMC Genomics</i> , 2022, 23, 40.	1.2	4
2603	Systematic Analysis and Functional Characterization of the PLATZ Transcription Factors in Moso Bamboo ( <i>Phyllostachys edulis</i> ). <i>Journal of Plant Growth Regulation</i> , 2023, 42, 218-236.	2.8	6
2604	Genome-Wide Identification of JRL Genes in Moso Bamboo and Their Expression Profiles in Response to Multiple Hormones and Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2021, 12, 809666.	1.7	4
2605	Genome-Wide Identification and Expression Analysis of the 14-3-3 Gene Family in Mango ( <i>Mangifera</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	1.8	9
2606	Genome-Wide Prediction, Functional Divergence, and Characterization of Stress-Responsive BZR Transcription Factors in <i>B. napus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 790655.	1.7	12
2607	New Insights into the Roles of <i>Osmanthus Fragrans</i> Heat-Shock Transcription Factors in Cold and Other Stress Responses. <i>Horticulturae</i> , 2022, 8, 80.	1.2	3
2608	Comprehensive analysis of the BES1 gene family and its expression under abiotic stress and hormone treatment in <i>Populus trichocarpa</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 173, 1-13.	2.8	8
2609	Genome-wide identification of auxin response factor (ARF) gene family and the miR160-ARF18-mediated response to salt stress in peanut ( <i>Arachis hypogaea</i> L.). <i>Genomics</i> , 2022, 114, 171-184.	1.3	30
2610	Systematic analysis reveals O-methyltransferase gene family members involved in flavonoid biosynthesis in grape. <i>Plant Physiology and Biochemistry</i> , 2022, 173, 33-45.	2.8	8
2611	Salicylic acid mitigates salt induced toxicity through the modifications of biochemical attributes and some key antioxidants in <i>capsicum annum</i> . <i>Saudi Journal of Biological Sciences</i> , 2022, , .	1.8	0

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2613	Phenylalanine ammonia lyase is more relevant than Chalcone synthase and Chalcone isomerase in the biosynthesis of flavonoids during postharvest senescence of broccoli. <i>Journal of Food Biochemistry</i> , 2022, 46, e14054.	1.2	13
2614	Genome-wide analysis of TALE superfamily in <i>Triticum aestivum</i> reveals <i>TaKNOX11-A</i> is involved in abiotic stress response. <i>BMC Genomics</i> , 2022, 23, 89.	1.2	7
2615	Molecular characterization and differential expression of an aromatic heptaketide producing type III plant polyketide synthase from Himalayan rhubarb. <i>Plant Biotechnology Reports</i> , 2023, 17, 255-273.	0.9	1
2616	Genome wide analysis of <i>DWARF27</i> genes in soybean and functional characterization of <i>GmD27c</i> reveals eminent role of strigolactones in rhizobia interaction and nodulation in <i>Glycine max</i> . <i>Molecular Biology Reports</i> , 2022, 49, 5405-5417.	1.0	3
2617	Molecular traits and functional analysis of Rapid Alkalinization Factors (RALFs) in four <i>Gossypium</i> species. <i>International Journal of Biological Macromolecules</i> , 2022, 194, 84-99.	3.6	4
2618	Meta-analysis and validation of genomic loci governing seedling and reproductive stage salinity tolerance in rice. <i>Physiologia Plantarum</i> , 2022, 174, e13629.	2.6	22
2619	Expression of <i>ZjPSY</i> , a Phytoene Synthase Gene from <i>Zoysia japonica</i> Affects Plant Height and Photosynthetic Pigment Contents. <i>Plants</i> , 2022, 11, 395.	1.6	3
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2621	Molecular structures and functional exploration of NDA family genes respond tolerant to alkaline stress in <i>Gossypium hirsutum</i> L. <i>Biological Research</i> , 2022, 55, 4.	1.5	4
2622	Genome-Wide Identification and Co-Expression Analysis of ARF and IAA Family Genes in <i>Euscaphis konishii</i> : Potential Regulators of Triterpenoids and Anthocyanin Biosynthesis. <i>Frontiers in Genetics</i> , 2021, 12, 737293.	1.1	1
2623	The molecular events underpinning cultivar differences in melatonin counteracting salt damage in. <i>Functional Plant Biology</i> , 2022, 49, 201-217.	1.1	6
2624	Genome-Wide Analysis of KNOX Transcription Factors and Expression Pattern of Dwarf-Related KNOX Genes in Pear. <i>Frontiers in Plant Science</i> , 2022, 13, 806765.	1.7	10
2625	Genome-Wide Identification of Maize Aquaporin and Functional Analysis During Seed Germination and Seedling Establishment. <i>Frontiers in Plant Science</i> , 2022, 13, 831916.	1.7	6
2626	Insights into the gene and protein structures of the CaSWEET family members in chickpea ( <i>Cicer</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 acid treatments. <i>Gene</i> , 2022, 819, 146210.	1.0	5
2627	Systematic analysis of the Serine/Arginine-Rich Protein Splicing Factors (SRs) and focus on salt tolerance of <i>PtSC27</i> in <i>Populus trichocarpa</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 173, 97-109.	2.8	5
2628	Genome-Wide Investigation of the Zinc Finger-Homeodomain Family Genes Reveals Potential Roles in Apple Fruit Ripening. <i>Frontiers in Genetics</i> , 2021, 12, 783482.	1.1	3
2629	Overexpression of <i>ZmPCK2</i> , a phosphoenolpyruvate carboxykinase gene from maize confers enhanced tolerance to water deficit stress in rice. <i>Plant Science</i> , 2022, 317, 111195.	1.7	2



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2631	Genome-wide identification and expression pattern analysis of the TCP transcription factor family in <i>Ginkgo biloba</i> . <i>Plant Signaling and Behavior</i> , 2022, 17, 1994248.	1.2	8
2632	Identification and characterization of stress responsive homeodomain leucine zipper transcription factors in <i>Medicago truncatula</i> . <i>Molecular Biology Reports</i> , 2022, , 1.	1.0	5
2633	Genome-Wide Identification and Comparative Analysis of WRKY Transcription Factors Related to Momilactone Biosynthesis in <i>Calohyphnum plumiforme</i> . <i>Frontiers in Ecology and Evolution</i> , 2022, 9, .	1.1	3
2634	Insight into VvGH3 genes evolutionary relationship from monocotyledons and dicotyledons reveals that VvGH3-9 negatively regulates the drought tolerance in transgenic <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2022, 172, 70-86.	2.8	4
2635	Genome-wide identification and expression analysis of the bZIP gene family in silver birch ( <i>Betula</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1.7 4	1.7	4
2636	Identification, Molecular Characteristics, and Evolution of GRF Gene Family in Foxtail Millet ( <i>Setaria</i> ) Tj ETQq0 0 0 9.1 /Overlock 10 Tf 5	9.1	10
2637	Genome-Wide Identification and Characterization of GASA Gene Family in <i>Nicotiana tabacum</i> . <i>Frontiers in Genetics</i> , 2021, 12, 768942.	1.1	14
2638	Genome-Wide Identification and Expression Analysis of VviYABs Family Reveal Its Potential Functions in the Developmental Switch and Stresses Response During Grapevine Development. <i>Frontiers in Genetics</i> , 2021, 12, 762221.	1.1	2
2639	Genomic Analysis of Soybean PP2A-B $\alpha$ Family and Its Effects on Drought and Salt Tolerance. <i>Frontiers in Plant Science</i> , 2021, 12, 784038.	1.7	5
2640	Nodulin 26-like intrinsic protein CsNIP2;2 is a silicon influx transporter in <i>Cucumis sativus</i> L.. <i>Journal of Integrative Agriculture</i> , 2022, 21, 685-696.	1.7	3
2641	GhODO1, an R2R3-type MYB transcription factor, positively regulates cotton resistance to <i>Verticillium dahliae</i> via the lignin biosynthesis and jasmonic acid signaling pathway. <i>International Journal of Biological Macromolecules</i> , 2022, 201, 580-591.	3.6	31
2642	AtQQS orphan gene and NtNF-YC4 boost protein accumulation and pest resistance in tobacco ( <i>Nicotiana tabacum</i> ). <i>Plant Science</i> , 2022, 317, 111198.	1.7	10
2643	Genome-wide identification, expression pattern and subcellular localization analysis of the JAZ gene family in <i>Toona ciliata</i> . <i>Industrial Crops and Products</i> , 2022, 178, 114582.	2.5	8
2644	MSD2, an apoplastic Mn-SOD, contributes to root skotomorphogenic growth by modulating ROS distribution in <i>Arabidopsis</i> . <i>Plant Science</i> , 2022, 317, 111192.	1.7	20
2645	Genome-wide identification and expression analysis of dirigent gene family in strawberry ( <i>Fragaria</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1.7 4	1.7	4
2646	CYP81A68 confers metabolic resistance to ALS and ACCase-inhibiting herbicides and its epigenetic regulation in <i>Echinochloa crus-galli</i> . <i>Journal of Hazardous Materials</i> , 2022, 428, 128225.	6.5	50
2647	Molecular characterisation of. <i>Crop and Pasture Science</i> , 2022, 73, 300-311.	0.7	9

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2649	Genome-wide identification and expression profiling analysis of maize AP2/ERF superfamily genes reveal essential roles in abiotic stress tolerance. <i>BMC Genomics</i> , 2022, 23, 125.	1.2	22
2650	A Novel Zn Transporter Gene (ClZIP1) from Turmeric ( <i>Curcuma longa</i> L.) and Expression Analysis in Presence of a Zn-Solubilizing Bacteria. <i>Plant Molecular Biology Reporter</i> , 0, , 1.	1.0	1
2651	Optogenetic and Chemical Induction Systems for Regulation of Transgene Expression in Plants: Use in Basic and Applied Research. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1737.	1.8	8
2652	Genome-wide identification and functional characterization of <i>CDPK</i> gene family reveal their involvement in response to drought stress in <i>Gossypium barbadense</i> . <i>PeerJ</i> , 2022, 10, e12883.	0.9	8
2653	Transcriptome shock in interspecific F1 allotriploid hybrids between Brassica species. <i>Journal of Experimental Botany</i> , 2022, , .	2.4	4
2654	Transcriptome Analysis of Bread Wheat Genotype KRL3-4 Provides a New Insight Into Regulatory Mechanisms Associated With Sodicity (High pH) Tolerance. <i>Frontiers in Genetics</i> , 2021, 12, 782366.	1.1	4
2655	Identification of Peanut Aux/IAA Genes and Functional Prediction during Seed Development and Maturation. <i>Plants</i> , 2022, 11, 472.	1.6	4
2656	Genome-wide identification, characterization, and expression analysis of the ammonium transporter gene family in tea plants ( <i>Camellia sinensis</i> L.). <i>Physiologia Plantarum</i> , 2022, 174, e13646.	2.6	9
2657	Molecular Characterization of the miR156/MsSPL Model in Regulating the Compound Leaf Development and Abiotic Stress Response in Alfalfa. <i>Genes</i> , 2022, 13, 331.	1.0	4
2658	Molecular cloning, characterization and expression analysis of two 12-oxophytodienoate reductases (NtOPR1 and NtOPR2) from <i>Nicotiana tabacum</i> . <i>Molecular Biology Reports</i> , 2022, 49, 5379-5387.	1.0	1
2659	Genome-Wide Evolution and Comparative Analysis of Superoxide Dismutase Gene Family in Cucurbitaceae and Expression Analysis of <i>Lagenaria siceraria</i> Under Multiple Abiotic Stresses. <i>Frontiers in Genetics</i> , 2021, 12, 784878.	1.1	6
2660	Identification and characterization of 20S proteasome genes and their relevance to heat/drought tolerance in bread wheat. <i>Gene Reports</i> , 2022, 27, 101552.	0.4	10
2661	Genome-wide analysis and expression profiling of Cation/H <sup>+</sup> exchanger (CAX) family genes reveal likely functions in cadmium stress responses in poplar. <i>International Journal of Biological Macromolecules</i> , 2022, 204, 76-88.	3.6	16
2662	Cotton genes GhMML1 and GhMML2 control trichome branching when ectopically expressed in tobacco. <i>Gene</i> , 2022, 820, 146308.	1.0	1
2663	Identification of PAL genes related to anthocyanin synthesis in tea plants and its correlation with anthocyanin content. <i>Horticultural Plant Journal</i> , 2022, 8, 381-394.	2.3	31
2664	Genome-wide association study identifies variants of <i>GhSAD1</i> conferring cold tolerance in cotton. <i>Journal of Experimental Botany</i> , 2022, 73, 2222-2237.	2.4	9
2665	The IbBBX24-IbTOE3-IbPRX17 module enhances abiotic stress tolerance by scavenging reactive oxygen species in sweet potato. <i>New Phytologist</i> , 2022, 233, 1133-1152.	3.5	37

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2668	Functional conservation and divergence in plant-specific <i>GRF</i> gene family revealed by sequences and expression analysis. Open Life Sciences, 2022, 17, 155-171.	0.6	3
2669	Stress Responsive <i>Shyprp16</i> Promoter Driven Early Expression of Resistance Gene <i>Pi54</i> Potentiate the Resistance Against <i>Magnaporthe Oryzae</i> In Transgenic Rice. SSRN Electronic Journal, 0, , .	0.4	0
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2671	Functional analysis of hot pepper ethylene responsive factor 1A in plant defense. Plant Signaling and Behavior, 2022, 17, 2027137.	1.2	3
2672	Genome-wide analysis of the rose ( <i>Rosa chinensis</i> ) NAC family and characterization of RcNAC091. Plant Molecular Biology, 2022, 108, 605-619.	2.0	4
2673	Genome-Wide Characterization of Serine/Arginine-Rich Gene Family and Its Genetic Effects on Agronomic Traits of Brassica napus. Frontiers in Plant Science, 2022, 13, 829668.	1.7	7
2674	Genome-Wide Identification and Gene Expression Analysis of the OTU DUB Family in <i>Oryza sativa</i> . Viruses, 2022, 14, 392.	1.5	3
2675	Genome-wide characterization of the sorghum JAZ gene family and their responses to phytohormone treatments and aphid infestation. Scientific Reports, 2022, 12, 3238.	1.6	8
2676	Characterization of SOD and GPX Gene Families in the Soybeans in Response to Drought and Salinity Stresses. Antioxidants, 2022, 11, 460.	2.2	25
2678	Genome-Wide Analysis of HSP70s in Hexaploid Wheat: Tandem Duplication, Heat Response, and Regulation. Cells, 2022, 11, 818.	1.8	5
2679	A new NLR gene for resistance to Tomato spotted wilt virus in tomato ( <i>Solanum lycopersicum</i> ). Theoretical and Applied Genetics, 2022, 135, 1493-1509.	1.8	12
2680	Genome-Wide Identification and Expression Profiling of Germin-Like Proteins Reveal Their Role in Regulating Abiotic Stress Response in Potato. Frontiers in Plant Science, 2021, 12, 831140.	1.7	9
2681	Genome-Wide Identification, Characterization and Expression Analysis of Lipoxygenase Gene Family in <i>Artemisia annua</i> L.. Plants, 2022, 11, 655.	1.6	6
2682	Genome-Wide Characterization and Anthocyanin-Related Expression Analysis of the B-BOX Gene Family in <i>Capsicum annuum</i> L.. Frontiers in Genetics, 2022, 13, 847328.	1.1	6
2683	In Silico Genome-Wide Characterisation of the Lipid Transfer Protein Multigenic Family in Sunflower ( <i>H. annuus</i> L.). Plants, 2022, 11, 664.	1.6	3
2684	Global Identification and Characterization of C2 Domain-Containing Proteins Associated with Abiotic Stress Response in Rice ( <i>Oryza sativa</i> L.). International Journal of Molecular Sciences, 2022, 23, 2221.	1.8	1
2685	Genome-wide analysis of sucrose synthase family in soybean and their expression in response to abiotic stress and seed development. PLoS ONE, 2022, 17, e0264269.	1.1	2

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2687	Genome-Wide Identification of Cotton ( <i>Gossypium</i> spp.) Glycerol-3-Phosphate Dehydrogenase (GPDH) Family Members and the Role of GhGPDH5 in Response to Drought Stress. <i>Plants</i> , 2022, 11, 592.	1.6	3
2688	Genome-wide identification of Tomato Golden 2-Like transcription factors and abiotic stress related members screening. <i>BMC Plant Biology</i> , 2022, 22, 82.	1.6	13
2689	Investigation of Roles of TaTALE Genes during Development and Stress Response in Bread Wheat. <i>Plants</i> , 2022, 11, 587.	1.6	14
2690	In Silico Study of Superoxide Dismutase Gene Family in Potato and Effects of Elevated Temperature and Salicylic Acid on Gene Expression. <i>Antioxidants</i> , 2022, 11, 488.	2.2	7
2691	Genome-wide evolution and expression analysis of the <i>MYB-CC</i> gene family in <i>Brassica</i> spp.. <i>PeerJ</i> , 2022, 10, e12882.	0.9	2
2692	Genome-Wide Analyses of Aspartic Proteases on Potato Genome ( <i>Solanum tuberosum</i> ): Generating New Tools to Improve the Resistance of Plants to Abiotic Stress. <i>Plants</i> , 2022, 11, 544.	1.6	4
2693	Expression profiling of the mitogen-activated protein kinase gene family reveals their diverse response pattern in two different salt-tolerant <i>Glycyrrhiza</i> species. <i>Genes and Genomics</i> , 2022, , 1.	0.5	0
2694	Genome-Wide Identification and Expression Analysis of the R2R3-MYB Transcription Factor Family Revealed Their Potential Roles in the Flowering Process in Longan ( <i>Dimocarpus longan</i> ). <i>Frontiers in Plant Science</i> , 2022, 13, 820439.	1.7	8
2695	Molecular Characterization, Evolutionary Analysis, and Expression Profiling of BOR Genes in Important Cereals. <i>Plants</i> , 2022, 11, 911.	1.6	14
2696	Metal Tolerance Protein Encoding Gene Family in <i>Fagopyrum tartaricum</i> : Genome-Wide Identification, Characterization and Expression under Multiple Metal Stresses. <i>Plants</i> , 2022, 11, 850.	1.6	3
2697	An Efficient and Universal Protoplast Isolation Protocol Suitable for Transient Gene Expression Analysis and Single-Cell RNA Sequencing. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3419.	1.8	19
2698	Fasulye bitkisinde phospholipase D gen ailesinin tuz ve kuraklık stresi altında genom karakterizasyonu. <i>European Journal of Science and Technology</i> , 0, , .	0.5	0
2699	<i>CiKN1</i> and <i>CiKN6</i> are involved in leaf development in citrus by regulating <i>CimiR164</i> . <i>Plant Journal</i> , 2022, 110, 828-848.	2.8	10
2700	Rapid Identification of Pollen- and Anther-Specific Genes in Response to High-Temperature Stress Based on Transcriptome Profiling Analysis in Cotton. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3378.	1.8	9
2701	GWAS to Identify Novel QTNs for WSCs Accumulation in Wheat Peduncle Under Different Water Regimes. <i>Frontiers in Plant Science</i> , 2022, 13, 825687.	1.7	5
2702	Systematic Analysis and Expression Profiles of the 4-Coumarate: CoA Ligase (4CL) Gene Family in Pomegranate ( <i>Punica granatum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 3509.	1.8	13
2703	Fasulye Genotiplerinde Tuz ve Kuraklık Stresleri Altında VPE Gen Ailesinin Genom Analizi ve Karakterizasyonu. <i>European Journal of Science and Technology</i> , 0, , .	0.5	1

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2705	Genome-Wide Identification of BAHD Superfamily and Functional Characterization of Bornyl Acetyltransferases Involved in the Bornyl Acetate Biosynthesis in <i>Wurfbainia villosa</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 860152.	1.7	5
2706	Genome-wide Identification, Expression, and Functional Analysis of MdMSI Genes in Apples ( <i>Malus</i> ). <i>Journal of Experimental Botany</i> , 2022, 73, 4129-4146.	1.1	2
2707	Tissue specificity and responses to abiotic stresses and hormones of PIN genes in rice. <i>Biologia (Poland)</i> , 2022, 77, 1459-1470.	0.8	7
2708	Identification and Characterization of Salt- and Drought-Responsive AQP Family Genes in <i>Medicago sativa</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3342.	1.8	5
2709	<i>Ugt7A1</i> , a TT19-like GST gene, is essential for accumulation of anthocyanins, but not proanthocyanins in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 4129-4146.	2.4	10
2710	Genome-Wide Identification and Characterization of CDPK Family Reveal Their Involvements in Growth and Development and Abiotic Stress in Sweet Potato and Its Two Diploid Relatives. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3088.	1.8	8
2711	Genome-Wide Identification and Expression Analysis of the Thioredoxin (Trx) Gene Family Reveals Its Role in Leaf Rust Resistance in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 2022, 13, 836030.	1.1	8
2712	The impacts of allopolyploidization on Methyl-CpG-Binding Domain (MBD) gene family in <i>Brassica napus</i> . <i>BMC Plant Biology</i> , 2022, 22, 103.	1.6	3
2713	PvTLP genlerinin genomik analiz ve karakterizasyonu. <i>European Journal of Science and Technology</i> , 2022, 13, 103-110.	0.5	0
2714	Systematic identification and expression profiles of the BAHD superfamily acyltransferases in barley ( <i>Hordeum vulgare</i> ). <i>Scientific Reports</i> , 2022, 12, 5063.	1.6	5
2715	Genome-wide analysis of the GRF gene family and their expression profiling in peach ( <i>Prunus</i> ). <i>Journal of Experimental Botany</i> , 2022, 73, 4129-4146.	1.0	10
2716	Functional analysis of a viral promoter from a strawberry vein banding virus isolate from China. <i>Virology Journal</i> , 2022, 19, 60.	1.4	0
2717	Enhancement of Drought Tolerance in Transgenic <i>Arabidopsis thaliana</i> Plants Overexpressing Chickpea Ca14-3-3 Gene. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 1544-1557.	2.8	3
2718	Medicarpin confers powdery mildew resistance in <i>Medicago truncatula</i> and activates the salicylic acid signalling pathway. <i>Molecular Plant Pathology</i> , 2022, 23, 966-983.	2.0	7
2719	Innovation and Emerging Roles of <i>Populus trichocarpa</i> TEOSINTE BRANCHED1/CYCLOIDEA/PROLIFERATING CELL FACTOR Transcription Factors in Abiotic Stresses by Whole-Genome Duplication. <i>Frontiers in Plant Science</i> , 2022, 13, 850064.	1.7	6
2720	Cross-kingdom microRNA transfer for the control of the anthracnose disease in cassava. <i>Tropical Plant Pathology</i> , 2022, 47, 362-377.	0.8	3
2721	Heat Shock Protein 20 Gene Superfamilies in Red Algae: Evolutionary and Functional Diversities. <i>Frontiers in Plant Science</i> , 2022, 13, 817852.	1.7	6

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2722	Genome-wide characterization of graft-transmissible mRNA-coding P450 genes of cucumber ( <i>Cucumis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10	2.38	1
2723	BURP domain-containing genes in legumes: genome-wide identification, structure, and expression analysis under stresses and development. <i>Plant Biotechnology Reports</i> , 2022, 16, 369-388.	0.9	4
2724	Identification of an anther-specific promoter from a male sterile AB line in Chinese cabbage ( <i>Brassica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	2
2725	Homologous Drought-Induced 19 Proteins, PtDi19-2 and PtDi19-7, Enhance Drought Tolerance in Transgenic Plants. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3371.	1.8	11
2726	Characterization of pectin methylesterase gene family and its possible role in juice sac granulation in navel orange ( <i>Citrus sinensis</i> Osbeck). <i>BMC Genomics</i> , 2022, 23, 185.	1.2	6
2727	Molecular cloning and characterization of Cinnamoylâ€CoA reductase promoter gene from <i>Asarum sieboldii</i> Miq. <i>Biotechnology and Applied Biochemistry</i> , 2022, , .	1.4	0
2728	Characterization of the TCP Gene Family in <i>Chrysanthemum nankingense</i> and the Role of CnTCP4 in Cold Tolerance. <i>Plants</i> , 2022, 11, 936.	1.6	7
2729	Overexpression of the <i>Salix matsudana</i> SmAP2-17 gene improves <i>Arabidopsis</i> salinity tolerance by enhancing the expression of SOS3 and ABI5. <i>BMC Plant Biology</i> , 2022, 22, 102.	1.6	8
2730	New insight into the roles of lipid transport protein and seed storage albumin gene families involved in oil and protein accumulation in rapeseed ( <i>Brassica napus</i> L.). <i>Botany</i> , 0, , .	0.5	0
2731	Genome-Wide Identification of APETALA2/ETHYLENE RESPONSIVE FACTOR Transcription Factors in <i>Cucurbita moschata</i> and Their Involvement in Ethylene Response. <i>Frontiers in Plant Science</i> , 2022, 13, 847754.	1.7	8
2732	Genome-Wide Analysis of the Protein Phosphatase 2C Genes in Tomato. <i>Genes</i> , 2022, 13, 604.	1.0	14
2733	Genome-Wide Identification of YABBY Gene Family in Cucurbitaceae and Expression Analysis in Cucumber ( <i>Cucumis sativus</i> L.). <i>Genes</i> , 2022, 13, 467.	1.0	12
2734	Gene Expression Analysis of Potato ( <i>Solanum tuberosum</i> L.) Lipoxygenase Cascade and Oxylipin Signature under Abiotic Stress. <i>Plants</i> , 2022, 11, 683.	1.6	5
2735	Genome-wide analysis of trehalose-6-phosphate phosphatases (TPP) gene family in wheat indicates their roles in plant development and stress response. <i>BMC Plant Biology</i> , 2022, 22, 120.	1.6	17
2736	Genome-Wide Identification, Evolution and Expression Analysis of the Glutathione S-Transferase Supergene Family in Euphorbiaceae. <i>Frontiers in Plant Science</i> , 2022, 13, 808279.	1.7	3
2737	Ethylene-induced potassium transporter AckUP2 gene is involved in kiwifruit postharvest ripening. <i>BMC Plant Biology</i> , 2022, 22, 108.	1.6	1
2738	Comprehensive identification and expression analysis of CRY gene family in <i>Gossypium</i> . <i>BMC Genomics</i> , 2022, 23, 231.	1.2	4
2739	Identification and expression analysis of phospholipase C family genes between different male fertility accessions in pepper. <i>Protoplasma</i> , 2022, , 1.	1.0	0

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2740	A SNP variation in an expansin ( <i>EgExp4</i> ) gene affects height in oil palm. <i>PeerJ</i> , 2022, 10, e13046.	0.9	4
2741	Identification, Expression, and Functional Study of Seven NAC Transcription Factor Genes Involved in Stress Response in Tartary Buckwheat ( <i>Fagopyrum tataricum</i> (L.) Gaertn.). <i>Agronomy</i> , 2022, 12, 849.	1.3	3
2742	VvTOR Responds to ABA Signal and Affects Sugar Related Genes Expression in Grape. <i>Russian Journal of Plant Physiology</i> , 2022, 69, 1.	0.5	0
2743	A Comprehensive Analysis of Calmodulin-Like Proteins of <i>Glycine max</i> Indicates Their Role in Calcium Signaling and Plant Defense Against Insect Attack. <i>Frontiers in Plant Science</i> , 2022, 13, 817950.	1.7	16
2744	Genome-wide identification and characterization of PdbHLH transcription factors related to anthocyanin biosynthesis in colored-leaf poplar ( <i>Populus deltoids</i> ). <i>BMC Genomics</i> , 2022, 23, 244.	1.2	14
2745	Genome-wide identification and expression analysis of the <i>RcYABBY</i> s reveals their potential functions in rose ( <i>Rosa chinensis</i> Jacq.). <i>Journal of Horticultural Science and Biotechnology</i> , 0, , 1-10.	0.9	1
2746	Tissue-Specific Expression of the Terpene Synthase Family Genes in <i>Rosa chinensis</i> and Effect of Abiotic Stress Conditions. <i>Genes</i> , 2022, 13, 547.	1.0	11
2747	Role of Wheat Phosphorus Starvation Tolerance 1 Genes in Phosphorus Acquisition and Root Architecture. <i>Genes</i> , 2022, 13, 487.	1.0	7
2748	Genome-wide analysis of <i>Solanum lycopersicum</i> L. cyclophilins. <i>Journal of Plant Biotechnology</i> , 2022, 49, 15-29.	0.1	0
2749	Genome-Wide Identification of GRAS Transcription Factors and Their Potential Roles in Growth and Development of Rose ( <i>Rosa chinensis</i> ). <i>Journal of Plant Growth Regulation</i> , 2023, 42, 1505-1521.	2.8	6
2750	Genome-wide characterization and expression analysis of Erf gene family in cotton. <i>BMC Plant Biology</i> , 2022, 22, 134.	1.6	23
2751	Global Survey, Expressions and Association Analysis of CBLL Genes in Peanut. <i>Frontiers in Genetics</i> , 2022, 13, 821163.	1.1	2
2752	Tyrosine Hydroxylase and DOPA Decarboxylase Are Associated With Pupal Melanization During Larval Pupal Transformation in <i>Antheraea pernyi</i> . <i>Frontiers in Physiology</i> , 2022, 13, 832730.	1.3	3
2753	Identification of the Wheat ( <i>Triticum aestivum</i> ) IQD Gene Family and an Expression Analysis of Candidate Genes Associated with Seed Dormancy and Germination. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4093.	1.8	3
2754	The Characterization of the Phloem Protein 2 Gene Family Associated with Resistance to <i>Sclerotinia sclerotiorum</i> in <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 3934.	1.8	4
2755	Genome-wide identification of glutathione S-transferase gene family members in tea plant ( <i>Camellia</i> ) Tj ETQq1 1 0.784314 rgBT /Overl Macromolecules, 2022, 205, 749-760.	3.6	17
2756	Loss of GSNOR increases abiotic stress sensitivity via regulating MAPK-ethylene cascade signaling in <i>Solanum lycopersicum</i> L.. <i>Environmental and Experimental Botany</i> , 2022, , 104872.	2.0	0
2757	Small RNA Sequencing Revealed that miR4415, a Legume-Specific miRNA, was Involved in the Cold Acclimation of <i>Ammopiptanthus nanus</i> by Targeting an L-Ascorbate Oxidase Gene and Regulating the Redox State of Apoplast. <i>Frontiers in Genetics</i> , 2022, 13, 870446.	1.1	8

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2758	Genome-Wide Identification of the B-Box Gene Family and Expression Analysis Suggests Their Potential Role in Photoperiod-Mediated l <sup>2</sup> -Carotene Accumulation in the Endocarp of Cucumber ( <i>Cucumis sativus</i> ) Tj ETQq0 0.0 rgBT /@verlock 10	1.0	0
2759	A new network containing MYB109-ZmCesA5 is involved in kernel development. <i>Biochemical and Biophysical Research Communications</i> , 2022, 602, 15-20.	1.0	1
2760	Genome-Wide Identification, Expression Pattern and Sequence Variation Analysis of SnRK Family Genes in Barley. <i>Plants</i> , 2022, 11, 975.	1.6	3
2761	Genome-wide identification and expression analysis of the plant-specific PLATZ gene family in Tartary buckwheat ( <i>Fagopyrum tataricum</i> ). <i>BMC Plant Biology</i> , 2022, 22, 160.	1.6	6
2762	Genome-Wide Identification of TLP Gene Family and Their Roles in <i>Carya cathayensis</i> Sarg in Response to <i>Botryosphaeria dothidea</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 849043.	1.7	2
2763	The non-specific lipid transfer protein GmLtpl.3 is involved in drought and salt tolerance in soybean. <i>Environmental and Experimental Botany</i> , 2022, 196, 104823.	2.0	3
2764	Genome-wide identification and characterization of bZIP gene family and cloning of candidate genes for anthocyanin biosynthesis in pomegranate ( <i>Punica granatum</i> ). <i>BMC Plant Biology</i> , 2022, 22, 170.	1.6	17
2765	Early wound-responsive cues regulate the expression of WRKY family genes in chickpea differently under wounded and unwounded conditions. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 719-735.	1.4	3
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2773	Evolutionary and functional characterisation of glutathione peroxidases showed splicing mediated stress responses in Maize. <i>Plant Physiology and Biochemistry</i> , 2022, 178, 40-54.	2.8	6
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3215	Identification and relative expression analysis of CaFRK gene family in pepper. <i>3 Biotech</i> , 2022, 12, .	1.1	2
3216	Genome-wide identification, characterization and expression analysis of the BRI1 gene family in <i>Triticum aestivum</i> L.. <i>Plant Biotechnology Reports</i> , 2022, 16, 777-791.	0.9	2
3218	Serine Hydroxymethyltransferase (SHMT) Gene Family in Wheat ( <i>Triticum aestivum</i> L.): Identification, Evolution, and Expression Analysis. <i>Agronomy</i> , 2022, 12, 1346.	1.3	1
3219	Genome-Wide Identification and Expression Pattern Analysis of KNOX Gene Family in Orchidaceae. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	12
3220	UDP-glucose pyrophosphorylase: genome-wide identification, expression and functional analyses in <i>Gossypium hirsutum</i> . <i>PeerJ</i> , 0, 10, e13460.	0.9	2
3221	Conservation and Divergence of Phosphoenolpyruvate Carboxylase Gene Family in Cotton. <i>Plants</i> , 2022, 11, 1482.	1.6	1
3222	Genome-Wide Identification and Analysis of the NAC Transcription Factor Gene Family in Garden Asparagus ( <i>Asparagus officinalis</i> ). <i>Genes</i> , 2022, 13, 976.	1.0	6
3223	Comparative Expression Profiling of Snf2 Family Genes During Reproductive Development and Stress Responses in Rice. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	2

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3224	Two homeologous MATE transporter genes, <i>NtMATE21</i> and <i>NtMATE22</i> , are involved in the modulation of plant growth and flavonol transport in <i>Nicotiana tabacum</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 6186-6206.	2.4	5
3225	Soybean F-Box-Like Protein GmFBL144 Interacts With Small Heat Shock Protein and Negatively Regulates Plant Drought Stress Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3226	Genome-Wide Identification and Functional Characterization of Auxin Response Factor (ARF) Genes in Eggplant. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6219.	1.8	11
3227	Rapeseed ( <i>Brassica napus</i> ) Mitogen-Activated Protein Kinase 1 Enhances Shading Tolerance by Regulating the Photosynthesis Capability of Photosystem II. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	1
3228	Genome Wide Identification and Characterization of Wheat GH9 Genes Reveals Their Roles in Pollen Development and Anther Dehiscence. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6324.	1.8	8
3229	Genome-Wide Identification and Analysis of Ariadne Gene Family Reveal Its Genetic Effects on Agronomic Traits of <i>Brassica napus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6265.	1.8	3
3230	Characterization and Functional Analysis of GhNAC82, A NAM Domain Gene, Coordinates the Leaf Senescence in Upland Cotton ( <i>Gossypium hirsutum</i> L.). <i>Plants</i> , 2022, 11, 1491.	1.6	3
3231	Genome-Wide Identification of m6A Writers, Erasers and Readers in Poplar 84K. <i>Genes</i> , 2022, 13, 1018.	1.0	4
3232	Characterization of sucrose binding protein as a seed-specific promoter in transgenic tobacco <i>Nicotiana tabacum</i> L. <i>PLoS ONE</i> , 2022, 17, e0268036.	1.1	2
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3234	Genome-wide identification of YABBY transcription factors in <i>Brachypodium distachyon</i> and functional characterization of Bd DROOPING LEAF. <i>Plant Physiology and Biochemistry</i> , 2022, 185, 13-24.	2.8	2
3235	Genome-wide identification of <i>Oryza sativa</i> : A new insight for advanced analysis of ABC transporter genes associated with the degradation of four pesticides. <i>Gene</i> , 2022, 834, 146613.	1.0	16
3236	Genome-wide analysis of cowpea NAC transcription factor family elucidating the genetic & molecular relationships that interface stress and growth regulatory signals. <i>Plant Gene</i> , 2022, 31, 100363.	1.4	2
3237	A jasmonate-responsive glutathione S-transferase gene SIGSTU24 mitigates cold-induced oxidative stress in tomato plants. <i>Scientia Horticulturae</i> , 2022, 303, 111231.	1.7	12
3240	In Silico Identification and Characterization of B12D Family Proteins in Viridiplantae. <i>Evolutionary Bioinformatics</i> , 2022, 18, 117693432211067.	0.6	1
3241	Genome-Wide Identification and Expression Analysis of Lcccr13 Reveals its Potential Role in Lignin Biosynthesis in <i>Liriodendron chinense</i> . <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
3242	Genome-Wide Identification and Expression Analysis Elucidates the Potential Role of PFK Gene Family in Drought Stress Tolerance and Sugar Metabolism in Cotton. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
3243	Genome-Wide Identification of NRT Gene Family and Expression Analysis of Nitrate Transporters in Response to Salt Stress in <i>Poncirus trifoliata</i> . <i>Genes</i> , 2022, 13, 1115.	1.0	9



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3245	Systematic Analysis of bHLH Transcription Factors in Cassava Uncovers Their Roles in Postharvest Physiological Deterioration and Cyanogenic Glycosides Biosynthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	15
3246	Identification of the CIPK-CBL family gene and functional characterization of CqCIPK14 gene under drought stress in quinoa. <i>BMC Genomics</i> , 2022, 23, .	1.2	14
3247	Genome-Wide Identification of NAP1 and Function Analysis in Moso Bamboo ( <i>Phyllostachys edulis</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 6491.	1.8	3
3248	Genome-Wide Identification of Genes Encoding for Rho-Related Proteins in "Duli"™ Pear ( <i>Pyrus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.6	1
3249	Characterization of two constitutive promoters RPS28 and EIF1 for studying soybean growth, development, and symbiotic nodule development. <i>ABIOTECH</i> , 0, , .	1.8	0
3250	Unraveling NPR-like Family Genes in <i>Fragaria</i> spp. Facilitated to Identify Putative NPR1 and NPR3/4 Orthologues Participating in Strawberry-Colletotrichum fructicola Interaction. <i>Plants</i> , 2022, 11, 1589.	1.6	2
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3252	Isolation of the 3 <sup>1</sup> -HSD promoter from <i>Digitalis ferruginea</i> subsp. <i>ferruginea</i> and its functional characterization in <i>Arabidopsis thaliana</i> . <i>Molecular Biology Reports</i> , 0, , .	1.0	0
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3256	A Non-Canonical MITE in the <i>WOX11</i> Promoter Is Associated with Robust Crown Root development in Rice. <i>Plant and Cell Physiology</i> , 2022, 63, 1052-1062.	1.5	1
3257	Genome-Wide Identification and Structural Characterization of Growth-Regulating Factors (GRFs) in <i>Actinidia eriantha</i> and <i>Actinidia chinensis</i> . <i>Plants</i> , 2022, 11, 1633.	1.6	4
3259	Genome-wide analysis of the strigolactone biosynthetic and signaling genes in grapevine and their response to salt and drought stresses. <i>PeerJ</i> , 0, 10, e13551.	0.9	7
3260	NbNAC42 and NbZFP3 Transcription Factors Regulate the Virus Inducible NbAGO5 Promoter in <i>Nicotiana benthamiana</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
3261	Systematic Analysis of Tobacco CrRLK1L Family Genes and Functional Identification of NtCrRLK1L47 in Environmental Stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3262	The Promoter Analysis of VvPR1 Gene: A Candidate Gene Identified through Transcriptional Profiling of Methyl Jasmonate Treated Grapevine ( <i>Vitis vinifera</i> L.). <i>Plants</i> , 2022, 11, 1540.	1.6	4

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3265	DNA Demethylation Induces Tree Peony Flowering with a Low Deformity Rate Compared to Gibberellin by Inducing PsFT Expression under Forcing Culture Conditions. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6632.	1.8	5
3266	Genome-Wide Characterization and Comprehensive Analysis of NAC Transcription Factor Family in <i>Nelumbo nucifera</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
3267	Systematic analysis and identification of regulators for SRS genes in <i>Capsicum annuum</i> . <i>Plant Growth Regulation</i> , 2022, 98, 51-64.	1.8	2
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3271	Genome-Wide Analysis of the GDSL Genes in Pecan ( <i>Carya illinoensis</i> K. Koch): Phylogeny, Structure, Promoter Cis-Elements, Co-Expression Networks, and Response to Salt Stresses. <i>Genes</i> , 2022, 13, 1103.	1.0	7
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3273	Comprehensive Analysis for GRF Transcription Factors in Sacred Lotus ( <i>Nelumbo nucifera</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 6673.	1.8	7
3274	Identification and Characterization of Abiotic Stress-Responsive NF-YB Family Genes in <i>Medicago</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6906.	1.8	3
3275	Genome-Wide Identification and Analysis of the Class III Peroxidase Gene Family in Tobacco ( <i>Nicotiana</i> ) Tj ETQq0 0 0 rgBT /Overlock 10	1.1	9
3276	Genome-Wide Identification of the LHC Gene Family in Kiwifruit and Regulatory Role of <i>AcLhcb3.1/3.2</i> for Chlorophyll a Content. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6528.	1.8	11
3277	Identification of TCP family in moso bamboo ( <i>Phyllostachys edulis</i> ) and salt tolerance analysis of PheTCP9 in transgenic <i>Arabidopsis</i> . <i>Planta</i> , 2022, 256, .	1.6	4
3278	<i>SELF PRUNING 3C</i> is a flowering repressor that modulates seed germination, root architecture, and drought responses. <i>Journal of Experimental Botany</i> , 2022, 73, 6226-6240.	2.4	5
3279	Genome-wide identification and expression analysis of the R2R3-MYB gene family in tobacco ( <i>Nicotiana</i> ) Tj ETQq0 0 0 rgBT /Overlock 10	1.2	13
3280	Genome-Wide Identification and Analysis of the NF-Y Transcription Factor Family Reveal Its Potential Roles in Salt Stress in Alfalfa ( <i>Medicago sativa</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 6426.	1.8	6

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3282	Genome-wide identification of PME gene family and expression of candidate genes associated with aluminum tolerance in tea plant ( <i>Camellia sinensis</i> ). <i>BMC Plant Biology</i> , 2022, 22, .	1.6	12
3283	Identification and expression analysis of xyloglucan endotransglucosylase/hydrolase (XTH) family in grapevine ( <i>Vitis vinifera</i> L.). <i>PeerJ</i> , 0, 10, e13546.	0.9	9
3284	Genome-wide analysis of the C2H2 zinc finger protein gene family and its response to salt stress in ginseng, <i>Panax ginseng</i> Meyer. <i>Scientific Reports</i> , 2022, 12, .	1.6	7
3285	Genome-wide identification and expression analysis of phospholipase D gene in leaves of sorghum in response to abiotic stresses. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 1261-1276.	1.4	4
3286	Genome-Wide Analysis of the Peptidase M24 Superfamily in <i>Triticum aestivum</i> Demonstrates That TaM24-9 Is Involved in Abiotic Stress Response. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6904.	1.8	0
3287	NtDREB-1BL1 Enhances Carotenoid Biosynthesis by Regulating Phytoene Synthase in <i>Nicotiana tabacum</i> . <i>Genes</i> , 2022, 13, 1134.	1.0	5
3288	A Comprehensive Identification and Expression Analysis of VQ Motif-Containing Proteins in Sugarcane ( <i>Saccharum spontaneum</i> L.) under Phytohormone Treatment and Cold Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6334.	1.8	10
3289	Integrative Analysis of the GRAS Genes From Chinese White Pear ( <i>Pyrus bretschneideri</i> ): A Critical Role in Leaf Regeneration. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3290	Genome-Wide Identification and Characterization of Growth Regulatory Factor Family Genes in <i>Medicago</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 6905.	1.8	7
3291	Genome-Wide Identification and Characterization of CPR5 Genes in <i>Gossypium</i> Reveals Their Potential Role in Trichome Development. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
3292	Comprehensive molecular evaluation of the histone methyltransferase gene family and their important roles in two-line hybrid wheat. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	0
3293	Genome-wide identification, expression analyses of Wuschel-related homeobox (WOX) genes in <i>Brachypodium distachyon</i> and functional characterization of BdWOX12. <i>Gene</i> , 2022, 836, 146691.	1.0	1
3294	Genome wide analysis of the heavy-metal-associated (HMA) gene family in tomato and expression profiles under different stresses. <i>Gene</i> , 2022, 835, 146664.	1.0	4
3295	Systematical characterization of GRF gene family in sorghum, and their potential functions in aphid resistance. <i>Gene</i> , 2022, 836, 146669.	1.0	6
3296	A novel root-specific Di19 transcription factor from <i>Glycine max</i> compromises drought tolerance in <i>Arabidopsis thaliana</i> through suppression of auxin-related pathway. <i>Environmental and Experimental Botany</i> , 2022, 201, 104951.	2.0	1
3297	Identification and expression analysis of AP2/ERF superfamily in pecan ( <i>Carya illinoensis</i> ). <i>Scientia Horticulturae</i> , 2022, 303, 111255.	1.7	3
3298	Genome-wide identification of CmaGH3 family genes, and expression analysis in response to cold and hormonal stresses in <i>Cucurbita maxima</i> . <i>Scientia Horticulturae</i> , 2022, 304, 111256.	1.7	3

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3301	Genome Wide Identification and Annotation of NGATHA Transcription Factor Family in Crop Plants. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7063.	1.8	5
3302	PtrWOX13A Promotes Wood Formation and Bioactive Gibberellins Biosynthesis in <i>Populus trichocarpa</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3303	Drought-induced proline is mainly synthesized in leaves and transported to roots in watermelon under water deficit. <i>Horticultural Plant Journal</i> , 2022, 8, 615-626.	2.3	22
3305	Genome-Wide Identification and Comparative Analysis of WOX Genes in Four Euphorbiaceae Species and Their Expression Patterns in <i>Jatropha curcas</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
3306	The qLTG1.1 candidate gene CsGAI regulates low temperature seed germination in cucumber. <i>Theoretical and Applied Genetics</i> , 2022, 135, 2593-2607.	1.8	5
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3308	Analysis of GSH1-GSH3 Genes by Comprehensive Use of Bioinformatics Method in Tomato. , 0, 2, 151-161.		0
3309	Integrating Multiple Omics Identifies <i>Phaeoacremonium rubrigenum</i> Acting as <i>Aquilaria sinensis</i> Marker Fungus to Promote Agarwood Sesquiterpene Accumulation by Inducing Plant Host Phosphorylation. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
3310	Comprehensive Genome-Wide Identification and Expression Profiling of Eceriferum (CER) Gene Family in Passion Fruit ( <i>Passiflora edulis</i> ) Under <i>Fusarium kyushuense</i> and Drought Stress Conditions. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	12
3311	Genome-Wide Analysis and Profile of UDP-Glycosyltransferases Family in Alfalfa ( <i>Medicago sativa</i> L.) under Drought Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7243.	1.8	8
3312	Genome-wide identification, expression, and characterization of CaLysM-RLKs in chickpea root nodule symbiosis. <i>Environmental and Experimental Botany</i> , 2022, 202, 104999.	2.0	4
3313	Identification and expression analysis of chlorophyll a/b binding protein gene family in grape ( <i>Vitis</i> ) Tj ETQq1 1 0.784314 rgBT <sub>3</sub> /Overlook	1.4	1,4
3314	Analysis of TCP Transcription Factors Revealed Potential Roles in Plant Growth and <i>Fusarium oxysporum</i> f.sp. <i>cubense</i> Resistance in Banana (cv. Rasthali). <i>Applied Biochemistry and Biotechnology</i> , 2022, 194, 5456-5473.	1.4	5
3315	AtMYB31 is a wax regulator associated with reproductive development in <i>Arabidopsis</i> . <i>Planta</i> , 2022, 256, .	1.6	2
3316	Genome-Wide Classification and Evolutionary Analysis Reveal Diverged Patterns of Chalcone Isomerase in Plants. <i>Biomolecules</i> , 2022, 12, 961.	1.8	3
3317	Genome-Wide Identification, Characterization, and Expression Profile Analysis of CONSTANS-like Genes in Woodland Strawberry ( <i>Fragaria vesca</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4

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3319	Genome-wide Identification of the GRAS Family Genes in <i>Melilotus albus</i> and Expression Analysis under Various Tissues and Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7403.	1.8	12
3320	Identification of BcARR Genes and CTK Effects on Stalk Development of Flowering Chinese Cabbage. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7412.	1.8	5
3321	Genome-Wide Identification and Characterization of Receptor-Like Protein Kinase 1 (RPK1) Gene Family in <i>Triticum aestivum</i> Under Drought Stress. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
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3323	Genome wide and evolutionary analysis of heat shock protein 70 proteins in tomato and their role in response to heat and drought stress. <i>Molecular Biology Reports</i> , 2022, 49, 11229-11241.	1.0	3
3324	Molecular Cloning, Characterization, and Expression Analysis of SIMILAR TO RCD-ONE (SRO) Family Genes Responding to Abiotic and Biotic Stress in Cucumber. <i>Horticulturae</i> , 2022, 8, 634.	1.2	1
3325	Evolutionary and Integrative Analysis of Gibberellin-Dioxygenase Gene Family and Their Expression Profile in Three Rosaceae Genomes ( <i>F. vesca</i> , <i>P. mume</i> , and <i>P. avium</i> ) Under Phytohormone Stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
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3328	Identification and Comprehensive Genome-Wide Analysis of Glutathione S-Transferase Gene Family in Sweet Cherry ( <i>Prunus avium</i> ) and Their Expression Profiling Reveals a Likely Role in Anthocyanin Accumulation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
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3331	The Epigenetic Regulation in Plant Specialized Metabolism: DNA Methylation Limits Paclitaxel in vitro Biotechnological Production. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
3332	Genome-wide identification, phylogenetic analysis, and expression profiles of trihelix transcription factor family genes in quinoa ( <i>Chenopodium quinoa</i> Willd.) under abiotic stress conditions. <i>BMC Genomics</i> , 2022, 23, .	1.2	8
3333	Small heat shock protein (Hsp20) gene family in <i>Phaseolus vulgaris</i> L.: Genome-wide identification, evolutionary and expression analysis. <i>Plant Gene</i> , 2022, 31, 100370.	1.4	2
3334	Genome-Wide Analysis of Anthocyanin Biosynthesis Regulatory WD40 Gene FcTTG1 and Related Family in <i>Ficus carica</i> L.. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
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3337	Genome-Wide Identification of Glutathione S-Transferase and Expression Analysis in Response to Anthocyanin Transport in the Flesh of the New Teinturier Grape Germplasm "Zhongshan-HongYu"™. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7717.	1.8	4
3338	Genome-Wide Analysis of DoSPX Genes and the Function of DoSPX4 in Low Phosphorus Response in <i>Dendrobium officinale</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
3339	Genome-Wide Characterization of the Aquaporin Gene Family in Radish and Functional Analysis of RsPIP2-6 Involved in Salt Stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
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3342	Diverse function of the PISTILLATA, APETALA 3, and AGAMOUS-like MADS-box genes involved in the floral development in <i>Alpinia hainanensis</i> (Zingiberaceae). <i>Gene</i> , 2022, 839, 146732.	1.0	0
3343	Amino acid transporter (AAT) gene family in Tartary buckwheat ( <i>Fagopyrum tataricum</i> L. Gaertn.): Characterization, expression analysis and functional prediction. <i>International Journal of Biological Macromolecules</i> , 2022, 217, 330-344.	3.6	4
3344	Genome-wide identification and expression analysis of the annexin gene family in rye ( <i>Secale cereale</i> ) Tj ETQq0 0 0 reBT /Overlock 10 Tf	1.0	3
3345	Genome-wide identification of the cytochrome P450 superfamily in <i>Olea europaea</i> helps elucidate the synthesis pathway of oleuropein to improve the quality of olive oil. <i>Scientia Horticulturae</i> , 2022, 304, 111291.	1.7	4
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3352	Molecular Characterization, Evolutionary and Phylogenetic Analyses of Rice ACT/BAT-type Amino Acid Transporters. <i>Computational Biology and Chemistry</i> , 2022, , 107745.	1.1	1
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3363	Genome-Wide Identification of Eucalyptus Heat Shock Transcription Factor Family and Their Transcriptional Analysis under Salt and Temperature Stresses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8044.	1.8	5
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3368	The Single-Stranded DNA-Binding Gene Whirly (Why1) with a Strong Pathogen-Induced Promoter from <i>Vitis pseudoreticulata</i> Enhances Resistance to <i>Phytophthora capsici</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 8052.	1.8	3
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3370	Genome-wide identification and characterization of GATA family genes in wheat. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	14
3371	Genome-Wide Identification and Characterization of Members of the ACS Gene Family in <i>Cucurbita maxima</i> and Their Transcriptional Responses to the Specific Treatments. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8476.	1.8	4

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3385	The interplay of DNA methyltransferases and demethylases with tuberization genes in potato ( <i>Solanum tuberosum</i> L.) genotypes under high temperature. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
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3399	Genome-Wide Characterization of Ascorbate Peroxidase Gene Family in Peanut ( <i>Arachis hypogea</i> L.) Revealed Their Crucial Role in Growth and Multiple Stress Tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	17
3400	The clock component OsLUX regulates rice heading through recruiting OsELF3-1 and OsELF4s to repress Hd1 and Ghd7. <i>Journal of Advanced Research</i> , 2023, 48, 17-31.	4.4	6
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3410	Expression of a Hydroxycinnamoyl-CoA Shikimate/Quinate Hydroxycinnamoyl Transferase 4 Gene from <i>Zoysia japonica</i> (ZjHCT4) Causes Excessive Elongation and Lignin Composition Changes in <i>Agrostis stolonifera</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 9500.	1.8	2
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3412	The <i>Sclerotinia sclerotiorum</i> -inducible promoter <i>pBnGH17</i> <i>D7</i> in <i>Brassica napus</i> : isolation, characterization, and application in host-induced gene silencing. <i>Journal of Experimental Botany</i> , 2022, 73, 6663-6677.	2.4	3
3413	Consensus genomic regions associated with multiple abiotic stress tolerance in wheat and implications for wheat breeding. <i>Scientific Reports</i> , 2022, 12, .	1.6	35

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3416	Multiple roles of wheat calmodulin genes during stress treatment and TaCAM2-D as a positive regulator in response to drought and salt tolerance. <i>International Journal of Biological Macromolecules</i> , 2022, 220, 985-997.	3.6	9
3417	<scp>GRP</scp> genes in potato genome and their expression response to phytohormone and <i>Ralstonia solanacearum</i>. <i>Journal of Phytopathology</i> , 2022, 170, 724-737.	0.5	2
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3427	Genome-Wide Identification and Expression Analysis of Eggplant DIR Gene Family in Response to Biotic and Abiotic Stresses. <i>Horticulturae</i> , 2022, 8, 732.	1.2	4
3428	Genome-Wide Analysis and Evolutionary Perspective of the Cytokinin Dehydrogenase Gene Family in Wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
3429	Transcript profiling of glutathione metabolizing genes reveals abiotic stress and glutathione-specific alteration in Arabidopsis and rice. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 1375-1390.	1.4	2
3431	Genome-Wide Analysis of the Type-B Authentic Response Regulator Gene Family in Brassica napus. <i>Genes</i> , 2022, 13, 1449.	1.0	2
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3434	Identification of receptor-like proteins induced by <i>Sclerotinia sclerotiorum</i> in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3435	Genome-wide investigation and comparative expression profiling reveal R2R3-MYB genes involved in <i>Sclerotinia sclerotiorum</i> defence in tomato. <i>Physiological and Molecular Plant Pathology</i> , 2022, 121, 101873.	1.3	5
3436	Multi-algorithm cooperation comprehensive research of bZIP genes under nitrogen stress in <i>Panax notoginseng</i> . <i>Gene</i> , 2022, 841, 146768.	1.0	4
3438	Identification of QTLs controlling cold tolerance in cucumber ( <i>Cucumis sativus</i> L.) seedlings. <i>Scientia Horticulturae</i> , 2022, 305, 111383.	1.7	2
3439	Stress responsive OsHyPRP16 promoter driven early expression of resistance gene Pi54 potentiate the resistance against <i>Magnaporthe oryzae</i> in transgenic rice. <i>Plant Science</i> , 2022, 324, 111413.	1.7	3
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3441	Genome-wide identification and expression analysis of WRKY family genes under soft rot in Chinese cabbage. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1
3442	Genome-Wide Identification and Expression Patterns of the SWEET Gene Family in <i>Bletilla striata</i> and its Responses to Low Temperature and Oxidative Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10057.	1.8	5
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3444	Genome-wide characterization of the MBF1 gene family and its expression pattern in different tissues and stresses in <i>Zanthoxylum armatum</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	3
3445	Functional characterization of the Serine acetyltransferase family genes uncovers the diversification and conservation of cysteine biosynthesis in tomato. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
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3447	Two R2R3-MYB transcription factors, CsMYB33 and CsMYB78 are involved in the regulation of anthocyanin biosynthesis in <i>Cannabis sativa</i> L.. <i>Industrial Crops and Products</i> , 2022, 188, 115546.	2.5	10
3448	Overexpression of mango MiMFT inhibits seed germination and enhances abiotic stress tolerance in transgenic <i>Arabidopsis</i> . <i>Scientia Horticulturae</i> , 2023, 307, 111495.	1.7	7
3449	Genome-wide identification of B3 superfamily in pecan ( <i>Carya illinoensis</i> ): In silico and experimental analyses. <i>Scientia Horticulturae</i> , 2023, 307, 111533.	1.7	2
3450	Genomic and Bioinformatic Resources for Next-Generation Breeding Approaches Towards Enhanced Stress Tolerance in Cereals. , 2022, , 453-493.		2
3451	Genome-wide identification of MAPK family genes and their response to abiotic stresses in tea plant ( <i>Camellia sinensis</i> ). <i>Open Life Sciences</i> , 2022, 17, 1064-1074.	0.6	5

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3453	Genome wide analysis of BnAPs gene family in <i>Brassica napus</i> . <i>Acta Agronomica Sinica(China)</i> , 2022, 48, 597-607.	0.1	1
3454	Genome-wide identification of BnCNGC and the gene expression analysis in <i>Brassica napus</i> challenged with <i>Sclerotinia sclerotiorum</i> and PEG-simulated drought. <i>Acta Agronomica Sinica(China)</i> , 2022, 48, 1357-1371.	0.1	0
3455	Comparative and expression analysis of MYB transcription factor genes in groundnut ( <i>Arachis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.9	0
3456	Genome-Wide Characterization of Remorin Genes in Terms of Their Evolution and Expression in Response to Hormone Signals and Abiotic Stresses in Foxtail Millet ( <i>Setaria italica</i> ). <i>Diversity</i> , 2022, 14, 711.	0.7	3
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3458	Genome-Wide Identification and Expression Analysis of eIF Family Genes from <i>Brassica rapa</i> in Response to TuMV Resistance. <i>Plants</i> , 2022, 11, 2248.	1.6	0
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3463	Profiling of transcriptional regulators associated with starch biosynthesis in sorghum ( <i>Sorghum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.7	4
3464	Genome-wide identification of the trehalose-6-phosphate synthase gene family in sweet orange ( <i>Citrus sinensis</i> ) and expression analysis in response to phytohormones and abiotic stresses. <i>PeerJ</i> , 0, 10, e13934.	0.9	3
3465	Genetic architecture of morin (pentahydroxyflavone) biosynthetic pathway in mulberry ( <i>Morus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.7	1
3466	The heat stress transcription factor family in <i>Aegilops tauschii</i> : genome-wide identification and expression analysis under various abiotic stresses and light conditions. <i>Molecular Genetics and Genomics</i> , 2022, 297, 1689-1709.	1.0	5
3467	ATP-citrate lyase B (ACLB) negatively affects cell death and resistance to <i>Verticillium</i> wilt. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
3468	Genome-Wide Identification of Membrane-Bound Fatty Acid Desaturase Genes in Three Peanut Species and Their Expression in <i>Arachis hypogaea</i> during Drought Stress. <i>Genes</i> , 2022, 13, 1718.	1.0	3
3469	Genome-wide analysis of the JAZ subfamily of transcription factors and functional verification of BnC08.JAZ1-1 in <i>Brassica napus</i> . , 2022, 15, .		2
3471	Identification of thioredoxin genes and analysis of their expression under abiotic stresses in <i>Medicago truncatula</i> . <i>Acta Physiologiae Plantarum</i> , 2022, 44, .	1.0	1
3472	Systematic Characterization of <i>Brassica napus</i> HIR Gene Family Reveals a Positive Role of BnHIR2.7 in <i>Sclerotinia sclerotiorum</i> Resistance. <i>Horticulturae</i> , 2022, 8, 874.	1.2	2

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3473	Comprehensive Analysis of GRAS Gene Family and Their Expression under GA3, Drought Stress and ABA Treatment in <i>Larix kaempferi</i> . <i>Forests</i> , 2022, 13, 1424.	0.9	2
3474	Genome-wide identification and expression analysis of the GRAS transcription in eggplant ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.1	1
3475	Genome-Wide Identification of Histone Modification (HM) Gene Family and Their Expression Patterns Under Abiotic Stress and Different Developmental Stages of Tea ( <i>Camellia assamica</i> ). <i>Journal of Plant Growth Regulation</i> , 2023, 42, 2960-2982.	2.8	2
3476	Functional divergence of GLP genes between <i>G. barbadense</i> and <i>G. hirsutum</i> in response to <i>Verticillium dahliae</i> infection. <i>Genomics</i> , 2022, 114, 110470.	1.3	3
3477	Genome-Wide Identification and Analysis of the MADS-Box Gene Family in Almond Reveal Its Expression Features in Different Flowering Periods. <i>Genes</i> , 2022, 13, 1764.	1.0	1
3478	Insights to the superoxide dismutase genes and its roles in <i>Hevea brasiliensis</i> under abiotic stress. <i>3 Biotech</i> , 2022, 12, .	1.1	3
3480	Characterization of the CqCAMTA gene family reveals the role of CqCAMTA03 in drought tolerance. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	5
3481	Genome wide identification and characterization of nodulation related genes in <i>Arachis hypogaea</i> . <i>PLoS ONE</i> , 2022, 17, e0273768.	1.1	0
3482	Multimiomics reveals an essential role of long-distance translocation in regulating plant cadmium resistance and grain accumulation in allohexaploid wheat ( <i>Triticum aestivum</i> ). <i>Journal of Experimental Botany</i> , 2022, 73, 7516-7537.	2.4	7
3483	Genome-Wide Identification, Characterization, and Expression Analysis of Glutamate Receptor-like Gene (GLR) Family in Sugarcane. <i>Plants</i> , 2022, 11, 2440.	1.6	6
3484	GmbZIP152, a Soybean bZIP Transcription Factor, Confers Multiple Biotic and Abiotic Stress Responses in Plant. <i>International Journal of Molecular Sciences</i> , 2022, 23, 10935.	1.8	6
3485	Identification, Genomic Organization, and Comprehensive Expression Analysis Reveals the Implication of <i>Cicer arietinum</i> SKP1-like Genes in Abiotic Stress. <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	1
3486	Genome-wide analysis of serine carboxypeptidase-like protein (SCPL) family and functional validation of Gh_SCPL42 unchromosome conferring cotton <i>Verticillium der Verticillium</i> wilt stress in <i>Gossypium hirsutum</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	6
3487	Identification and Characterization of Malate Dehydrogenases in Tomato ( <i>Solanum lycopersicum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 10028.	1.8	8
3488	Identification and Functional Analysis of the Promoter of a Leucoanthocyanidin Reductase Gene from <i>Gossypium hirsutum</i> . <i>Molecular Biotechnology</i> , 0, , .	1.3	0
3489	Genome-Wide Identification and Characterization of Heat Shock Protein 20 Genes in Maize. <i>Life</i> , 2022, 12, 1397.	1.1	3
3490	The transcriptional coactivator CmMBF1c is required for waterlogging tolerance in <i>Chrysanthemum morifolium</i> . <i>Horticulture Research</i> , 2022, 9, .	2.9	5
3491	Classification and Expression Profile of the U-Box E3 Ubiquitin Ligase Enzyme Gene Family in Maize ( <i>Zea</i> ) Tj ETQq1 1 0.784314 rgBT /Ov	1.6	6

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3493	Comparative Analysis of Promoters of DREB2B Transcription Factor Genes in <i>Deschampsia antarctica</i> and Other Grasses. <i>Cytology and Genetics</i> , 2022, 56, 399-409.	0.2	2
3494	Genome-wide identification and expression analysis of the WRKY gene family in cabbage ( <i>Brassica</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.5	2
3495	Genome-Wide Identification and Molecular Evolution of the Magnesium Transporter (MGT) Gene Family in <i>Citrullus lanatus</i> and <i>Cucumis sativus</i> . <i>Agronomy</i> , 2022, 12, 2253.	1.3	16
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3499	Genome wide identification and characterization of MAPK genes reveals their potential in enhancing drought and salt stress tolerance in <i>Gossypium hirsutum</i> . <i>Journal of Cotton Research</i> , 2022, 5, .	1.0	5
3500	Identification, characterization, and expression profiling of the putative U-box E3 ubiquitin ligase gene family in <i>Sorghum bicolor</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
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3504	Computational insights into diverse aspects of glutathione S-transferase gene family in <i>Papaver somniferum</i> . <i>Journal of Plant Research</i> , 2022, 135, 823-852.	1.2	1
3505	Phylogenomic analysis of phenylalanine ammonia-lyase (PAL) multigene family and their differential expression analysis in wheat ( <i>Triticum aestivum</i> L.) suggested their roles during different stress responses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	12
3506	Systematic analysis of the pectin methylesterase gene family in <i>Nicotiana tabacum</i> and reveal their multiple roles in plant development and abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3507	Genome-wide identification and analysis of anthocyanin synthesis-related R2R3-MYB genes in <i>Cymbidium goeringii</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
3508	Genome-wide identification of AOX family genes in Moso bamboo and functional analysis of PeAOX1b_2 in drought and salinity stress tolerance. <i>Plant Cell Reports</i> , 2022, 41, 2321-2339.	2.8	5
3509	Evolutionary relationship analysis of <sc>STARD</sc> gene family and <sc> <i>VvSTARD5</i> </sc> improves tolerance of salt stress in transgenic tomatoes. <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	1
3510	Genome-wide identification and characterization of AP2/ERF gene superfamily during flower development in <i>Actinidia eriantha</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	12

#	ARTICLE	IF	CITATIONS
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3512	Genome-wide identification, characterization, and expression analysis of UDP-glycosyltransferase genes associated with secondary metabolism in alfalfa ( <i>Medicago sativa</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
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3516	Genome-wide analysis of OFP gene family in pepper ( <i>Capsicum annuum</i> L.). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
3517	Identification and Characterization of Trihelix Transcription Factors and Expression Changes during Flower Development in Pineapple. <i>Horticulturae</i> , 2022, 8, 894.	1.2	5
3518	Cold-inducible promoter-driven knockdown of <i>Brachypodium</i> antifreeze proteins confers freezing and phytopathogen susceptibility. <i>Plant Direct</i> , 2022, 6, .	0.8	0
3519	Insights into sweet potato SR proteins: from evolution to species-specific expression and alternative splicing. <i>Planta</i> , 2022, 256, .	1.6	3
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3522	Genome-wide characterization and sequence polymorphism analyses of cysteine-rich poly comb-like protein in <i>Glycine max</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
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3525	Two central circadian oscillators OsPRR59 and OsPRR95 modulate magnesium homeostasis and carbon fixation in rice. <i>Molecular Plant</i> , 2022, 15, 1602-1614.	3.9	14
3526	Chickpea Defensin Gene Family: Promising Candidates for Resistance Against Soil-Borne Chickpea Fungal Pathogens. <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	0
3527	Genome-wide identification and expression of TIFY family in cassava ( <i>Manihot esculenta</i> Crantz). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3528	Genome-wide characterization of soybean RALF genes and their expression responses to <i>Fusarium oxysporum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3530	Molecular characterization of the genome-wide BOR transporter family and their responses to boron conditions in common wheat ( <i>Triticum aestivum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3531	Genome-wide identification and analysis of LOX genes in soybean cultivar "Zhonghuang 13". <i>Frontiers in Genetics</i> , 0, 13, .	1.1	1

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3533	Pepper (&i&gt;Capsicum annum&i&gt;) xylogen-like arabinogalactan protein (XYLP) 1 and XYLP2 promote synthesis of lignin during stem development to cope with stresses. <i>Vegetable Research</i> , 2022, 2, 1-10.	0.2	2
3534	Molecular characterization of SUT Gene Family in Solanaceae with emphasis on expression analysis of pepper genes during development and stresses. <i>Bioengineered</i> , 2022, 13, 14780-14798.	1.4	2
3535	Genome-wide identification and analysis of the cytokinin oxidase/dehydrogenase (ckx) gene family in finger millet ( <i>Eleusine coracana</i> ). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
3536	Identification of Dof Transcription Factors in the Genome of <i>Rosa chinensis</i> . <i>Journal of the American Society for Horticultural Science</i> , 2022, 147, 239-248.	0.5	0
3537	Genome-Wide Identification and Salt Stress Response Analysis of the bZIP Transcription Factor Family in Sugar Beet. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11573.	1.8	3
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3539	Genome-Wide Investigation and Expression Analysis of the <i>Nitraria sibirica</i> Pall. CIPK Gene Family. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11599.	1.8	3
3540	Natural variation of Alfinâ€like family affects seed size and drought tolerance in rice. <i>Plant Journal</i> , 2022, 112, 1176-1193.	2.8	6
3541	Genome-wide identification and expression analysis of the bHLH gene family in cauliflower ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.4	2
3542	The Barley Heavy Metal Associated Isoprenylated Plant Protein HvFP1 Is Involved in a Crosstalk between the Leaf Development and Abscisic Acid-Related Drought Stress Responses. <i>Plants</i> , 2022, 11, 2851.	1.6	6
3543	Genome-Wide Analysis of the Almond AP2/ERF Superfamily and Its Functional Prediction during Dormancy in Response to Freezing Stress. <i>Biology</i> , 2022, 11, 1520.	1.3	5
3544	Deciphering the roles of tobacco MYB transcription factors in environmental stress tolerance. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
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3546	Molecular Characterization of bHLH Transcription Factor Family in Rose ( <i>Rosa chinensis</i> Jacq.) under <i>Botrytis cinerea</i> Infection. <i>Horticulturae</i> , 2022, 8, 989.	1.2	3
3547	Genome-Wide Identification, Expression and Interaction Analysis of GmSnRK2 and Type A PP2C Genes in Response to Abscisic Acid Treatment and Drought Stress in Soybean Plant. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13166.	1.8	3
3548	Sequence Characteristics and Expression Analysis of GhCIPK23 Gene in Upland Cotton ( <i>Gossypium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	0
3549	Heterologous Expression of the Apple MdbZIP26 Gene in <i>Arabidopsis thaliana</i> Improves Resistance to High Salinity and Drought Stress. <i>Agronomy</i> , 2022, 12, 2624.	1.3	0



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3551	Genome-Wide Identification and Characterization of the Oat ( <i>Avena sativa</i> L.) WRKY Transcription Factor Family. <i>Genes</i> , 2022, 13, 1918.	1.0	6
3552	Comparative Genomic and Expression Analysis Insight into Evolutionary Characteristics of PEBP Genes in Cultivated Peanuts and Their Roles in Floral Induction. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12429.	1.8	1
3553	Genome-wide identification and expression profiling of WUSCHEL-related homeobox (WOX) genes confer their roles in somatic embryogenesis, growth and abiotic stresses in banana. <i>3 Biotech</i> , 2022, 12, .	1.1	4
3554	Genome-wide identification of the rubber tree superoxide dismutase ( <i>SOD</i> ) gene family and analysis of its expression under abiotic stress. <i>PeerJ</i> , 0, 10, e14251.	0.9	7
3555	<i>Chrysanthemum</i> MAF2 regulates flowering by repressing gibberellin biosynthesis in response to low temperature. <i>Plant Journal</i> , 2022, 112, 1159-1175.	2.8	7
3556	Genome-wide identification and expression analysis of <i>SBP-box</i> gene family reveal their involvement in hormone response and abiotic stresses in <i>Chrysanthemum nankingense</i> . <i>PeerJ</i> , 0, 10, e14241.	0.9	2
3558	AtELP4 a subunit of the Elongator complex in <i>Arabidopsis</i> , mediates cell proliferation and dorsoventral polarity during leaf morphogenesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
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3561	Genome-Wide Identification of Maize Protein Arginine Methyltransferase Genes and Functional Analysis of ZmPRMT1 Reveal Essential Roles in <i>Arabidopsis</i> Flowering Regulation and Abiotic Stress Tolerance. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12793.	1.8	5
3562	The Function of BBX Gene Family under Multiple Stresses in <i>Nicotiana tabacum</i> . <i>Genes</i> , 2022, 13, 1841.	1.0	4
3563	Genome-wide identification and comparative analysis of CLE family in rapeseed and its diploid progenitors. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3564	LbMYB48 positively regulates salt gland development of <i>Limonium bicolor</i> and salt tolerance of plants. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
3565	Identification and Expression Analysis of the <i>Solanum tuberosum</i> StATG8 Family Associated with the WRKY Transcription Factor. <i>Plants</i> , 2022, 11, 2858.	1.6	2
3566	Genome-wide identification and characterization of NPF family reveals NtNPF6.13 involving in salt stress in <i>Nicotiana tabacum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
3567	The auxin response factor TaARF15-A1 negatively regulates senescence in common wheat ( <i>Triticum</i> ) Tj ETQq1 1,0,784314 rgBT /Ove 2,3 125		
3568	Characterization and expression analysis of MATEs in <i>Cannabis sativa</i> L. reveals genes involving in cannabinoid synthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3569	Genome-Wide Analysis and Expression Profiling of Glutathione Reductase Gene Family in Oat ( <i>Avena</i> ) Tj ETQq1 1 0.784314 rgBT /Ove 1.8 1		

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3572	Mapping and Validation of BrGOLDEN: A Dominant Gene Regulating Carotenoid Accumulation in Brassica rapa. International Journal of Molecular Sciences, 2022, 23, 12442.	1.8	3
3573	The genome of single-petal jasmine ( <i>Jasminum sambac</i> ) provides insights into heat stress tolerance and aroma compound biosynthesis. Frontiers in Plant Science, 0, 13, .	1.7	2
3574	Genome-Wide Identification and Expression Profiling Analysis of the Long-Chain Acyl-CoA Synthetases Reveal Their Potential Roles in Wheat Male Fertility. International Journal of Molecular Sciences, 2022, 23, 11942.	1.8	1
3575	Genome-Wide Identification, Cloning and Expression Profile of RanBP2-Type Zinc Finger Protein Genes in Tomato. Horticulturae, 2022, 8, 985.	1.2	1
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3577	Genome-Wide Identification of C2H2 ZFPs and Functional Analysis of BRZAT12 under Low-Temperature Stress in Winter Rapeseed ( <i>Brassica rapa</i> ). International Journal of Molecular Sciences, 2022, 23, 12218.	1.8	7
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3579	Low-acidity <i>ALUMINUM-DEPENDENT MALATE TRANSPORTER4</i> genotype determines malate content in cultivated jujube. Plant Physiology, 2023, 191, 414-427.	2.3	6
3580	Genome-wide analysis of MADS-box families and their expressions in flower organs development of pineapple ( <i>Ananas comosus</i> (L.) Merr.). Frontiers in Plant Science, 0, 13, .	1.7	3
3581	Genome-wide identification of biotin carboxyl carrier subunits of acetyl-CoA carboxylase in Brassica and their role in stress tolerance in oilseed Brassica napus. BMC Genomics, 2022, 23, .	1.2	9
3582	The Poplar ( <i>Populus trichocarpa</i> ) Dehydrin Gene PtrDHN-3 Enhances Tolerance to Salt Stress in Arabidopsis. Plants, 2022, 11, 2700.	1.6	4
3583	Genome-Wide Identification and Expression Analysis of Wall-Associated Kinase (WAK) Gene Family in Cannabis sativa L.. Plants, 2022, 11, 2703.	1.6	4
3584	Fasulyede Tuz ve Kuraklık Stresi Altında PIF Gen Ailesinin Genomunda Analizi ve Karakterizasyonu. Trkiye Tarımsal Arařtırmalar Dergisi, 0, , .	0.5	0
3586	WRKY transcription factor family in lettuce plant ( <i>Lactuca sativa</i> ): Genome-wide characterization, chromosome location, phylogeny structures, and expression patterns. PeerJ, 0, 10, e14136.	0.9	5
3587	Genome-wide identification of the mango CONSTANS (CO) family and functional analysis of two MICOL9 genes in transgenic Arabidopsis. Frontiers in Plant Science, 0, 13, .	1.7	7
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3590	Transcriptome analysis reveals pathogenesis-related gene 1 pathway against salicylic acid treatment in grapevine ( <i>Vitis vinifera</i> L). <i>Frontiers in Genetics</i> , 0, 13, .	1.1	7
3591	Genome-wide characterization of DcHsp90 gene family in carnation ( <i>Dianthus caryophyllus</i> L.) and functional analysis of DcHsp90-6 in heat tolerance. <i>Protoplasma</i> , 2023, 260, 807-819.	1.0	2
3592	Genome-Wide Identification and Characterization of the CCT Gene Family in Foxtail Millet ( <i>Setaria</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.0	5
3593	The miR156-Targeted SQUAMOSA PROMOTER BINDING PROTEIN (PmSBP) Transcription Factor Regulates the Flowering Time by Binding to the Promoter of SUPPRESSOR OF OVEREXPRESSION OF CO1 (PmSOC1) in <i>Prunus mume</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 11976.	1.8	2
3594	Pangenome-wide analysis of cyclic nucleotide-gated channel (CNGC) gene family in citrus Spp. Revealed their intraspecies diversity and potential roles in abiotic stress tolerance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	9
3595	Genome-Wide Identification and Expression Analysis of Senescence-Associated Genes in Grapevine ( <i>Vitis</i> ) Tj ETQq0 0 0 rgBT /Overlock 1	1.8	0
3596	Genome-wide identification of Aux/IAA gene family and their expression analysis in <i>Prunus mume</i> . <i>Frontiers in Genetics</i> , 0, 13, .	1.1	4
3597	Genome-Wide Analysis of the MYB-Related Transcription Factor Family in Pepper and Functional Studies of CaMYB37 Involvement in Capsaicin Biosynthesis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11667.	1.8	6
3598	Protein S-Acyl Transferase GhPAT27 Was Associated with Verticillium wilt Resistance in Cotton. <i>Plants</i> , 2022, 11, 2758.	1.6	1
3599	Genome-wide characterization of the UDP-glycosyltransferase gene family reveals their potential roles in leaf senescence in cotton. <i>International Journal of Biological Macromolecules</i> , 2022, 222, 2648-2660.	3.6	6
3600	Genome-Wide Analysis and Characterization of SABATH Gene Family in <i>Phaseolus vulgaris</i> Genotypes Subject to Melatonin under Drought and Salinity Stresses. <i>Plant Molecular Biology Reporter</i> , 2023, 41, 242-259.	1.0	5
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3603	Genome-wide analysis of polyamine biosynthesis genes in wheat reveals gene expression specificity and involvement of STRE and MYB-elements in regulating polyamines under drought. <i>BMC Genomics</i> , 2022, 23, .	1.2	9
3604	Genome-Wide Identification of ERF Transcription Factor Family and Functional Analysis of the Drought Stress-Responsive Genes in <i>Melilotus albus</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 12023.	1.8	4
3605	Comprehensive Identification and Analyses of the GRF Gene Family in the Whole-Genome of Four Juglandaceae Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12663.	1.8	4
3606	Genome-Wide Identification of Auxin-Responsive GH3 Gene Family in <i>Saccharum</i> and the Expression of ScGH3-1 in Stress Response. <i>International Journal of Molecular Sciences</i> , 2022, 23, 12750.	1.8	6

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3607	Genome-wide analysis of autophagy-related gene family and PagATG18a enhances salt tolerance by regulating ROS homeostasis in poplar. <i>International Journal of Biological Macromolecules</i> , 2023, 224, 1524-1540.	3.6	6
3608	Exploration of the genomic atlas of Dof transcription factor family across genus <i>Oryza</i> provides novel insights on rice breeding in changing climate. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3609	Metabolome and transcriptome analysis of terpene synthase genes and their putative role in floral aroma production in <i>Litchi chinensis</i> . <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	9
3610	Genome-Wide Identification and Expression Analysis of AMT and NRT Gene Family in Pecan ( <i>Carya</i> ) Tj ETQq1 1 0.784314 rgBT /Overlook Sciences, 2022, 23, 13314.	1.8	4
3611	Identification and comprehensive analysis of MIPSs in Rosaceae and their expression under abiotic stresses in rose ( <i>Rosa chinensis</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3612	The heat shock factor GhHsFA4a positively regulates cotton resistance to <i>Verticillium dahliae</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3613	Genome-Wide Identification and Characterization of USP Gene Family in Grapes ( <i>Vitis vinifera</i> L.). <i>Horticulturae</i> , 2022, 8, 1024.	1.2	2
3614	Genome-wide identification of RsGRAS gene family reveals positive role of RsSHRc gene in chilling stress response in radish ( <i>Raphanus sativus</i> L.). <i>Plant Physiology and Biochemistry</i> , 2022, 192, 285-297.	2.8	2
3615	Effect of the photoperiod on bud dormancy in <i>Liriodendron chinense</i> . <i>Journal of Plant Physiology</i> , 2022, 279, 153835.	1.6	0
3616	Genome Wide Characterization of CBL-CIPK Family Genes and Their Responsive Expression in <i>Rosa chinensis</i> . <i>Phyton</i> , 2023, 92, 349-368.	0.4	0
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3618	Genome-wide analysis of the CSN genes in land plants and their expression under various abiotic stress and phytohormone conditions in rice. <i>Gene</i> , 2023, 850, 146905.	1.0	2
3619	Molecular characterization of the GH3 family in alfalfa under abiotic stress. <i>Gene</i> , 2023, 851, 146982.	1.0	3
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3621	Blue light and its receptor white collar complex (FwWCC) regulates mycelial growth and fruiting body development in <i>Flammulina filiformis</i> . <i>Scientia Horticulturae</i> , 2023, 309, 111623.	1.7	2
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3631	Genome-wide identification of WD40 superfamily in <i>Cerasus humilis</i> and functional characteristics of ChTTG1. <i>International Journal of Biological Macromolecules</i> , 2023, 225, 376-388.	3.6	3
3632	Transcriptome and Regional Association Analyses Reveal the Effects of Oleosin Genes on the Accumulation of Oil Content in <i>Brassica napus</i> . <i>Plants</i> , 2022, 11, 3140.	1.6	5
3635	Evolution patterns of NBS genes in the genus <i>Dendrobium</i> and NBS-LRR gene expression in <i>D. officinale</i> by salicylic acid treatment. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
3636	Glandular trichome specificity of menthol biosynthesis pathway gene promoters from <i>Mentha piperita</i> . <i>Planta</i> , 2022, 256, .	1.6	3
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3641	Genome-Wide Identification of the SAUR Gene Family in Wax Gourd ( <i>Benincasa hispida</i> ) and Functional Characterization of BhSAUR60 during Fruit Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14021.	1.8	3
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3647	Comprehensive Genomic Survey, Structural Classification, and Expression Analysis of WRKY Transcription Factor Family in <i>Rhododendron simsii</i> . <i>Plants</i> , 2022, 11, 2967.	1.6	2
3648	Physiological Responses of Cigar Tobacco Crop to Nitrogen Deficiency and Genome-Wide Characterization of the NtNPF Family Genes. <i>Plants</i> , 2022, 11, 3064.	1.6	2
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3651	Genome-wide analysis of MADS-box gene family in kiwifruit ( <i>Actinidia chinensis</i> var. <i>chinensis</i> ) and their potential role in floral sex differentiation. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	5
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3654	Orphan Genes in Crop Improvement: Enhancing Potato Tuber Protein without Impacting Yield. <i>Plants</i> , 2022, 11, 3076.	1.6	5
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3658	Genome-wide identification and characterization profile of phosphatidyl ethanolamine-binding protein family genes in carrot. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
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3660	Genome-wide identification and expression analysis of PIN gene family under phytohormone and abiotic stresses in <i>Vitis Vinifera</i> L.. <i>Physiology and Molecular Biology of Plants</i> , 2022, 28, 1905-1919.	1.4	3
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3662	Genome-Wide Identification, Characterization, and Expression Analysis of CHS Gene Family Members in <i>Chrysanthemum nankingense</i> . <i>Genes</i> , 2022, 13, 2145.	1.0	3
3663	Genome-Wide Identification and Characterization of the SBP Gene Family in Passion Fruit ( <i>Passiflora</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	1.8	5

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3665	In-silico analysis of WRKY Transcription Factors gene family in healthy and malformed stages of mango ( <i>Mangifera indica</i> ). , 2019, 89, .		0
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3667	Multicopper oxidases GbAO and GbSKS are involved in the <i>Verticillium dahliae</i> resistance in <i>Gossypium barbadense</i> . <i>Journal of Plant Physiology</i> , 2023, 280, 153887.	1.6	3
3668	Identification of bHLH family genes in <i>Agaricus bisporus</i> and transcriptional regulation of arginine catabolism-related genes by <i>AbbHLH1</i> after harvest. <i>International Journal of Biological Macromolecules</i> , 2023, 226, 496-509.	3.6	3
3669	Identification and characterization of WAK gene family in <i>Saccharum</i> and the negative roles of <i>ScWAK1</i> under the pathogen stress. <i>International Journal of Biological Macromolecules</i> , 2023, 224, 1-19.	3.6	9
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3671	The chloroplast GATA-motif of <i>Mahonia bealei</i> participates in alkaloid-mediated photosystem inhibition during dark to light transition. <i>Journal of Plant Physiology</i> , 2023, 280, 153894.	1.6	5
3672	Characterization and evolutionary analysis of phosphate starvation response genes in wheat and other major gramineous plants. <i>International Journal of Biological Macromolecules</i> , 2023, 225, 63-78.	3.6	0
3673	Transcriptional and post-transcriptional controls for tuning gene expression in plants. <i>Current Opinion in Plant Biology</i> , 2023, 71, 102315.	3.5	10
3674	The allene oxide synthase gene family in sugarcane and its involvement in disease resistance. <i>Industrial Crops and Products</i> , 2023, 192, 116136.	2.5	9
3675	Grape BES1 transcription factor gene <i>VvBES1-3</i> confers salt tolerance in transgenic <i>Arabidopsis</i> . <i>Gene</i> , 2023, 854, 147059.	1.0	2
3676	Genome-wide identification, characterization, and expression profile of NBS-LRR gene family in sweet orange ( <i>Citrus sinensis</i> ). <i>Gene</i> , 2023, 854, 147117.	1.0	10
3677	<i>ChPAS1</i> , a bHLH transcription factor in upland cotton ( <i>Gossypium hirsutum</i> ), positively regulates <i>Verticillium dahliae</i> resistance. <i>Industrial Crops and Products</i> , 2023, 192, 116077.	2.5	0
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3679	Decipher the molecular evolution and expression patterns of Cupin family genes in oilseed rape. <i>International Journal of Biological Macromolecules</i> , 2023, 227, 437-452.	3.6	2
3680	Genome-wide analysis of the Early Flowering 4 (ELF4) gene family in short-juvenile persimmon ( <i>Diospyros deyangensis</i> ) and its role of <i>DdELF4</i> during flowering control. <i>Scientia Horticulturae</i> , 2023, 310, 111736.	1.7	1
3681	Comparative phylogenomic analysis of 5'UTR-regulatory elements (CREs) of miR160 gene family in diploid and allopolyploid cotton ( <i>Gossypium</i> ). <i>Gene Reports</i> , 2023, 30, 101721.	0.4	0

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3684	Genome Wide Analysis and Characterization of NPR-like Gene Family of <i>Phaseolus vulgaris</i> L. , 0, , .		1
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3686	Genome-wide survey of Calcium-Dependent Protein Kinases (CPKs) in five Brassica species and identification of CPKs induced by <i>Plasmodiophora brassicae</i> in <i>B. rapa</i> , <i>B. oleracea</i> , and <i>B. napus</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
3687	Genome-Wide Identification and Analysis of FKBP Gene Family in Wheat ( <i>Triticum aestivum</i> ). <i>International Journal of Molecular Sciences</i> , 2022, 23, 14501.	1.8	1
3688	Identification, Classification and Characterization Analysis of FBXL Gene in Cotton. <i>Genes</i> , 2022, 13, 2194.	1.0	1
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3690	Genome-wide identification, molecular evolution and expression analysis of the non-specific lipid transfer protein (nsLTP) family in <i>Setaria italica</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	4
3691	Genome-wide identification of calcium-dependent protein kinases (CDPKs) in pear ( <i>Pyrus bretschneideri</i> ) Tj ETQq1 1 0.784314 rgBT /Ov Environment and Biotechnology, 2022, 63, 903-915.	0.7	2
3692	Characterization and response of two potato receptor-like kinases to cyst nematode infection. <i>Plant Signaling and Behavior</i> , 2022, 17, .	1.2	1
3693	Identification and expression profiles of xylogen-like arabinogalactan protein (XYLP) gene family in <i>Phyllostachys edulis</i> in different developmental tissues and under various abiotic stresses. <i>International Journal of Biological Macromolecules</i> , 2023, 227, 1098-1118.	3.6	1
3694	Genome-Wide Identification and Expression Profile of the HD-Zip Transcription Factor Family Associated with Seed Germination and Abiotic Stress Response in <i>Miscanthus sinensis</i> . <i>Genes</i> , 2022, 13, 2256.	1.0	1
3695	Genome-wide identification and expression analysis of the GRAS gene family in <i>Dendrobium chrysotoxum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	7
3696	Mining key genes related to root morphogenesis through genome-wide identification and expression analysis of RR gene family in citrus. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3697	Genome-wide identification, comprehensive characterization of transcription factors, cis-regulatory elements, protein homology, and protein interaction network of DREB gene family in <i>Solanum lycopersicum</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3698	The $\beta$ -1-pyrroline-5-carboxylate synthetase family performs diverse physiological functions in stress responses in pear ( <i>Pyrus betulifolia</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3699	Genome-wide identification and analysis of LEA_2 gene family in alfalfa ( <i>Medicago sativa</i> L.) under aluminum stress. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1



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3700	Genome-Wide Identification and Expression Analysis of the CAD Gene Family in Walnut ( <i>Juglans regia</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 T	0.8	0
3701	Identification, evolution, and expression analysis of OsBSK gene family in <i>Oryza sativa</i> Japonica. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
3702	Unleashing the power within short-read RNA-seq for plant research: Beyond differential expression analysis and toward regulomics. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3703	Genome-wide characterization and expression analysis of the HAK gene family in response to abiotic stresses in <i>Medicago</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	1
3704	Investigation and Expression Analysis of R2R3-MYBs and Anthocyanin Biosynthesis-Related Genes during Seed Color Development of Common Bean ( <i>Phaseolus vulgaris</i> ). <i>Plants</i> , 2022, 11, 3386.	1.6	4
3705	Comprehensive Analysis of GASA Family Members in the Peanut Genome: Identification, Characterization, and Their Expressions in Response to Pod Development. <i>Agronomy</i> , 2022, 12, 3067.	1.3	2
3706	Genome-Wide Identification of AP2/ERF Superfamily Genes in <i>Juglans mandshurica</i> and Expression Analysis under Cold Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15225.	1.8	3
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3708	Identification of the Xyloglucan Endotransglycosylase/Hydrolase (XTH) Gene Family Members Expressed in <i>Boehmeria nivea</i> in Response to Cadmium Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16104.	1.8	4
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3710	Jasmonate Positively Regulates Cold Tolerance by Promoting ABA Biosynthesis in Tomato. <i>Plants</i> , 2023, 12, 60.	1.6	11
3711	Identification, Characterization and Expression Profiling of the RS Gene Family during the Withering Process of White Tea in the Tea Plant ( <i>Camellia sinensis</i> ) Reveal the Transcriptional Regulation of CsRS8. <i>International Journal of Molecular Sciences</i> , 2023, 24, 202.	1.8	2
3712	Genome-Wide Analysis of the Rab Gene Family in <i>Melilotus albus</i> Reveals Their Role in Salt Tolerance. <i>International Journal of Molecular Sciences</i> , 2023, 24, 126.	1.8	2
3713	The NF-Y Transcription Factor Family in Watermelon: Re-Characterization, Assembly of CINP-Y Complexes, Hormone- and Pathogen-Inducible Expression and Putative Functions in Disease Resistance. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15778.	1.8	0
3714	Comprehensive analysis of the carboxylesterase gene reveals that NtCXE22 regulates axillary bud growth through strigolactone metabolism in tobacco. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3715	Genome-Wide Identification and Expression Analysis of SWEET Family Genes in Sweet Potato and Its Two Diploid Relatives. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15848.	1.8	8
3716	Genome-wide identification and expression pattern analysis of quinoa BBX family. <i>PeerJ</i> , 0, 10, e14463.	0.9	1
3717	Genome-Wide Identification and Expression Pattern of the GRAS Gene Family in <i>Pitaya</i> ( <i>Selenicereus</i> ) Tj ETQq1 1 0,784314 rgBT /Overlo	1.3	8

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3718	In silico Analysis of OsNRT2.3 Reveals OsAMT1.3, OsZIFL9, OsbZIP27, and OsIRT1 as Potential Drought-related Genes During Nitrogen Use Efficiency in <i>Oryza sativa</i> L.. <i>Pertanika Journal of Science and Technology</i> , 2022, 46, .	0.1	0
3719	CmHY5 functions in apigenin biosynthesis by regulating flavone synthase II expression in <i>chrysanthemum</i> flowers. <i>Planta</i> , 2023, 257, .	1.6	0
3720	Genome-wide investigation on metal tolerance protein (MTP) genes in leguminous plants: <i>Glycine max</i> , <i>Medicago truncatula</i> , and <i>Lotus japonicus</i> . <i>Acta Physiologiae Plantarum</i> , 2023, 45, .	1.0	4
3721	Caffeoyl-CoA 3-O-methyltransferase gene family in jute: Genome-wide identification, evolutionary progression and transcript profiling under different quandaries. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3722	Genome-wide analysis of hyperosmolality-gated calcium-permeable channel (OSCA) family members and their involvement in various osmotic stresses in <i>Brassica napus</i> . <i>Gene</i> , 2023, 856, 147137.	1.0	2
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3724	Identification and Functional Characterization of the RcFAH12 Promoter from Castor Bean in <i>Arabidopsis thaliana</i> . <i>Separations</i> , 2023, 10, 2.	1.1	0
3725	Genome-Wide Identification of <i>Brassica napus</i> PEN1-LIKE Genes and Their Expression Profiling in Insect-Susceptible and Resistant Cultivars. <i>Current Issues in Molecular Biology</i> , 2022, 44, 6385-6396.	1.0	0
3726	Genome-Wide Analysis of Specific PFR2R3-MYB Genes Related to <i>Paulownia Witchesâ€™ Broom</i> . <i>Genes</i> , 2023, 14, 7.	1.0	1
3727	Evolution and functional analysis of the GRAS family genes in six Rosaceae species. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	3
3728	Genome-Wide Characterization and Function Analysis of ZmERD15 Genesâ€™ Response to Saline Stress in <i>Zea mays</i> L.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15721.	1.8	0
3729	Genome-Wide Identification of Wheat KNOX Gene Family and Functional Characterization of TaKNOX14-D in Plants. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15918.	1.8	4
3730	Genome-wide identification and expression analysis of <i>SlRR</i> genes in response to abiotic stresses in tomato. <i>Plant Biology</i> , 0, , .	1.8	0
3731	Transcription factor TaGAMYB from wheat ( <i>Triticum aestivum</i> L.) regulates flowering time and fertility in transgenic <i>Arabidopsis thaliana</i> . <i>Planta</i> , 2023, 257, .	1.6	1
3732	Genome-Wide Characterization of Trehalose-6-Phosphate Synthase Gene Family of <i>Brassica napus</i> and Potential Links with Agronomic Traits. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15714.	1.8	2
3733	Discovery of cadmium-tolerant biomacromolecule (StCAX1/4 transportproteins) in potato and its potential regulatory relationship with WRKY transcription factors. <i>International Journal of Biological Macromolecules</i> , 2023, 228, 385-399.	3.6	7
3734	Genome-Wide Identification and Expression Analysis of Kinesin Family in Barley ( <i>Hordeum vulgare</i> ). <i>Genes</i> , 2022, 13, 2376.	1.0	2
3735	Identification of WRKYs using in silico tools for unraveling the modulation during abiotic stress response in <i>Tef</i> [ <i>Eragrostis tef</i> (Zucc.) Trotter] a super grain. <i>Genetic Resources and Crop Evolution</i> , 0, , .	0.8	0

#	ARTICLE	IF	CITATIONS
3736	Genome-wide survey of catalase genes in <i>Brassica rapa</i> , <i>Brassica oleracea</i> , and <i>Brassica napus</i> : identification, characterization, molecular evolution, and expression profiling of BnCATs in response to salt and cadmium stress. <i>Protoplasma</i> , 2023, 260, 899-917.	1.0	4
3737	Characterization of a Stress-Enhanced Promoter from the Grass Halophyte, <i>Spartina alterniflora</i> L.. <i>Biology</i> , 2022, 11, 1828.	1.3	3
3738	Genome-wide analysis of the TCP gene family and their expression pattern in <i>Cymbidium goeringii</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
3739	Identification of Peanut AhMYB44 Transcription Factors and Their Multiple Roles in Drought Stress Responses. <i>Plants</i> , 2022, 11, 3522.	1.6	4
3740	Beta-galactosidase gene family genome-wide identification and expression analysis of members related to fruit softening in melon ( <i>Cucumis melo</i> L.). <i>BMC Genomics</i> , 2022, 23, .	1.2	4
3741	Genome-Wide Identification of AMT2-Type Ammonium Transporters Reveal That CsAMT2.2 and CsAMT2.3 Potentially Regulate NH <sub>4</sub> <sup>+</sup> Absorption among Three Different Cultivars of <i>Camellia sinensis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 15661.	1.8	4
3742	Transcriptional Regulation of zma-MIR528a by Action of Nitrate and Auxin in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15718.	1.8	2
3743	CRISPR/Cas9-induced modification of the conservative promoter region of VRN-A1 alters the heading time of hexaploid bread wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
3744	SbMYB3 transcription factor promotes root-specific flavone biosynthesis in <i>Scutellaria baicalensis</i> . <i>Horticulture Research</i> , 2023, 10, .	2.9	7
3745	Genome-wide characterization of the NLR gene family in tomato ( <i>Solanum lycopersicum</i> ) and their relatedness to disease resistance. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	3
3746	Genome-wide identification and characterization of <i>NHL</i> gene family in response to alkaline stress, ABA and MEJA treatments in wild soybean ( <i>Glycine soja</i> ). <i>PeerJ</i> , 0, 10, e14451.	0.9	4
3747	Genome-Wide Survey and Expression Analysis of the Basic Leucine Zipper (bZIP) Gene Family in Eggplant ( <i>Solanum melongena</i> L.). <i>Horticulturae</i> , 2022, 8, 1153.	1.2	0
3748	Genome-Wide Identification and Expression Analysis of TUA and TUB Genes in Wheat ( <i>Triticum aestivum</i> ) Tj ETQq0,0,0 rgBT /Overlock 1	1.6	1
3749	Evolutionary Relationships and Divergence of Filamin Gene Family Involved in Development and Stress in Cotton ( <i>Gossypium hirsutum</i> L.). <i>Genes</i> , 2022, 13, 2313.	1.0	0
3750	An uncharacterized gene Lb1G04794 from <i>Limonium bicolor</i> promotes salt tolerance and trichome development in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
3751	Identification and Functional Analysis of Transcription Factor NF-Y Family during Flower Bud Dormancy in <i>Prunus mume</i> . <i>Horticulturae</i> , 2022, 8, 1180.	1.2	0
3752	Genome-wide identification, characterization, and genetic diversity of CCR gene family in <i>Dalbergia odorifera</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3753	In Silico Genome-Wide Mining and Analysis of Terpene Synthase Gene Family in <i>Hevea Brasiliensis</i> . <i>Biochemical Genetics</i> , 2023, 61, 1185-1209.	0.8	1

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3756	CRISPR/Cas9 Mutant Rice Ospm12 Involved in Growth, Cell Wall Development, and Response to Phytohormone and Heavy Metal Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 16082.	1.8	5
3758	Genome-Wide Identification of SnRK1 Catalytic Î± Subunit and FLZ Proteins in <i>Glycyrrhiza inflata</i> Bat. Highlights Their Potential Roles in Licorice Growth and Abiotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2023, 24, 121.	1.8	7
3759	Systematic genome-wide and expression analysis of RNA-directed DNA methylation pathway genes in grapes predicts their involvement in multiple biological processes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3760	CcMYB12 Positively Regulates Flavonoid Accumulation during Fruit Development in <i>Carya cathayensis</i> and Has a Role in Abiotic Stress Responses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15618.	1.8	4
3761	Genome-wide identification and comprehensive analysis of tubby-like protein gene family in multiple crops. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3762	Bracelet salt glands of the recretahalophyte <i>Limonium bicolor</i> : Distribution, morphology, and induction. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 950-966.	4.1	9
3763	Genome-wide identification of sucrose non-fermenting-1-related protein kinase genes in maize and their responses to abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3764	Identification and Evolutionary Analysis of the GOLDEN 2-LIKE Gene Family in Foxtail Millet. <i>Tropical Plant Biology</i> , 0, , .	1.0	0
3765	Multi-locus genome-wide association studies reveal genomic regions and putative candidate genes associated with leaf spot diseases in African groundnut ( <i>Arachis hypogaea</i> L.) germplasm. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3767	Postharvest chilling diminishes melon flavor via effects on volatile acetate ester biosynthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3768	<i>PhAAT1</i> , encoding an anthocyanin acyltransferase, is transcriptionally regulated by <i>PhAN2</i> in petunia. <i>Physiologia Plantarum</i> , 0, , .	2.6	1
3769	Genome-wide identification of acyl-CoA binding proteins and possible functional prediction in legumes. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	2
3770	Genome-wide identification and expression analysis of metal tolerance protein (MTP) gene family in soybean ( <i>Glycine max</i> ) under heavy metal stress. <i>Molecular Biology Reports</i> , 2023, 50, 2975-2990.	1.0	12
3771	In silico analysis of steviol glycoside biosynthesis related genes of <i>Helianthus annuus</i> shows its potential for sweetener production. <i>Genetic Resources and Crop Evolution</i> , 0, , .	0.8	1
3772	Genome-Wide Identification and Analysis of the Maize Serine Peptidase S8 Family Genes in Response to Drought at Seedling Stage. <i>Plants</i> , 2023, 12, 369.	1.6	2
3773	Genome-wide characterization, chromosome localization, and expression profile analysis of poplar nonspecific lipid transfer proteins. <i>International Journal of Biological Macromolecules</i> , 2023, , 123226.	3.6	2
3774	Genome-wide identification and characterization of LcCCR13 reveals its potential role in lignin biosynthesis in <i>Liriodendron chinense</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3775	Promoter of Nitrate Reductase Gene Behaves Differently Under Salinity Stress in Contrasting Rice Genotype. <i>Journal of Plant Growth Regulation</i> , 0, , .	2.8	0

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3776	Genome-Wide Identification and Expression Analysis of WRKY Transcription Factors in <i>Siraitia siamensis</i> . <i>Plants</i> , 2023, 12, 288.	1.6	7
3777	In silico analysis of NAC gene family in the mangrove plant <i>Avicennia marina</i> provides clues for adaptation to intertidal habitats. <i>Plant Molecular Biology</i> , 2023, 111, 393-413.	2.0	2
3778	Overexpression of a DUF740 family gene (LOC_Os04g59420) imparts enhanced climate resilience through multiple stress tolerance in rice. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
3779	Identification of Alfalfa SPL gene family and expression analysis under biotic and abiotic stresses. <i>Scientific Reports</i> , 2023, 13, .	1.6	9
3780	Systematic identification and characterization of the soybean ( <i>Glycine max</i> ) B-box transcription factor family. <i>Biotechnology and Biotechnological Equipment</i> , 2023, 37, 104-116.	0.5	1
3781	Silencing of GhORP_A02 enhances drought tolerance in <i>Gossypium hirsutum</i> . <i>BMC Genomics</i> , 2023, 24, .	1.2	2
3782	Genome-wide identification and expression analysis of calmodulin-like proteins in cucumber. <i>PeerJ</i> , 0, 11, e14637.	0.9	0
3783	Genome-Wide Identification and Analysis of NF-Y Gene Family Reveal Its Potential Roles in Stress-Resistance in <i>Chrysanthemum</i> . <i>Horticulturae</i> , 2023, 9, 70.	1.2	2
3784	The class B heat shock factor HSF1 regulates heat tolerance in grapevine. <i>Horticulture Research</i> , 2023, 10, .	2.9	6
3785	Evolutionary analysis and expression profiling of the <i>HSP70</i> gene family in response to abiotic stresses in tomato ( <i>Solanum lycopersicum</i> ). <i>Science Progress</i> , 2023, 106, 003685042211488.	1.0	1
3786	Comprehensive Analysis of Major Latex-Like Protein Family Genes in Cucumber ( <i>Cucumis sativus</i> L.) and Their Potential Roles in Phytophthora Blight Resistance. <i>International Journal of Molecular Sciences</i> , 2023, 24, 784.	1.8	5
3787	Genome-Wide Identification and Expression Analysis of the Xyloglucan Endotransglucosylase/Hydrolase Gene Family in Sweet Potato [ <i>Ipomoea batatas</i> (L.) Lam]. <i>International Journal of Molecular Sciences</i> , 2023, 24, 775.	1.8	8
3788	The functional analysis of sugar transporter proteins in sugar accumulation and pollen tube growth in pummelo ( <i>Citrus grandis</i> ). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
3789	Characterization and Expression Analysis of the UDP Glycosyltransferase Family in Pomegranate ( <i>Punica granatum</i> L.). <i>Horticulturae</i> , 2023, 9, 119.	1.2	2
3790	Genome-Wide Identification and Expression Analysis Reveals Roles of the NRAMP Gene Family in Iron/Cadmium Interactions in Peanut. <i>International Journal of Molecular Sciences</i> , 2023, 24, 1713.	1.8	10
3792	NF-YB family transcription factors in <i>Arabidopsis</i> : Structure, phylogeny, and expression analysis in biotic and abiotic stresses. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	3
3793	Genome-wide identification and analysis of wheat LRR-RLK family genes following Chinese wheat mosaic virus infection. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
3794	Genome-wide identification of HD-ZIP gene family and screening of genes related to prickly development in <i>Zanthoxylum armatum</i> . <i>Plant Genome</i> , 2023, 16, .	1.6	3

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3795	Genome-Wide Identification of 14-3-3 gene family reveals their diverse responses to abiotic stress by interacting with StABI5 in Potato ( <i>Solanum tuberosum</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3796	Genome-wide identification and expression analysis of AUX/LAX family genes in Chinese hickory ( <i>Carya</i> ) Tj ETQq1 1,0,784314 <sub>2</sub> rgBT /Ome	1.7	1
3797	Functional Characterization of TkSRPP Promoter in Response to Hormones and Wounding Stress in Transgenic Tobacco. <i>Plants</i> , 2023, 12, 252.	1.6	4
3798	Genome-wide identification and expression profile analysis of SWEET genes in Chinese jujube. <i>PeerJ</i> , 0, 11, e14704.	0.9	5
3799	Genome-Wide Analysis of Aquaporin Gene Family in <i>Triticum turgidum</i> and Its Expression Profile in Response to Salt Stress. <i>Genes</i> , 2023, 14, 202.	1.0	24
3800	Genome-wide analysis of the <i>Populus trichocarpa</i> laccase gene family and functional identification of PtrLAC23. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3801	Genome-Wide Identification and Characterization of the GRF Gene Family in <i>Melastoma dodecandrum</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 1261.	1.8	5
3802	Genome-wide identification and expression analysis of two-component system genes in sweet potato ( <i>Ipomoea batatas</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
3803	Genome-Wide Identification and Expression Analysis of Response Regulators Family Genes in Chinese Hickory ( <i>Carya cathayensis</i> ) Suggests Their Potential Roles during Grafting. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 5099-5115.	2.8	2
3804	Genome wide identification of GDSL gene family explores a novel GhirGDSL26 gene enhancing drought stress tolerance in cotton. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
3805	Annotation of the <i>Turnera subulata</i> (Passifloraceae) Draft Genome Reveals the S-Locus Evolved after the Divergence of Turneroideae from Passifloroideae in a Stepwise Manner. <i>Plants</i> , 2023, 12, 286.	1.6	2
3806	The NtSPL Gene Family in <i>Nicotiana tabacum</i> : Genome-Wide Investigation and Expression Analysis in Response to Cadmium Stress. <i>Genes</i> , 2023, 14, 183.	1.0	4
3807	Cloning of the promoter of rice brown planthopper feedingâ€¦inducible gene <sc><i>OsTPS31</i></sc> and identification of related <sc><i>cis</i></sc>â€¦regulatory elements. <i>Pest Management Science</i> , 2023, 79, 1809-1819.	1.7	2
3808	Genome-wide characterization of the inositol transporters gene family in <i>Populus</i> and functional characterization of PtINT1b in response to salt stress. <i>International Journal of Biological Macromolecules</i> , 2023, 228, 197-206.	3.6	1
3809	Unravelling structural, functional, evolutionary and genetic basis of SWEET transporters regulating abiotic stress tolerance in maize. <i>International Journal of Biological Macromolecules</i> , 2023, 229, 539-560.	3.6	4
3810	Genome-wide analysis of wheat Di19 gene family and functional analysis of TaDi19-7 in transgenic <i>Arabidopsis</i> . <i>Environmental and Experimental Botany</i> , 2023, 206, 105192.	2.0	0
3811	Genome-wide analysis of the 6B-INTERACTING PROTEIN1 gene family with functional characterization of MdSIP1-2 in <i>Malus domestica</i> . <i>Plant Physiology and Biochemistry</i> , 2023, 195, 89-100.	2.8	4
3812	Squalene synthase in plants â€œ Functional intricacy and evolutionary divergence while retaining a core catalytic structure. <i>Plant Gene</i> , 2023, 33, 100403.	1.4	2

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3813	Molecular characterization of a chalcone synthase gene RhCHS from <i>Rhododendron</i> × <i>Hybridum</i> Hort. Gene, 2023, 857, 147176.	1.0	2
3814	Gnawing pressure led to the expansion of JAZ genes in angiosperms. International Journal of Biological Macromolecules, 2023, 230, 123165.	3.6	0
3815	Arsenic-induced galactinol synthase1 gene, AtGolS1, provides arsenic stress tolerance in <i>Arabidopsis thaliana</i> . Environmental and Experimental Botany, 2023, 207, 105217.	2.0	7
3816	Identification of HubHLH family and key role of HubHLH159 in betalain biosynthesis by activating the transcription of HuADH1, HuCYP76AD1-1, and HuDODA1 in pitaya. Plant Science, 2023, 328, 111595.	1.7	5
3817	Genome wide analysis of BREVIS RADIX gene family from wheat ( <i>Triticum aestivum</i> ): A conserved gene family differentially regulated by hormones and abiotic stresses. International Journal of Biological Macromolecules, 2023, 232, 123081.	3.6	4
3818	Genome-wide studies of PAL genes in sorghum and their responses to aphid infestation. Scientific Reports, 2022, 12, .	1.6	6
3819	The nuclear effector ArPEC25 from the necrotrophic fungus <i>Ascochyta rabiei</i> targets the chickpea transcription factor Ca <sup>2+</sup> LIM1a and negatively modulates lignin biosynthesis, increasing host susceptibility. Plant Cell, 2023, 35, 1134-1159.	3.1	12
3820	Genome-Wide Identification and Expression Analysis of the KCS Gene Family in Yellow Horn Reveal Their Putative Function on Abiotic Stress Responses and Wax Accumulation. Horticulturae, 2023, 9, 25.	1.2	3
3821	Genome-Wide Identification and Characterization of the AlkB Gene Family in Sweet Orange ( <i>Citrus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	1
3822	Analysis of the C2H2 Gene Family in Maize ( <i>Zea mays</i> L.) under Cold Stress: Identification and Expression. Life, 2023, 13, 122.	1.1	3
3823	Full-Length Transcriptome Characterization and Functional Analysis of Pathogenesis-Related Proteins in <i>Lilium</i> Oriental Hybrid "Sorbonne"™ Infected with <i>Botrytis elliptica</i> . International Journal of Molecular Sciences, 2023, 24, 425.	1.8	1
3824	Genome-wide identification of the PYL gene family and expression of PYL genes under abiotic stresses in Chinese cabbage. Biologia Plantarum, 0, 66, 322-332.	1.9	0
3825	Genome-Wide Analysis of the AAAP Gene Family in <i>Populus</i> and Functional Analysis of PsAAAP21 in Root Growth and Amino Acid Transport. International Journal of Molecular Sciences, 2023, 24, 624.	1.8	1
3826	Functional Characterization of the Cystine-Rich-Receptor-like Kinases (CRKs) and Their Expression Response to <i>Sclerotinia sclerotiorum</i> and Abiotic Stresses in <i>Brassica napus</i> . International Journal of Molecular Sciences, 2023, 24, 511.	1.8	2
3827	Genome-Wide Identification and Analysis of the GRAS Transcription Factor Gene Family in <i>Theobroma cacao</i> . Genes, 2023, 14, 57.	1.0	3
3828	Characteristics and Expression Analysis of Invertase Gene Family in Common Wheat ( <i>Triticum aestivum</i> ) Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 5	1.0	4
3829	Genome-Wide Identification of Kiwifruit SGR Family Members and Functional Characterization of SGR2 Protein for Chlorophyll Degradation. International Journal of Molecular Sciences, 2023, 24, 1993.	1.8	3
3831	Genome-wide identification of germin-like proteins in peanut ( <i>Arachis hypogea</i> L.) and expression analysis under different abiotic stresses. Frontiers in Plant Science, 0, 13, .	1.7	2

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3832	Genome-wide identification, evolutionary and expression analysis of the cyclin-dependent kinase gene family in peanut. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
3833	Genome-wide identification of the MATE gene family and functional characterization of PbrMATE9 related to anthocyanin in pear. <i>Horticultural Plant Journal</i> , 2023, 9, 1079-1094.	2.3	3
3834	Genome-wide characterization of the PP2C gene family in peanut ( <i>Arachis hypogaea</i> L.) and the identification of candidate genes involved in salinity-stress response. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	8
3835	Genome-Wide Identification, Characterization, and Expression Analysis of the U-Box Gene Family in <i>Punica granatum</i> L.. <i>Agronomy</i> , 2023, 13, 332.	1.3	1
3836	Genome wide identification and evolutionary analysis of vat like NBS-LRR genes potentially associated with resistance to aphids in cotton. <i>Genetica</i> , 0, , .	0.5	0
3837	Genome-wide identification of the class III peroxidase gene family of sugarcane and its expression profiles under stresses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
3838	Genome-wide identification and expression reveal the involvement of the FCS-like zinc finger (FLZ) gene family in <i>Gossypium hirsutum</i> at low temperature. <i>PeerJ</i> , 0, 11, e14690.	0.9	1
3839	Grapevine-Associated Lipid Signalling Is Specifically Activated in an Rpv3 Background in Response to an Aggressive <i>P. viticola</i> Pathovar. <i>Cells</i> , 2023, 12, 394.	1.8	1
3840	PyuARF16/33 Are Involved in the Regulation of Lignin Synthesis and Rapid Growth in <i>Populus yunnanensis</i> . <i>Genes</i> , 2023, 14, 278.	1.0	3
3841	Characterization of the 1-Deoxy-D-xylulose 5-Phosphate synthase Genes in <i>Toona ciliata</i> Suggests Their Role in Insect Defense. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2339.	1.8	0
3842	Genome-wide identification of BONZAI (BON) genes in <i>Glycine max</i> L. and their regulated expression patterns under saline environment. <i>Current Plant Biology</i> , 2023, 33, 100273.	2.3	3
3843	Decoding allelic diversity, transcript variants and transcriptional complexity of CENH3 gene in <i>Brassica oleracea</i> var. <i>botrytis</i> . <i>Protoplasma</i> , 0, , .	1.0	0
3844	Genome-Wide Identification and Expression Analysis of UBiA Family Genes Associated with Abiotic Stress in Sunflowers ( <i>Helianthus annuus</i> L.). <i>International Journal of Molecular Sciences</i> , 2023, 24, 1883.	1.8	1
3845	Analysis of PAT1 subfamily members in the GRAS family of upland cotton and functional characterization of GhSCL13-2A in <i>Verticillium dahliae</i> resistance. <i>Plant Cell Reports</i> , 0, , .	2.8	1
3846	Genome-Wide Identification and Phylogenetic and Expression Analyses of the PLATZ Gene Family in <i>Medicago sativa</i> L.. <i>International Journal of Molecular Sciences</i> , 2023, 24, 2388.	1.8	3
3847	Genome-Wide Characterization of the Sulfate Transporter Gene Family in Oilseed Crops: <i>Camelina sativa</i> and <i>Brassica napus</i> . <i>Plants</i> , 2023, 12, 628.	1.6	5
3848	Identification and Molecular Characterization of RWP-RK Transcription Factors in Soybean. <i>Genes</i> , 2023, 14, 369.	1.0	5
3849	Genome-wide analysis of WRKY transcription factor genes in <i>Toona sinensis</i> : An insight into evolutionary characteristics and terpene synthesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3



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3850	Genome-Wide Characterization of B-Box Gene Family in <i>Salvia miltiorrhiza</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 2146.	1.8	2
3851	Characterization of the REVEILLE family in Rosaceae and role of PblHY in flowering time regulation. <i>BMC Genomics</i> , 2023, 24, .	1.2	7
3852	Identification and co-expression network analysis of plumule-preferentially expressed genes in <i>Oryza sativa</i> . <i>Genes and Genomics</i> , 0, , .	0.5	0
3853	Identification of CmbHLH Transcription Factor Family and Excavation of CmbHLHs Resistant to Necrotrophic Fungus <i>Alternaria</i> in <i>Chrysanthemum</i> . <i>Genes</i> , 2023, 14, 275.	1.0	1
3854	Genome-wide analysis and characterization of <i>Dendrocalamus farinosus</i> SUT gene family reveal DfSUT4 involvement in sucrose transportation in plants. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
3855	Computational analysis and expression profiling of potassium transport-related gene families in mango ( <i>Mangifera indica</i> ) indicate their role in stress response and fruit development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
3856	Genome-Wide Characterization of HSP90 Gene Family in Chinese Pumpkin ( <i>Cucurbita moschata</i> Duch.) and Their Expression Patterns in Response to Heat and Cold Stresses. <i>Agronomy</i> , 2023, 13, 430.	1.3	0
3857	Strigolactones positively regulate <i>Verticillium</i> wilt resistance in cotton via crosstalk with other hormones. <i>Plant Physiology</i> , 2023, 192, 945-966.	2.3	6
3858	Genome-wide analysis of annexin gene family in <i>Schrenkiella parvula</i> and <i>Eutrema salsugineum</i> suggests their roles in salt stress response. <i>PLoS ONE</i> , 2023, 18, e0280246.	1.1	4
3859	Genome-Wide Identification Analysis of the R2R3-MYB Transcription Factor Family in <i>Cymbidium sinense</i> for Insights into Drought Stress Responses. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3235.	1.8	4
3860	Diversity and expression analysis of ZIP transporters and associated metabolites under zinc and iron stress in <i>Capsicum</i> . <i>Plant Physiology and Biochemistry</i> , 2023, 196, 415-430.	2.8	3
3861	Overexpression of CsATG3a improves tolerance to nitrogen deficiency and increases nitrogen use efficiency in <i>Arabidopsis</i> . <i>Plant Physiology and Biochemistry</i> , 2023, 196, 328-338.	2.8	2
3862	Genome wide Analysis and Characterization of <i>Eucalyptus grandis</i> TCP Transcription Factors. <i>Tarim Bilimleri Dergisi</i> , 0, , .	0.4	2
3863	The SAH7 Homologue of the Allergen Ole e 1 Interacts with the Putative Stress Sensor SBP1 (Selenium-Binding Protein 1) in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 3580.	1.8	1
3864	Genome-wide identification and expression analysis of the HD2 protein family and its response to drought and salt stress in <i>Gossypium</i> species. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
3865	Evolutionary Analysis of Respiratory Burst Oxidase Homolog (RBOH) Genes in Plants and Characterization of ZmRBOHs. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3858.	1.8	9
3866	Novel inducible promoter DREB1G cloned from date palm exhibits high fold expression over AtRD29 to drought and salinity stress. <i>Plant Cell, Tissue and Organ Culture</i> , 0, , .	1.2	1
3867	Identification of the BcLEA Gene Family and Functional Analysis of the BcLEA73 Gene in Wucai ( <i>Brassica</i> ) Tj ETQq1 1.0.784314 rgBT / Ov	1.0	2

#	ARTICLE	IF	CITATIONS
3868	Genomic Insights into the Origin of a Thermotolerant Tomato Line and Identification of Candidate Genes for Heat Stress. <i>Genes</i> , 2023, 14, 535.	1.0	1
3869	Genome-wide identification and expression pattern analysis of R2R3-MYB transcription factor gene family involved in puerarin biosynthesis and response to hormone in <i>Pueraria lobata</i> var. <i>thomsonii</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
3870	Genome-wide analysis of the laccase (LAC) gene family in <i>Aeluropus littoralis</i> : A focus on identification, evolution and expression patterns in response to abiotic stresses and ABA treatment. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	17
3871	Genome-wide identification, evolution and expression analysis of NAC gene family under salt stress in wild emmer wheat ( <i>Triticum dicoccoides</i> . L). <i>International Journal of Biological Macromolecules</i> , 2023, 230, 123376.	3.6	3
3873	Evolutionary Analysis of the Melon ( <i>Cucumis melo</i> L.) GH3 Gene Family and Identification of GH3 Genes Related to Fruit Growth and Development. <i>Plants</i> , 2023, 12, 1382.	1.6	2
3874	Genome-Wide Analysis, Characterization, Expression and Function of SERK Gene Family in <i>Phyllostachys edulis</i> . <i>Forests</i> , 2023, 14, 540.	0.9	0
3875	Genome-wide analysis of the GLP gene family and overexpression of GLP1-5â€“1 to promote lignin accumulation during early somatic embryo development in <i>Dimocarpus longan</i> . <i>BMC Genomics</i> , 2023, 24, .	1.2	5
3876	Genome-wide identification of the geranylgeranyl pyrophosphate synthase (GGPS) gene family involved in chlorophyll synthesis in cotton. <i>BMC Genomics</i> , 2023, 24, .	1.2	3
3877	<i>OsRboh1</i> Regulates Rice Growth and Development through Jasmonic Acid Signal. <i>Plant and Cell Physiology</i> , 0, , .	1.5	0
3878	Genome-wide characterization and expression analysis of Î±-amylase and Î²-amylase genes underlying drought tolerance in cassava. <i>BMC Genomics</i> , 2023, 24, .	1.2	2
3879	Genome-wide investigation of Cytochrome P450 superfamily of <i>Aquilaria agallocha</i> : Association with terpenoids and phenylpropanoids biosynthesis. <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123758.	3.6	9
3880	Genome-wide identification of PR10 family members and expression profile analysis of PvPR10 in common bean ( <i>Phaseolus vulgaris</i> L.) in response to hormones and several abiotic stress conditions. <i>Plant Growth Regulation</i> , 2024, 102, 279-295.	1.8	1
3881	Genome-Wide Identification and Expression Analysis of the SHI-Related Sequence Family in Cassava. <i>Genes</i> , 2023, 14, 870.	1.0	2
3882	Genome-wide identification of the ABA receptor PYL gene family and expression analysis in <i>Prunus avium</i> L.. <i>Scientia Horticulturae</i> , 2023, 313, 111919.	1.7	5
3883	Genome-wide identification of cytokinin oxidase family members in common bean ( <i>Phaseolus vulgaris</i> ): identification, phylogeny, expansion, and expression pattern analyses at the sprout stage under abiotic stress. <i>Scientia Horticulturae</i> , 2023, 315, 111974.	1.7	2
3884	Genome-wide identification of papain-like cysteine protease family genes in cultivated peanut ( <i>Arachis</i> ) Tj ETQq1 1 0.784314 rgBT /Over Environmental and Experimental Botany, 2023, 209, 105272.	2.0	2
3885	The MYB transcription factor LbCPC of <i>Limonium bicolor</i> negatively regulates salt gland development and salt tolerance. <i>Environmental and Experimental Botany</i> , 2023, 209, 105310.	2.0	4
3886	Recent genome-wide replication promoted expansion and functional differentiation of the JAZs in soybeans. <i>International Journal of Biological Macromolecules</i> , 2023, 238, 124064.	3.6	0

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3887	Genome-wide identification, classification and expression analysis of the JmjC domain-containing histone demethylase gene family in Moso bamboo ( <i>Phyllostachys edulis</i> ). <i>South African Journal of Botany</i> , 2023, 157, 335-345.	1.2	2
3888	Genome-wide identification and expression analysis of SUT gene family members in sugar beet (Beta) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	1
3889	Characterization of the Fasciclin-like arabinogalactan gene family in <i>Brassica napus</i> and the negative regulatory role of BnFLA39 in response to clubroot disease stress. <i>Industrial Crops and Products</i> , 2023, 196, 116400.	2.5	2
3890	The BrAFP1 promoter drives gene-specific expression in leaves and stems of winter rapeseed ( <i>Brassica</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.7	3
3891	Genome-wide comparative analysis of Glycolate oxidase (GOX) gene family in plants. <i>Plant Gene</i> , 2023, 34, 100407.	1.4	2
3892	RNA interference-core proteins from the Actinidiaceae: Evolution, structure, and functional differentiation. <i>Plant Gene</i> , 2023, 34, 100419.	1.4	0
3893	Characterization of the m6A gene family in sorghum and its function in growth, development and stress resistance. <i>Industrial Crops and Products</i> , 2023, 198, 116625.	2.5	1
3894	Functional divergence of Heat Shock Factors (Hsfs) during heat stress and recovery at the tissue and developmental scales in C4 grain amaranth ( <i>Amaranthus hypochondriacus</i> ). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
3895	Genome-wide identification of MATE, functional analysis and molecular dynamics of DcMATE21 involved in anthocyanin accumulation in <i>Daucus carota</i> . <i>Phytochemistry</i> , 2023, 210, 113676.	1.4	2
3896	Overexpression of banana GDP-L-galactose phosphorylase (GGP) modulates the biosynthesis of ascorbic acid in <i>Arabidopsis thaliana</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 237, 124124.	3.6	8
3899	Synthetic sub-genomic transcript promoter from Horseradish Latent Virus (HRLV). <i>Planta</i> , 2023, 257, .	1.6	2
3900	Identification of SHORT VEGETATIVE PHASE (SVP)-like genes and necessary responsibility of CmSVPc for the development of lateral branches in melon ( <i>Cucumis melo</i> L.). <i>Scientia Horticulturae</i> , 2023, 312, 111845.	1.7	1
3901	Genome-wide characterization of sugarcane catalase gene family identifies a ScCAT1 gene associated disease resistance. <i>International Journal of Biological Macromolecules</i> , 2023, 232, 123398.	3.6	13
3902	Genome-Wide Analyses of Thaumatin-like Protein Family Genes Reveal the Involvement in the Response to Low-Temperature Stress in <i>Ammopiptanthus nanus</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 2209.	1.8	8
3903	Genome-wide characterization, phylogenetic and expression analysis of Histone gene family in cucumber ( <i>Cucumis sativus</i> L.). <i>International Journal of Biological Macromolecules</i> , 2023, 230, 123401.	3.6	3
3904	Overexpression of mango MirZFP34 confers early flowering and stress tolerance in transgenic <i>Arabidopsis</i> . <i>Scientia Horticulturae</i> , 2023, 312, 111868.	1.7	1
3905	Identification and characterization of aldehyde dehydrogenase (ALDH) gene superfamily in garlic and expression profiling in response to drought, salinity, and ABA. <i>Gene</i> , 2023, 860, 147215.	1.0	0
3906	Insights into the Sulfate Transporter Gene Family and Its Expression Patterns in Durum Wheat Seedlings under Salinity. <i>Genes</i> , 2023, 14, 333.	1.0	4

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3907	Identification and molecular characterization of novel sucrose transporters in the hexaploid wheat ( <i>Triticum aestivum</i> L.). <i>Gene</i> , 2023, 860, 147245.	1.0	2
3908	Comprehensive analysis of <i>MAPK</i> gene family in <i>Populus trichocarpa</i> and physiological characterization of <i>PtMAPK3</i> in response to MeJA induction. <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	6
3909	Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut ( <i>Juglans nigra</i> ). <i>Horticulture Research</i> , 2023, 10, .	2.9	11
3910	Genomic identification of cotton SAC genes branched ovule and stress-related key genes in <i>Gossypium hirsutum</i> . <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
3911	Gene Profiling of the Ascorbate Oxidase Family Genes under Osmotic and Cold Stress Reveals the Role of AnAO5 in Cold Adaptation in <i>Ammopiptanthus nanus</i> . <i>Plants</i> , 2023, 12, 677.	1.6	6
3912	Instability of extrachromosomal DNA transformed into the diatom <i>Phaeodactylum tricornutum</i> . <i>Algal Research</i> , 2023, 70, 102998.	2.4	4
3913	Dehydrogenase MnGutB1 catalyzes 1-deoxynojirimycin biosynthesis in mulberry. <i>Plant Physiology</i> , 2023, 192, 1307-1320.	2.3	5
3914	Genome-Wide Re-Identification and Analysis of CrRLK1Ls in Tomato. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3142.	1.8	6
3915	Genome Identification of the Tea Plant ( <i>Camellia sinensis</i> ) ASMT Gene Family and Its Expression Analysis under Abiotic Stress. <i>Genes</i> , 2023, 14, 409.	1.0	4
3916	Analysis in silico of superoxide dismutase genes family provides insights into the evolution of this gene family in <i>Coffea</i> spp.. <i>Journal of Crop Science and Biotechnology</i> , 0, , .	0.7	0
3917	Uncovering the role of wheat magnesium transporter family genes in abiotic responses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
3918	The Bcl-2-associated athanogene gene family in tobacco ( <i>Nicotiana tabacum</i> ) and the function of NtBAG5 in leaf senescence. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
3919	Integrated transcriptomic and metabolomic profiles reveal anthocyanin accumulation in <i>Scutellaria baicalensis</i> petal coloration. <i>Industrial Crops and Products</i> , 2023, 194, 116144.	2.5	4
3920	Designing artificial synthetic promoters for accurate, smart, and versatile gene expression in plants. <i>Plant Communications</i> , 2023, 4, 100558.	3.6	9
3921	Genome-wide identification and characterization of parthenocarpic fruit set-related gene homologs in cucumber ( <i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2023, 13, .	1.6	5
3922	The genome of <i>Magnolia hypoleuca</i> provides a new insight into cold tolerance and the evolutionary position of magnoliids. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
3923	Chickpea R2R3 Transcription Factor CaMYB78 Enhances Abiotic Stress Tolerance in Tobacco. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 4511-4527.	2.8	1
3924	Single-cell transcriptomic analysis reveals the developmental trajectory and transcriptional regulatory networks of pigment glands in <i>Gossypium bickii</i> . <i>Molecular Plant</i> , 2023, 16, 694-708.	3.9	12

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3925	Changes in physio-biochemical parameters and expression of metallothioneins in <i>Avena sativa</i> L. in response to drought. <i>Scientific Reports</i> , 2023, 13, .	1.6	7
3926	The LHT Gene Family in Rice: Molecular Characterization, Transport Functions and Expression Analysis. <i>Plants</i> , 2023, 12, 817.	1.6	0
3927	Genome-Wide Analysis of the Molecular Functions of B3 Superfamily in Oil Biosynthesis in Olive ( <i>Olea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.9	2
3928	Freezing transcriptome analysis showed that GhZAT10 regulates freezing tolerance through a partially CBF-dependent pathway in upland cotton ( <i>Gossypium hirsutum</i> L.). <i>Environmental and Experimental Botany</i> , 2023, 208, 105263.	2.0	1
3929	Genome-Wide Identification and Characterization of the PPO Gene Family in Cotton ( <i>Gossypium</i> ) and Their Expression Variations Responding to <i>Verticillium</i> Wilt Infection. <i>Genes</i> , 2023, 14, 477.	1.0	2
3930	Genome-Wide Identification and Expression Analysis of Calmodulin-Like Gene Family in <i>Paspalum vaginatum</i> Revealed Their Role in Response to Salt and Cold Stress. <i>Current Issues in Molecular Biology</i> , 2023, 45, 1693-1711.	1.0	2
3932	Genome-wide characterization of aldehyde dehydrogenase gene family members in groundnut ( <i>Arachis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.7	4
3933	Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, <i>Quercus dentata</i> . <i>New Phytologist</i> , 2023, 238, 2016-2032.	3.5	13
3934	Genome-Wide Identification, Characterization, and Expression Analysis of SPIRAL1 Family Genes in Legume Species. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3958.	1.8	0
3935	Genome-Wide Identification and Expression Analysis of the Ammonium Transporter Family Genes in Soybean. <i>International Journal of Molecular Sciences</i> , 2023, 24, 3991.	1.8	3
3936	pCtFSG2, a flower-specific promoter with suitable promoter activity in safflower. <i>Journal of Plant Biochemistry and Biotechnology</i> , 0, , .	0.9	1
3938	Characterization and expression profiles of the B-box gene family during plant growth and under low-nitrogen stress in <i>Saccharum</i> . <i>BMC Genomics</i> , 2023, 24, .	1.2	0
3939	Characterization of the Passion Fruit ( <i>Passiflora edulis</i> Sim) bHLH Family in Fruit Development and Abiotic Stress and Functional Analysis of PebHLH56 in Cold Stress. <i>Horticulturae</i> , 2023, 9, 272.	1.2	4
3940	Genome-wide analysis of NBS-LRR genes revealed contribution of disease resistance from <i>Saccharum spontaneum</i> to modern sugarcane cultivar. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	0
3941	Genome-Wide Analysis of SIMILAR TO RCD ONE (SRO) Family Revealed Their Roles in Abiotic Stress in Poplar. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4146.	1.8	5
3942	Genome-wide identification of the fibrillin gene family in chickpea ( <i>Cicer arietinum</i> L.) and its response to drought stress. <i>International Journal of Biological Macromolecules</i> , 2023, 234, 123757.	3.6	1
3943	Identification of a Rice Leaf Width Gene Narrow Leaf 22 (NAL22) through Genome-Wide Association Study and Gene Editing Technology. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4073.	1.8	4
3944	Genome-wide analysis of MYB family in <i>Nicotiana benthamiana</i> and the functional role of the key members in resistance to <i>Bemisia tabaci</i> . <i>International Journal of Biological Macromolecules</i> , 2023, 235, 123759.	3.6	3

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3945	Genome-Wide Identification and Abiotic Stress Response Analysis of PP2C Gene Family in Woodland and Pineapple Strawberries. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4049.	1.8	6
3946	High-quality <i>Cymbidium mannii</i> genome and multifaceted regulation of crassulacean acid metabolism in epiphytes. <i>Plant Communications</i> , 2023, 4, 100564.	3.6	5
3947	Genome-Wide Analysis of the <i>Rhododendron</i> AP2/ERF Gene Family: Identification and Expression Profiles in Response to Cold, Salt and Drought Stress. <i>Plants</i> , 2023, 12, 994.	1.6	6
3948	Whole genome identification of CBF gene families and expression analysis in <i>Vitis vinifera</i> L.. <i>Czech Journal of Genetics and Plant Breeding</i> , 2023, 59, 119-132.	0.4	2
3949	Identification of Pyrabactin resistance 1-like (PYL) genes in <i>Brachypodium distachyon</i> and functional characterization of BdPYL5. <i>Journal of Plant Physiology</i> , 2023, 283, 153949.	1.6	0
3950	Genome-wide analysis of MdGeBP family and functional identification of MdGeBP3 in <i>Malus domestica</i> . <i>Environmental and Experimental Botany</i> , 2023, 208, 105262.	2.0	1
3951	Genome-wide identification and expression analysis of the CHYR gene family in <i>Phaseolus vulgaris</i> under abiotic stress at the seeding stage. <i>Journal of Plant Interactions</i> , 2023, 18, .	1.0	0
3952	The CmMYB3 transcription factors isolated from the <i>Chrysanthemum morifolium</i> regulate flavonol biosynthesis in <i>Arabidopsis thaliana</i> . <i>Plant Cell Reports</i> , 2023, 42, 791-803.	2.8	1
3953	Genetic variation in ZmSO contributes to ABA response and drought tolerance in maize seedlings. <i>Crop Journal</i> , 2023, 11, 1106-1114.	2.3	2
3954	Genome-Wide Investigation of the NAC Transcription Factor Family in <i>Apocynum venetum</i> Revealed Their Synergistic Roles in Abiotic Stress Response and Trehalose Metabolism. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4578.	1.8	2
3955	Identification and Characterization of Phytoeyanin Family Genes in Cotton Genomes. <i>Genes</i> , 2023, 14, 611.	1.0	4
3956	Integrated bioinformatic and physiological analyses reveal the pivotal role of hydrogen sulfide in enhancing low-temperature tolerance in alfalfa. <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	2
3957	Genome-Wide Identification and Expression Analysis of RCC1 Gene Family under Abiotic Stresses in Rice ( <i>Oryza sativa</i> L.). <i>Agronomy</i> , 2023, 13, 703.	1.3	1
3958	Genome-Wide Investigation of Apyrase (APY) Genes in Peanut ( <i>Arachis hypogaea</i> L.) and Functional Characterization of a Pod-Abundant Expression Promoter AhAPY2-1p. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4622.	1.8	2
3961	A subset of highly responsive transcription factors upon tomato infection by pepino mosaic virus. <i>Plant Biology</i> , 2023, 25, 529-540.	1.8	1
3962	Phytochromes mediate germination inhibition under red, far-red, and white light in <i>Aethionema arabicum</i> . <i>Plant Physiology</i> , 2023, 192, 1584-1602.	2.3	4
3963	Genome-wide identification, bioinformatics and expression analysis of HD-Zip gene family in peach. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	5
3964	Comparative phylogenomic insights of KCS and ELO gene families in Brassica species indicate their role in seed development and stress responsiveness. <i>Scientific Reports</i> , 2023, 13, .	1.6	3

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3965	Genome-Wide Identification and Expression Analysis of ESPs and NSPs Involved in Glucosinolate Hydrolysis and Insect Attack Defense in Chinese Cabbage ( <i>Brassica rapa</i> subsp. <i>pekinensis</i> ). <i>Plants</i> , 2023, 12, 1123.	1.6	1
3966	Genome-Wide Identification and Expression Characteristics of Cytokinin Response Factors in Soybean. <i>Journal of Plant Growth Regulation</i> , 2023, 42, 4484-4496.	2.8	1
3967	Identification and expression analysis of C2H2-zinc finger protein genes reveals their role in stress tolerance in <i>Brassica napus</i> . <i>Genome</i> , 2023, 66, 91-107.	0.9	2
3968	Identification of citrus APX gene family and their response to CYVCV infection. <i>Journal of Plant Research</i> , 0, , .	1.2	1
3969	Zinc/iron-regulated transporter-like protein gene family in <i>Theobroma cacao</i> L: Characteristics, evolution, function and 3D structure analysis. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
3970	Genome-Wide Identification and Expression Analysis of the HSF Gene Family in Poplar. <i>Forests</i> , 2023, 14, 510.	0.9	4
3971	Genome-wide identification and expression analysis of the HVA22 gene family in cotton and functional analysis of GhHVA22E1D in drought and salt tolerance. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
3972	Genome-Wide Identification and Evolutionary Analysis of Gossypium YTH Domain-Containing RNA-Binding Protein Family and the Role of GhYTH8 in Response to Drought Stress. <i>Plants</i> , 2023, 12, 1198.	1.6	1
3973	Meta-QTL and haplo-pheno analysis reveal superior haplotype combinations associated with low grain chalkiness under high temperature in rice. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	4
3974	Identification and Expression Analysis of Hexokinases Family in <i>Saccharum spontaneum</i> L. under Drought and Cold Stresses. <i>Plants</i> , 2023, 12, 1215.	1.6	1
3976	UBC gene family and their potential functions on the cellular homeostasis under the elevated pCO <sub>2</sub> stress in the diatom <i>Phaeodactylum tricornutum</i> . <i>Ecological Indicators</i> , 2023, 148, 110106.	2.6	0
3977	Genome-Wide Identification and Expression Analysis of the TIR-NBS-LRR Gene Family and Its Response to Fungal Disease in Rose ( <i>Rosa chinensis</i> ). <i>Biology</i> , 2023, 12, 426.	1.3	1
3978	Genome-Wide Identification and Expression Analysis of NPF Genes in Cucumber ( <i>Cucumis sativus</i> L.). <i>Plants</i> , 2023, 12, 1252.	1.6	3
3979	Citrus ACC synthase CiACS4 regulates plant height by inhibiting gibberellin biosynthesis. <i>Plant Physiology</i> , 2023, 192, 1947-1968.	2.3	5
3980	Comprehensive Analysis of Universal Stress Protein Family Genes and Their Expression in <i>Fusarium oxysporum</i> Response of <i>Populus davidiana</i> Å— <i>P. alba</i> var. <i>pyramidalis</i> Louche Based on the Transcriptome. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5405.	1.8	4
3981	SiMYBS3, Encoding a <i>Setaria italica</i> Heterosis-Related MYB Transcription Factor, Confers Drought Tolerance in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 5418.	1.8	4
3982	Genome-wide analysis of TPX2 gene family in <i>Populus trichocarpa</i> and its specific response genes under various abiotic stresses. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
3983	Fine mapping and candidate gene analysis of qFL-A12-5: a fiber length-related QTL introgressed from <i>Gossypium barbadense</i> into <i>Gossypium hirsutum</i> . <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	1

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3984	Identification of CNGCs in Glycine max and Screening of Related Resistance Genes after Fusarium solani Infection. <i>Biology</i> , 2023, 12, 439.	1.3	1
3985	Genome-wide identification and comparative analyses of key genes involved in C4 photosynthesis in five main gramineous crops. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
3986	Allelic Variation in GmPAP14 Alters Gene Expression to Affect Acid Phosphatase Activity in Soybean. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5398.	1.8	0
3987	The proposed role of MSL-lncRNAs in causing sex lability of female poplars. <i>Horticulture Research</i> , 2023, 10, .	2.9	0
3988	Promoter Cis-Element Analyses Reveal the Function of $\hat{\pm}$ VPE in Drought Stress Response of Arabidopsis. <i>Biology</i> , 2023, 12, 430.	1.3	3
3989	Genome-wide identification of NHX (Na <sup>+</sup> /H <sup>+</sup> antiporter) gene family in Cucurbita L. and functional analysis of CmoNHX1 under salt stress. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
3990	Genome-wide analysis of BrbHLH gene family and functional identification of the involvement of BcbHLH57 in abiotic stress in wucaï (Brassica campestris L.). <i>Plant Cell, Tissue and Organ Culture</i> , 2023, 154, 457-479.	1.2	1
3992	BCH1 expression pattern contributes to the fruit carotenoid diversity between peach and apricot. <i>Plant Physiology and Biochemistry</i> , 2023, 197, 107647.	2.8	1
3993	Genome-Wide Identification of Superoxide Dismutase and Expression in Response to Fruit Development and Biological Stress in Akebia trifoliata: A Bioinformatics Study. <i>Antioxidants</i> , 2023, 12, 726.	2.2	2
3996	Natural variations of chlorophyll fluorescence and ion transporter genes influenced the differential response of japonica rice germplasm with different salt tolerances. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
3998	Genome-wide identification and expression analysis of the U-box E3 ubiquitin ligase gene family related to salt tolerance in sorghum ( <i>Sorghum bicolor</i> L.). <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	3
3999	Genome-wide identification, characterization, and validation of the bHLH transcription factors in grass pea. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	4
4001	Genome-wide characterization of ubiquitin-conjugating enzyme gene family explores its genetic effects on the oil content and yield of Brassica napus. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1
4002	Genome-Wide Identification of the Sweet Orange bZIP Gene Family and Analysis of Their Expression in Response to Infection by <i>Penicillium digitatum</i> . <i>Horticulturae</i> , 2023, 9, 393.	1.2	1
4003	Comparative analysis of the MYB gene family in seven Ipomoea species. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	7
4004	The Identification and Expression Analysis of the Liriodendron chinense (Hemsl.) Sarg. SOD Gene Family. <i>Forests</i> , 2023, 14, 628.	0.9	3
4005	Genome-wide identification and characterization of lipoxygenase genes related to the English grain aphid infestation response in wheat. <i>Planta</i> , 2023, 257, .	1.6	4
4006	Heterologous WvDREB2c Expression Improves Heat Tolerance in Arabidopsis by Inducing Photoprotective Responses. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5989.	1.8	1



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4007	Genome-Wide Identification and Expression Analysis of TPS Gene Family in <i>Liriodendron chinense</i> . <i>Genes</i> , 2023, 14, 770.	1.0	2
4008	Genome-Wide Identification and Analysis of the MADS-Box Transcription Factor Genes in Blueberry ( <i>Vaccinium</i> spp.) and Their Expression Pattern during Fruit Ripening. <i>Plants</i> , 2023, 12, 1424.	1.6	5
4009	Functional characterization and transcriptional activity analysis of <i>Dryopteris fragrans</i> farnesyl diphosphate synthase genes. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
4010	Genome-wide identification and comparative expression profiling of the WRKY transcription factor family in two Citrus species with different <i>Candidatus Liberibacter asiaticus</i> susceptibility. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
4011	Genome-Wide Identification of the U-Box E3 Ubiquitin Ligase Gene Family in Cabbage ( <i>Brassica oleracea</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 2023, 12, 1437.	1.6	2
4012	How to start a <sc>LINE</sc>: 5â€² switching rejuvenates <sc>LINE</sc> retrotransposons in tobacco and related <i>Nicotiana</i> species. <i>Plant Journal</i> , 2023, 115, 52-67.	2.8	0
4013	Genome-wide analysis of pathogenesis-related protein-1 (PR-1) genes from Qingke ( <i>Hordeum vulgare</i> L.) Tj ETQq0 0 0 rgBT /Q1overlock 10	1.4	1
4014	Rapid production of novel beneficial alleles for improving rice appearance quality by targeting a regulatory element of <sc><i>SLG7</i></sc>. <i>Plant Biotechnology Journal</i> , 2023, 21, 1305-1307.	4.1	7
4015	Genome-wide identification and expression analysis of wall-associated kinase (WAK) and WAK-like kinase gene family in response to tomato yellow leaf curl virus infection in <i>Nicotiana benthamiana</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
4016	Genome-wide identification of the TIFY family reveals JAZ subfamily function in response to hormone treatment in <i>Betula platyphylla</i> . <i>BMC Plant Biology</i> , 2023, 23, .	1.6	2
4018	Comprehensive Analysis of the INDETERMINATE DOMAIN (IDD) Gene Family and Their Response to Abiotic Stress in <i>Zea mays</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 6185.	1.8	1
4019	Recent progress and challenges in CRISPR-Cas9 engineered algae and cyanobacteria. <i>Algal Research</i> , 2023, 71, 103068.	2.4	6
4020	Systematic Investigation of TCP Gene Family: Genome-Wide Identification and Light-Regulated Gene Expression Analysis in Pepino ( <i>Solanum Muricatum</i> ). <i>Cells</i> , 2023, 12, 1015.	1.8	3
4021	Comprehensive Identification and Expression Analysis of the YTH Family of RNA-Binding Proteins in Strawberry. <i>Plants</i> , 2023, 12, 1449.	1.6	0
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4031	Genomic diversity of aquaporins across genus <i>Oryza</i> provides a rich genetic resource for development of climate resilient rice cultivars. <i>BMC Plant Biology</i> , 2023, 23, .	1.6	3
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4067	Functional studies of four MiFPF genes in mango revealed their function in promoting flowering in transgenic <i>Arabidopsis</i> . <i>Journal of Plant Physiology</i> , 2023, 285, 153994.	1.6	0
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