

agriGO: a GO analysis toolkit for the agricultural commu

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Effect of purified somatomedins on thymidine incorporation into lectin-activated human lymphocytes. <i>European Journal of Endocrinology</i> , 1983, 102, 21-26.	1.9	40
3	ProFITS of maize: a database of protein families involved in the transduction of signalling in the maize genome. <i>BMC Genomics</i> , 2010, 11, 580.	1.2	8
4	Comparative transcriptomics of drought responses in <i>Populus</i> : a meta-analysis of genome-wide expression profiling in mature leaves and root apices across two genotypes. <i>BMC Genomics</i> , 2010, 11, 630.	1.2	179
5	Habituation to thaxtomin A in hybrid poplar cell suspensions provides enhanced and durable resistance to inhibitors of cellulose synthesis. <i>BMC Plant Biology</i> , 2010, 10, 272.	1.6	16
6	Meiosis-specific gene discovery in plants: RNA-Seq applied to isolated <i>Arabidopsis</i> male meiocytes. <i>BMC Plant Biology</i> , 2010, 10, 280.	1.6	133
7	Differential expression of the microRNAs in superior and inferior spikelets in rice ( <i>Oryza sativa</i> ). <i>Journal of Experimental Botany</i> , 2011, 62, 4943-4954.	2.4	95
8	Barley Leaf Transcriptome and Metabolite Analysis Reveals New Aspects of Compatibility and Piriformospora indica-Mediated Systemic Induced Resistance to Powdery Mildew. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1427-1439.	1.4	125
9	Implementation of a de novo genome-wide computational approach for updating <i>Brachypodium</i> miRNAs. <i>Genomics</i> , 2011, 97, 282-293.	1.3	17
10	Identification of candidate genes in <i>Arabidopsis</i> and <i>Populus</i> cell wall biosynthesis using text-mining, co-expression network analysis and comparative genomics. <i>Plant Science</i> , 2011, 181, 675-687.	1.7	44
11	The bZIP Transcription Factor PERIANTHIA: A Multifunctional Hub for Meristem Control. <i>Frontiers in Plant Science</i> , 2011, 2, 79.	1.7	41
12	Comparison of Four CHIP-Seq Analytical Algorithms Using Rice Endosperm H3K27 Trimethylation Profiling Data. <i>PLoS ONE</i> , 2011, 6, e25260.	1.1	54
13	Identification and Characterization of microRNAs from Peanut ( <i>Arachis hypogaea</i> L.) by High-Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e27530.	1.1	131
14	Transcriptome Phase Distribution Analysis Reveals Diurnal Regulated Biological Processes and Key Pathways in Rice Flag Leaves and Seedling Leaves. <i>PLoS ONE</i> , 2011, 6, e17613.	1.1	37
15	Ancestral polyploidy in seed plants and angiosperms. <i>Nature</i> , 2011, 473, 97-100.	13.7	1,862
16	Transcriptional responses to flooding stress in roots including hypocotyl of soybean seedlings. <i>Plant Molecular Biology</i> , 2011, 77, 129-144.	2.0	103
17	TaNf-YB3 is involved in the regulation of photosynthesis genes in <i>Triticum aestivum</i> . <i>Functional and Integrative Genomics</i> , 2011, 11, 327-340.	1.4	74
18	Comparative analysis of root transcriptome profiles of two pairs of drought-tolerant and susceptible rice near-isogenic lines under different drought stress. <i>BMC Plant Biology</i> , 2011, 11, 174.	1.6	134
19	Identification of miRNAs and their target genes in developing soybean seeds by deep sequencing. <i>BMC Plant Biology</i> , 2011, 11, 5.	1.6	287

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20	A label-free quantitative shotgun proteomics analysis of rice grain development. <i>Proteome Science</i> , 2011, 9, 61.	0.7	42
21	Identification of novel soybean microRNAs involved in abiotic and biotic stresses. <i>BMC Genomics</i> , 2011, 12, 307.	1.2	313
22	Comparative analysis of neural transcriptomes and functional implication of unannotated intronic expression. <i>BMC Genomics</i> , 2011, 12, 494.	1.2	3
23	Functional annotation of the transcriptome of <i>Sorghum bicolor</i> in response to osmotic stress and abscisic acid. <i>BMC Genomics</i> , 2011, 12, 514.	1.2	197
24	Whole genome resequencing of black Angus and Holstein cattle for SNP and CNV discovery. <i>BMC Genomics</i> , 2011, 12, 559.	1.2	153
25	Genetic architecture of gene expression in ovine skeletal muscle. <i>BMC Genomics</i> , 2011, 12, 607.	1.2	18
26	Next generation functional proteomics in non-model plants: A survey on techniques and applications for the analysis of protein complexes and post-translational modifications. <i>Phytochemistry</i> , 2011, 72, 1192-1218.	1.4	28
27	REVIGO Summarizes and Visualizes Long Lists of Gene Ontology Terms. <i>PLoS ONE</i> , 2011, 6, e21800.	1.1	5,347
28	NOA: a novel Network Ontology Analysis method. <i>Nucleic Acids Research</i> , 2011, 39, e87-e87.	6.5	101
29	Digital Gene Expression Profiling of the <i>Phytophthora sojae</i> Transcriptome. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1530-1539.	1.4	119
30	AgBase: supporting functional modeling in agricultural organisms. <i>Nucleic Acids Research</i> , 2011, 39, D497-D506.	6.5	56
31	Transcriptome analysis of rice mature root tissue and root tips in early development by massive parallel sequencing. <i>Journal of Experimental Botany</i> , 2012, 63, 2141-2157.	2.4	41
32	Uncovering Arabidopsis Membrane Protein Interactome Enriched in Transporters Using Mating-Based Split Ubiquitin Assays and Classification Models. <i>Frontiers in Plant Science</i> , 2012, 3, 124.	1.7	42
33	Transcript and metabolite signature of maize source leaves suggests a link between transitory starch to sucrose balance and the autonomous floral transition. <i>Journal of Experimental Botany</i> , 2012, 63, 5079-5092.	2.4	34
34	Ten Years of Pathway Analysis: Current Approaches and Outstanding Challenges. <i>PLoS Computational Biology</i> , 2012, 8, e1002375.	1.5	1,267
35	Tissue-Specific Functional Networks for Prioritizing Phenotype and Disease Genes. <i>PLoS Computational Biology</i> , 2012, 8, e1002694.	1.5	137
36	The SET-Domain Protein SUV5 Mediates H3K9me2 Deposition and Silencing at Stimulus Response Genes in a DNA Methylation-Independent Manner. <i>PLoS Genetics</i> , 2012, 8, e1002995.	1.5	54
37	Analysis of <i>Arabidopsis</i> genome-wide variations before and after meiosis and meiotic recombination by resequencing Landsberg <i>erecta</i> and all four products of a single meiosis. <i>Genome Research</i> , 2012, 22, 508-518.	2.4	125

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38	<i>In silico</i> analyses of pericycle cell populations reinforce their relation with associated vasculature in <i>Arabidopsis</i> . <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 1479-1488.	1.8	27
39	Promotion of Hepatocarcinogenesis by Perfluoroalkyl Acids in Rainbow Trout. <i>Toxicological Sciences</i> , 2012, 125, 69-78.	1.4	34
40	Drastic expression change of transposon-derived piRNA-like RNAs and microRNAs in early stages of chicken embryos implies a role in gastrulation. <i>RNA Biology</i> , 2012, 9, 212-227.	1.5	39
41	Maize Source Leaf Adaptation to Nitrogen Deficiency Affects Not Only Nitrogen and Carbon Metabolism But Also Control of Phosphate Homeostasis. <i>Plant Physiology</i> , 2012, 160, 1384-1406.	2.3	170
42	A comparative transcriptomic study of an allotetraploid and its diploid progenitors illustrates the unique advantages and challenges of RNA-seq in plant species. <i>American Journal of Botany</i> , 2012, 99, 383-396.	0.8	80
43	Assessing the Biosynthetic Capabilities of Secretory Glands in <i>Citrus</i> Peel. <i>Plant Physiology</i> , 2012, 159, 81-94.	2.3	82
44	Transcriptional profiling analysis in <i>Populus yunnanensis</i> provides insights into molecular mechanisms of sexual differences in salinity tolerance. <i>Journal of Experimental Botany</i> , 2012, 63, 3709-3726.	2.4	43
45	Transcriptional profiling reveals sexual differences of the leaf transcriptomes in response to drought stress in <i>Populus yunnanensis</i> . <i>Tree Physiology</i> , 2012, 32, 1541-1555.	1.4	44
46	Transcriptome Analysis of Age-Related Gain of Callus-Forming Capacity in <i>Arabidopsis Hypocotyls</i> . <i>Plant and Cell Physiology</i> , 2012, 53, 1457-1469.	1.5	16
47	Characterization of a Viral Synergism in the Monocot <i>Brachypodium distachyon</i> Reveals Distinctly Altered Host Molecular Processes Associated with Disease. <i>Plant Physiology</i> , 2012, 160, 1432-1452.	2.3	60
48	Inducible Maize Defense Mechanisms Against the Corn Borer <i>Sesamia nonagrioides</i> : A Transcriptome and Biochemical Approach. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 61-68.	1.4	22
49	Taking the Next Step: Building an <i>Arabidopsis</i> Information Portal. <i>Plant Cell</i> , 2012, 24, 2248-2256.	3.1	38
50	Global Analysis of Tomato Gene Expression During <i>Potato spindle tuber viroid</i> Infection Reveals a Complex Array of Changes Affecting Hormone Signaling. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 582-598.	1.4	97
51	A Systems Approach for Identifying Resistance Factors to Rice stripe virus. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 534-545.	1.4	8
52	Regulation of the <i>Arabidopsis</i> anther transcriptome by DYT1 for pollen development. <i>Plant Journal</i> , 2012, 72, 612-624.	2.8	138
53	Transcriptional reprogramming by root knot and migratory nematode infection in rice. <i>New Phytologist</i> , 2012, 196, 887-900.	3.5	157
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55	SKIP Is a Component of the Spliceosome Linking Alternative Splicing and the Circadian Clock in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 3278-3295.	3.1	198

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57	Transcriptome analysis of fruit development of a citrus late-ripening mutant by microarray. <i>Scientia Horticulturae</i> , 2012, 134, 32-39.	1.7	10
58	Basic leucine zipper transcription factor OsbZIP16 positively regulates drought resistance in rice. <i>Plant Science</i> , 2012, 193-194, 8-17.	1.7	98
59	Somatic small RNA pathways promote the mitotic events of megagametogenesis during female reproductive development in <i>Arabidopsis</i> . <i>Development (Cambridge)</i> , 2012, 139, 1399-1404.	1.2	145
60	Mutations in an <i>Arabidopsis</i> Mitochondrial Transcription Termination Factor-Related Protein Enhance Thermotolerance in the Absence of the Major Molecular Chaperone HSP101. <i>Plant Cell</i> , 2012, 24, 3349-3365.	3.1	94
61	Comparative transcriptome analysis of transporters, phytohormone and lipid metabolism pathways in response to arsenic stress in rice ( <i>Oryza sativa</i> ). <i>New Phytologist</i> , 2012, 195, 97-112.	3.5	193
62	OLSVis: an animated, interactive visual browser for bio-ontologies. <i>BMC Bioinformatics</i> , 2012, 13, 116.	1.2	20
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66	Identification of genes specifically or preferentially expressed in maize silk reveals similarity and diversity in transcript abundance of different dry stigmas. <i>BMC Genomics</i> , 2012, 13, 294.	1.2	33
67	Identification of soybean seed developmental stage-specific and tissue-specific miRNA targets by degradome sequencing. <i>BMC Genomics</i> , 2012, 13, 310.	1.2	115
68	Chips and tags suggest plant-environment interactions differ for two alpine <i>Pachycladon</i> species. <i>BMC Genomics</i> , 2012, 13, 322.	1.2	5
69	Transcriptome analysis at four developmental stages of grape berry ( <i>Vitis vinifera</i> cv. Shiraz) provides insights into regulated and coordinated gene expression. <i>BMC Genomics</i> , 2012, 13, 691.	1.2	125
70	Transcriptome analysis of rice root responses to potassium deficiency. <i>BMC Plant Biology</i> , 2012, 12, 161.	1.6	176
71	Identification of wild soybean miRNAs and their target genes responsive to aluminum stress. <i>BMC Plant Biology</i> , 2012, 12, 182.	1.6	137
72	Transcriptome analysis of intraspecific competition in <i>Arabidopsis thaliana</i> reveals organ-specific signatures related to nutrient acquisition and general stress response pathways. <i>BMC Plant Biology</i> , 2012, 12, 227.	1.6	33
73	Comparative analysis of microarray data in <i>Arabidopsis</i> transcriptome during compatible interactions with plant viruses. <i>Virology Journal</i> , 2012, 9, 101.	1.4	51

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75	Transcriptomic Analysis of the Highly Heterotic Maize Hybrid Zhengdan 958 and Its Parents During Spikelet and Floscule Differentiation. <i>Journal of Integrative Agriculture</i> , 2012, 11, 1783-1793.	1.7	3
76	Transcriptome Comparison of Susceptible and Resistant Wheat in Response to Powdery Mildew Infection. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 94-106.	3.0	90
77	Differential accumulation of host mRNAs on polyribosomes during obligate pathogen-plant interactions. <i>Molecular BioSystems</i> , 2012, 8, 2153.	2.9	31
78	Genome-wide identification and analysis of early heat stress responsive genes in rice. <i>Journal of Plant Biology</i> , 2012, 55, 458-468.	0.9	44
79	PICARA, an Analytical Pipeline Providing Probabilistic Inference about A Priori Candidates Genes Underlying Genome-Wide Association QTL in Plants. <i>PLoS ONE</i> , 2012, 7, e46596.	1.1	23
80	Different Transcriptional Response to <i>Xanthomonas citri</i> subsp. <i>citri</i> between Kumquat and Sweet Orange with Contrasting Canker Tolerance. <i>PLoS ONE</i> , 2012, 7, e41790.	1.1	36
81	<i>Verticillium longisporum</i> Infection Affects the Leaf Apoplastic Proteome, Metabolome, and Cell Wall Properties in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2012, 7, e31435.	1.1	112
82	Identification of Gene Modules Associated with Drought Response in Rice by Network-Based Analysis. <i>PLoS ONE</i> , 2012, 7, e33748.	1.1	61
83	A Gene-Phenotype Network Based on Genetic Variability for Drought Responses Reveals Key Physiological Processes in Controlled and Natural Environments. <i>PLoS ONE</i> , 2012, 7, e45249.	1.1	58
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85	The Rice R2R3-MYB Transcription Factor OsMYB55 Is Involved in the Tolerance to High Temperature and Modulates Amino Acid Metabolism. <i>PLoS ONE</i> , 2012, 7, e52030.	1.1	163
86	Dissecting <i>Phaseolus vulgaris</i> Innate Immune System against <i>Colletotrichum lindemuthianum</i> Infection. <i>PLoS ONE</i> , 2012, 7, e43161.	1.1	36
87	PloGO: Plotting gene ontology annotation and abundance in multi-condition proteomics experiments. <i>Proteomics</i> , 2012, 12, 406-410.	1.3	30
88	Experimental sink removal induces stress responses, including shifts in amino acid and phenylpropanoid metabolism, in soybean leaves. <i>Planta</i> , 2012, 235, 939-954.	1.6	12
89	Root herbivory: molecular analysis of the maize transcriptome upon infestation by Southern corn rootworm, <i>Diabrotica undecimpunctata howardi</i> . <i>Physiologia Plantarum</i> , 2012, 144, 303-319.	2.6	21
90	Characterization of the early response of the orchid, <i>Phalaenopsis amabilis</i> , to <i>Erwinia chrysanthemi</i> infection using expression profiling. <i>Physiologia Plantarum</i> , 2012, 145, 406-425.	2.6	11
91	Genome-wide transcriptome dissection of the rice root system: implications for developmental and physiological functions. <i>Plant Journal</i> , 2012, 69, 126-140.	2.8	106

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93	A genome-wide survey of copy number variation regions in various chicken breeds by array comparative genomic hybridization method. <i>Animal Genetics</i> , 2012, 43, 282-289.	0.6	37
94	Genome-wide identification of SOC1 and SVP targets during the floral transition in Arabidopsis. <i>Plant Journal</i> , 2012, 70, 549-561.	2.8	161
95	Fructokinase is required for carbon partitioning to cellulose in aspen wood. <i>Plant Journal</i> , 2012, 70, 967-977.	2.8	64
96	Transcriptional programs regulating seed dormancy and its release by after-ripening in common wheat ( <i>Triticum aestivum</i> L.). <i>Plant Biotechnology Journal</i> , 2012, 10, 465-476.	4.1	56
97	Genomic survey, expression profile and co-expression network analysis of OsWD40 family in rice. <i>BMC Genomics</i> , 2012, 13, 100.	1.2	78
98	The role of the Arabidopsis FUSCA3 transcription factor during inhibition of seed germination at high temperature. <i>BMC Plant Biology</i> , 2012, 12, 15.	1.6	70
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100	Comparative transcriptome analysis of AP2/EREBP gene family under normal and hormone treatments, and under two drought stresses in NILs setup by Aday Selection and IR64. <i>Molecular Genetics and Genomics</i> , 2012, 287, 1-19.	1.0	30
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105	High-throughput genomics in sorghum: from whole-genome resequencing to a SNP screening array. <i>Plant Biotechnology Journal</i> , 2013, 11, 1112-1125.	4.1	63
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107	Linking the potato genome to the conserved ortholog set (COS) markers. <i>BMC Genetics</i> , 2013, 14, 51.	2.7	6
108	Transcriptional profiling of sweetpotato ( <i>Ipomoea batatas</i> ) roots indicates down-regulation of lignin biosynthesis and up-regulation of starch biosynthesis at an early stage of storage root formation. <i>BMC Genomics</i> , 2013, 14, 460.	1.2	154
109	Adaptation of maize source leaf metabolism to stress related disturbances in carbon, nitrogen and phosphorus balance. <i>BMC Genomics</i> , 2013, 14, 442.	1.2	100



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110	Transcript profiling by microarray and marker analysis of the short cotton ( <i>Gossypium hirsutum</i> L.) fiber mutant Ligon lintless-1 (Li 1 ). BMC Genomics, 2013, 14, 403.	1.2	43
111	Transcription profile of soybean-root-knot nematode interaction reveals a key role of phytohormones in the resistance reaction. BMC Genomics, 2013, 14, 322.	1.2	56
112	Identification of molecular processes needed for vascular formation through transcriptome analysis of different vascular systems. BMC Genomics, 2013, 14, 217.	1.2	21
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116	The integrative expression and co-expression analysis of the AGO gene family in rice. Gene, 2013, 528, 221-235.	1.0	24
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118	Genome-wide copy number variation in Hanwoo, Black Angus, and Holstein cattle. Mammalian Genome, 2013, 24, 151-163.	1.0	66
119	Application of an Improved Proteomics Method for Abundant Protein Cleanup: Molecular and Genomic Mechanisms Study in Plant Defense. Molecular and Cellular Proteomics, 2013, 12, 3431-3442.	2.5	24
120	A 34K <i>SNP</i> genotyping array for <i>Populus trichocarpa</i> : Design, application to the study of natural populations and transferability to other <i>Populus</i> species. Molecular Ecology Resources, 2013, 13, 306-323.	2.2	92
121	Molecular characterization of two small heat shock protein genes in rice: their expression patterns, localizations, networks, and heterogeneous overexpressions. Molecular Biology Reports, 2013, 40, 6709-6720.	1.0	26
122	Flower Development under Drought Stress: Morphological and Transcriptomic Analyses Reveal Acute Responses and Long-Term Acclimation in <i>Arabidopsis</i> . Plant Cell, 2013, 25, 3785-3807.	3.1	176
123	<i>Arabidopsis</i> KINETOCHORE NULL2 Is an Upstream Component for Centromeric Histone H3 Variant cenH3 Deposition at Centromeres. Plant Cell, 2013, 25, 3389-3404.	3.1	80
124	Asexual genome evolution in the apomictic <i>Ranunculus auricomus</i> complex: examining the effects of hybridization and mutation accumulation. Molecular Ecology, 2013, 22, 5908-5921.	2.0	118
125	Grafting with rootstocks induces extensive transcriptional re-programming in the shoot apical meristem of grapevine. BMC Plant Biology, 2013, 13, 147.	1.6	82
126	Transcriptome analysis of heat stress response in switchgrass ( <i>Panicum virgatum</i> L.). BMC Plant Biology, 2013, 13, 153.	1.6	91
127	Circles within circles: crosstalk between protein Ser/Thr/Tyr-phosphorylation and Met oxidation. BMC Bioinformatics, 2013, 14, S14.	1.2	13



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128	A global profiling of uncapped mRNAs under cold stress reveals specific decay patterns and endonucleolytic cleavages in <i>Brachypodium distachyon</i> . <i>Genome Biology</i> , 2013, 14, R92.	13.9	22
129	Transcriptomic analysis highlights epigenetic and transcriptional regulation during zygotic embryo development of <i>Pinus pinaster</i> . <i>BMC Plant Biology</i> , 2013, 13, 123.	1.6	37
130	GOParGenPy: a high throughput method to generate Gene Ontology data matrices. <i>BMC Bioinformatics</i> , 2013, 14, 242.	1.2	5
131	Transcriptional profiling of <i>Zea mays</i> roots reveals roles for jasmonic acid and terpenoids in resistance against <i>Phytophthora cinnamomi</i> . <i>Functional and Integrative Genomics</i> , 2013, 13, 217-228.	1.4	56
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134	Comprehensive transcriptomic study on horse gram ( <i>Macrotyloma uniflorum</i> ): De novo assembly, functional characterization and comparative analysis in relation to drought stress. <i>BMC Genomics</i> , 2013, 14, 647.	1.2	71
135	Incipient stem cell niche conversion in tissue culture: using a systems approach to probe early events in <i>WUSCHEL</i> -dependent conversion of lateral root primordia into shoot meristems. <i>Plant Journal</i> , 2013, 73, 798-813.	2.8	80
136	Whole genome sequencing of Gir cattle for identifying polymorphisms and loci under selection. <i>Genome</i> , 2013, 56, 592-598.	0.9	63
137	Early Transcriptomic Adaptation to Na <sup>2+</sup> CO <sup>3</sup> Stress Altered the Expression of a Quarter of the Total Genes in the Maize Genome and Exhibited Shared and Distinctive Profiles with Na <sup>C</sup> l and High p <sup>H</sup> Stresses. <i>Journal of Integrative Plant Biology</i> , 2013, 55, 1147-1165.	4.1	22
138	Transcriptome sequencing of the Antarctic vascular plant <i>Deschampsia antarctica</i> Desv. under abiotic stress. <i>Planta</i> , 2013, 237, 823-836.	1.6	44
139	<i>TALE</i> 1 from <i>Xanthomonas axonopodis</i> pv. <i>manihotis</i> acts as a transcriptional activator in plant cells and is important for pathogenicity in cassava plants. <i>Molecular Plant Pathology</i> , 2013, 14, 84-95.	2.0	37
140	Cell Type-Specific Transcriptome Analysis of the Soybean Leaf Paraveinal Mesophyll Layer. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 210-221.	1.0	4
141	Transcriptome analysis of <i>Chlamydomonas reinhardtii</i> during the process of lipid accumulation. <i>Genomics</i> , 2013, 101, 229-237.	1.3	102
142	Identification of Immunity-related Genes in <i>Arabidopsis</i> and Cassava Using Genomic Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 345-353.	3.0	8
143	Transcriptional Regulatory Network of <i>Arabidopsis</i> Starch Metabolism under Extensive Light Condition: A Potential Model of Transcription-modulated Starch Metabolism in Roots of Starchy Crops. <i>Procedia Computer Science</i> , 2013, 23, 113-121.	1.2	3
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316	Proteomics profiling of fiber development and domestication in upland cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 462 1.6 25	1.6	25
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603	Identification of Drought Tolerant Mechanisms in Maize Seedlings Based on Transcriptome Analysis of Recombination Inbred Lines. <i>Frontiers in Plant Science</i> , 2016, 7, 1080.	1.7	98
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622	Identification of Flowering-Related Genes Responsible for Differences in Bolting Time between Two Radish Inbred Lines. <i>Frontiers in Plant Science</i> , 2016, 7, 1844.	1.7	26
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625	Jasmonate Signalling and Defence Responses in the Model Legume <i>Medicago truncatula</i> —A Focus on Responses to <i>Fusarium</i> Wilt Disease. <i>Plants</i> , 2016, 5, 11.	1.6	9
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633	Natural variation of H3K27me3 modification in two <i>Arabidopsis</i> accessions and their hybrid. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 466-474.	4.1	17
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651	A novel mutant allele of SSI2 confers a better balance between disease resistance and plant growth inhibition on <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2016, 16, 208.	1.6	21
652	RNA-seq-based digital gene expression analysis reveals modification of host defense responses by rice stripe virus during disease symptom development in <i>Arabidopsis</i> . <i>Virology Journal</i> , 2016, 13, 202.	1.4	32
653	PoplarGene: poplar gene network and resource for mining functional information for genes from woody plants. <i>Scientific Reports</i> , 2016, 6, 31356.	1.6	11
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655	Co-expression network analyses identify functional modules associated with development and stress response in <i>Gossypium arboreum</i> . <i>Scientific Reports</i> , 2016, 6, 38436.	1.6	46
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660	Co-expression network analysis of duplicate genes in maize ( <i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , 2016, 17, 875.	1.2	36
661	Ty1-copia elements reveal diverse insertion sites linked to polymorphisms among flax ( <i>Linum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj	1.2	10
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665	De novo Transcriptome Analysis Reveals Distinct Defense Mechanisms by Young and Mature Leaves of <i>Hevea brasiliensis</i> (Para Rubber Tree). <i>Scientific Reports</i> , 2016, 6, 33151.	1.6	40
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670	Small RNA profiles in soybean primary root tips under water deficit. <i>BMC Systems Biology</i> , 2016, 10, 126.	3.0	33
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682	Variation in Linked Selection and Recombination Drive Genomic Divergence during Allopatric Speciation of European and American Aspens. <i>Molecular Biology and Evolution</i> , 2016, 33, 1754-1767.	3.5	83
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684	Differential miRNA expression in maize ear subjected to shading tolerance. <i>Acta Physiologiae Plantarum</i> , 2016, 38, 1.	1.0	5
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687	Cassava ( <i>Manihot esculenta</i> ) transcriptome analysis in response to infection by the fungus <i>Colletotrichum gloeosporioides</i> using an oligonucleotide-DNA microarray. <i>Journal of Plant Research</i> , 2016, 129, 711-726.	1.2	28
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690	Early transcriptomic response of <i>Arabidopsis thaliana</i> to polymetallic contamination: implications for the identification of potential biomarkers of metal exposure. <i>Metallomics</i> , 2016, 8, 518-531.	1.0	10
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700	Proteomic analysis of pear ( <i>Pyrus pyrifolia</i> ) ripening process provides new evidence for the sugar/acid metabolism difference between core and mesocarp. <i>Proteomics</i> , 2016, 16, 3025-3041.	1.3	16
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702	Transcriptomic analysis for elucidating the physiological effects of 5-aminolevulinic acid accumulation on <i>Corynebacterium glutamicum</i> . <i>Microbiological Research</i> , 2016, 192, 292-299.	2.5	8
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1130	Transcriptome analysis of root nematode ( <i>Meloidogyne incognita</i> )-infected tomato ( <i>Solanum lycopersicum</i> ) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses. <i>Molecular Plant Pathology</i> , 2018, 19, 615-633.	2.0	127
1131	Transcriptional analysis of the interaction between the oomycete biocontrol agent, <i>Pythium oligandrum</i> , and the roots of <i>Vitis vinifera</i> L.. <i>Biological Control</i> , 2018, 120, 26-35.	1.4	18
1132	Development of iFOX - hunting as a functional genomic tool and demonstration of its use to identify early senescence-related genes in the polyploid <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 591-602.	4.1	24
1133	Comparative transcriptome combined with morpho-physiological analyses revealed key factors for differential cadmium accumulation in two contrasting sweet sorghum genotypes. <i>Plant Biotechnology Journal</i> , 2018, 16, 558-571.	4.1	106
1134	Whole genome re-sequencing reveals evolutionary patterns of sacred lotus ( <i>Nelumbo</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	4.1	37
1135	PCSD: a plant chromatin state database. <i>Nucleic Acids Research</i> , 2018, 46, D1157-D1167.	6.5	107
1136	Successive evolutionary steps drove Poideae grasses from tropical to temperate regions. <i>New Phytologist</i> , 2018, 217, 925-938.	3.5	27

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1141	Three <i>AtCesA6</i> -like members enhance biomass production by distinctively promoting cell growth in <i>Arabidopsis</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 976-988.	4.1	49
1142	Comprehensive description of genomewide nucleotide and structural variation in short-season soya bean. <i>Plant Biotechnology Journal</i> , 2018, 16, 749-759.	4.1	46
1143	<i>Arabidopsis</i> NAP-related proteins (NRPs) contribute to the coordination of plant growth, developmental rate, and age-related pathogen resistance under short days. <i>Plant Science</i> , 2018, 267, 124-134.	1.7	15
1144	Comparative epigenomics reveals evolution of duplicated genes in potato and tomato. <i>Plant Journal</i> , 2018, 93, 460-471.	2.8	33
1145	Transcriptome Profiling of <i>Melaleuca quinquenervia</i> Challenged by Myrtle Rust Reveals Differences in Defense Responses Among Resistant Individuals. <i>Phytopathology</i> , 2018, 108, 495-509.	1.1	16
1146	Profiling of Accessible Chromatin Regions across Multiple Plant Species and Cell Types Reveals Common Gene Regulatory Principles and New Control Modules. <i>Plant Cell</i> , 2018, 30, 15-36.	3.1	226
1147	Identification of virus-derived siRNAs and their targets in RBSDV-infected rice by deep sequencing. <i>Journal of Basic Microbiology</i> , 2018, 58, 227-237.	1.8	23
1148	Stage-Specific Gene Profiling of Germinal Cells Helps Delineate the Mitosis/Meiosis Transition. <i>Plant Physiology</i> , 2018, 176, 1610-1626.	2.3	19
1149	Illuminating the role of the G $\beta\gamma$ heterotrimeric G protein subunit, RGA1, in regulating photoprotection and photoavoidance in rice. <i>Plant, Cell and Environment</i> , 2018, 41, 451-468.	2.8	36
1150	Drought stress responses in maize are diminished by <i>Piriformospora indica</i> . <i>Plant Signaling and Behavior</i> , 2018, 13, e1414121.	1.2	87
1151	Identification of tomato miRNAs responsive to root colonization by endophytic <i>Pochonia chlamydosporia</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 907-919.	1.7	19
1152	Identification of circular RNAs and their targets during tomato fruit ripening. <i>Postharvest Biology and Technology</i> , 2018, 136, 90-98.	2.9	74
1153	Prominent alterations of wild barley leaf transcriptome in response to individual and combined drought acclimation and heat shock conditions. <i>Physiologia Plantarum</i> , 2018, 163, 18-29.	2.6	16
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1156	Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. <i>New Phytologist</i> , 2018, 217, 1292-1306.	3.5	92
1157	Alternative polyadenylation is involved in auxin-based plant growth and development. <i>Plant Journal</i> , 2018, 93, 246-258.	2.8	38
1158	Fine-mapping of QTLs for individual and total isoflavone content in soybean ( <i>Glycine max</i> L.) using a high-density genetic map. <i>Theoretical and Applied Genetics</i> , 2018, 131, 555-568.	1.8	34
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1161	Systematic miRNome profiling reveals differential microRNAs in transgenic maize metabolism. <i>Environmental Sciences Europe</i> , 2018, 30, 37.	2.6	0
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1166	iTRAQ analysis of a mouse acute myocardial infarction model reveals that vitamin D binding protein promotes cardiomyocyte apoptosis after hypoxia. <i>Oncotarget</i> , 2018, 9, 1969-1979.	0.8	9
1167	Unravelling transcriptome changes between two distinct maize inbred lines using RNA-seq. <i>Journal of Integrative Agriculture</i> , 2018, 17, 1574-1584.	1.7	2
1168	Transcriptomic evidence for distinct mechanisms underlying abscission deficiency in the <i>Arabidopsis</i> mutants <i>haesa/haesa-like 2</i> and <i>nevershed</i> . <i>BMC Research Notes</i> , 2018, 11, 754.	0.6	6
1169	Comparative Transcriptome Analysis between a Resistant and a Susceptible Wild Tomato Accession in Response to <i>Phytophthora parasitica</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 3735.	1.8	29
1170	Transcriptome-wide identification of genes involved in Ascorbate-Glutathione cycle (Halliwell-Asada pathway) and related pathway for elucidating its role in antioxidative potential in finger millet ( <i>Eleusine coracana</i> (L.)). <i>3 Biotech</i> , 2018, 8, 499.	1.1	17
1171	Maize multi-omics reveal roles for autophagic recycling in proteome remodelling and lipid turnover. <i>Nature Plants</i> , 2018, 4, 1056-1070.	4.7	124
1172	Changes of gene expression but not cytosine methylation are associated with male parental care reflecting behavioural state, social context, and individual flexibility. <i>Journal of Experimental Biology</i> , 2019, 222, .	0.8	12

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1174	Proteomic and ecophysiological responses of soybean ( <i>Glycine max</i> L.) root nodules to Pb and hg stress. <i>BMC Plant Biology</i> , 2018, 18, 283.	1.6	26
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1193	Chronic Adrenergic Signaling Causes Abnormal RNA Expression of Proliferative Genes in Fetal Sheep Islets. <i>Endocrinology</i> , 2018, 159, 3565-3578.	1.4	13
1194	Transcriptome reprogramming of resistant and susceptible peach genotypes during <i>Xanthomonas arboricola</i> pv. <i>pruni</i> early leaf infection. <i>PLoS ONE</i> , 2018, 13, e0196590.	1.1	13
1195	Microarray dataset of after-ripening induced mRNA oxidation in wheat seeds. <i>Data in Brief</i> , 2018, 21, 852-855.	0.5	5
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1197	Biomarkers for Early Stages of <i>Johne</i> 's Disease Infection and Immunization in Goats. <i>Frontiers in Microbiology</i> , 2018, 9, 2284.	1.5	11
1198	Comparative proteomic analysis of <i>Ulva prolifera</i> response to high temperature stress. <i>Proteome Science</i> , 2018, 16, 17.	0.7	18
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1204	Effects of sugarcane aphid herbivory on transcriptional responses of resistant and susceptible sorghum. <i>BMC Genomics</i> , 2018, 19, 774.	1.2	40
1205	<i>Cis</i> -regulated alternative splicing divergence and its potential contribution to environmental responses in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2019, 97, 555-570.	2.8	33
1206	Phosphate Deficiency Negatively Affects Early Steps of the Symbiosis between Common Bean and Rhizobia. <i>Genes</i> , 2018, 9, 498.	1.0	25
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1208	Comparative analysis of circular RNAs between soybean cytoplasmic male-sterile line NJCMS1A and its maintainer NJCMS1B by high-throughput sequencing. <i>BMC Genomics</i> , 2018, 19, 663.	1.2	35



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1210	Extensive Genetic Diversity is Present within North American Switchgrass Germplasm. <i>Plant Genome</i> , 2018, 11, 170055.	1.6	35
1211	Proteomics dataset containing proteins that obscure identification of TOPLESS interactors in <i>Arabidopsis</i> . <i>Data in Brief</i> , 2018, 20, 909-916.	0.5	0
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1225	Identification of transcription factors from NF-Y, NAC, and SPL families responding to osmotic stress in multiple tomato varieties. <i>Plant Science</i> , 2018, 274, 441-450.	1.7	9
1226	Genome-Wide Association Analyses Reveal the Importance of Alternative Splicing in Diversifying Gene Function and Regulating Phenotypic Variation in Maize. <i>Plant Cell</i> , 2018, 30, 1404-1423.	3.1	66

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1228	Omics approaches revealed how arbuscular mycorrhizal symbiosis enhances yield and resistance to leaf pathogen in wheat. <i>Scientific Reports</i> , 2018, 8, 9625.	1.6	108
1229	Temporal Analyses of Barley Malting Stages Using Shotgun Proteomics. <i>Proteomics</i> , 2018, 18, e1800025.	1.3	21
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1231	Systems Biology Approach for Elucidation of Plant Responses to Salinity Stress. , 2018, , 307-326.		1
1232	Rice H2A.Z negatively regulates genes responsive to nutrient starvation but promotes expression of key housekeeping genes. <i>Journal of Experimental Botany</i> , 2018, 69, 4907-4919.	2.4	33
1233	Phytohormone participation during <i>Citrus sinensis</i> non-host response to <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> . <i>Plant Gene</i> , 2018, 15, 28-36.	1.4	7
1234	Global analysis of H3K4me3/H3K27me3 in <i>Brachypodium distachyon</i> reveals <i>VRN3</i> as critical epigenetic regulation point in vernalization and provides insights into epigenetic memory. <i>New Phytologist</i> , 2018, 219, 1373-1387.	3.5	36
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1239	In Silico Approach for Sustainable Agriculture. , 2018, , .		1
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1246	Transcriptomic analyses of rice ( <i>Oryza sativa</i> ) genes and non-coding RNAs under nitrogen starvation using multiple omics technologies. <i>BMC Genomics</i> , 2018, 19, 532.	1.2	100
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1249	When Transcriptomics and Metabolomics Work Hand in Hand: A Case Study Characterizing Plant CDF Transcription Factors. <i>High-Throughput</i> , 2018, 7, 7.	4.4	4
1250	Genome-Wide Identification and Characterization of Warming-Related Genes in <i>Brassica rapa</i> ssp. <i>pekinensis</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 1727.	1.8	10
1251	Transcriptome Analysis Provides Insight into the Molecular Mechanisms Underlying gametophyte factor 2-Mediated Cross-Incompatibility in Maize. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1757.	1.8	9
1252	RNA-seq analysis reveals alternative splicing under salt stress in cotton, <i>Gossypium davidsonii</i> . <i>BMC Genomics</i> , 2018, 19, 73.	1.2	72
1253	Silicon protects soybean plants against <i>Phytophthora sojae</i> by interfering with effector-receptor expression. <i>BMC Plant Biology</i> , 2018, 18, 97.	1.6	80
1254	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
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1257	MCENet: A database for maize conditional co-expression network and network characterization collaborated with multi-dimensional omics levels. <i>Journal of Genetics and Genomics</i> , 2018, 45, 351-360.	1.7	39
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1269	Identification and characterization of ncRNA-associated ceRNA networks in Arabidopsis leaf development. <i>BMC Genomics</i> , 2018, 19, 607.	1.2	52
1270	Identifying QTL-allele system of seed protein content in Chinese soybean landraces for population differentiation studies and optimal cross predictions. <i>Euphytica</i> , 2018, 214, 1.	0.6	7
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1274	Unravelling miRNA regulation in yield of rice ( <i>Oryza sativa</i> ) based on differential network model. <i>Scientific Reports</i> , 2018, 8, 8498.	1.6	28
1275	Transcriptome analysis during ripening of table grape berry cv. Thompson Seedless. <i>PLoS ONE</i> , 2018, 13, e0190087.	1.1	23
1276	Computational exploration of cis-regulatory modules in rhythmic expression data using the "Exploration of Distinctive CREs and CRMs" (EDCC) and "CRM Network Generator" (CNG) programs. <i>PLoS ONE</i> , 2018, 13, e0190421.	1.1	3
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1283	Transcriptomic analysis of <i>Aegilops tauschii</i> during long-term salinity stress. <i>Functional and Integrative Genomics</i> , 2019, 19, 13-28.	1.4	30
1284	Deep sequencing identified potential miRNAs involved in defence response, stress and plant growth characteristics of wild genotypes of cardamom. <i>Plant Biology</i> , 2019, 21, 3-14.	1.8	8
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1288	Male Sterility in Maize after Transient Heat Stress during the Tetrad Stage of Pollen Development. <i>Plant Physiology</i> , 2019, 181, 683-700.	2.3	139
1289	Time-dependent effects of <i>Pochonia chlamydosporia</i> endophytism on gene expression profiles of colonized tomato roots. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 8511-8527.	1.7	14
1290	A chromosome-anchored eggplant genome sequence reveals key events in Solanaceae evolution. <i>Scientific Reports</i> , 2019, 9, 11769.	1.6	179
1291	Mapping and analysis of QTLs related to seed length and seed width in <i>Glycine max</i> . <i>Plant Breeding</i> , 2019, 138, 733-740.	1.0	3
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1294	DiVenn: An Interactive and Integrated Web-Based Visualization Tool for Comparing Gene Lists. <i>Frontiers in Genetics</i> , 2019, 10, 421.	1.1	85
1295	A Genetic Algorithm to Optimize Weighted Gene Co-Expression Network Analysis. <i>Journal of Computational Biology</i> , 2019, 26, 1349-1366.	0.8	18
1296	Transcriptome Landscape Variation in the Genus <i>Thymus</i> . <i>Genes</i> , 2019, 10, 620.	1.0	11
1297	Physiological responses and small RNAs changes in maize under nitrogen deficiency and resupply. <i>Genes and Genomics</i> , 2019, 41, 1183-1194.	0.5	22
1298	A multivariate Poisson-log normal mixture model for clustering transcriptome sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 394.	1.2	25

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1300	Identification of microRNAs responding to cold stress in Dongxiang common wild rice. <i>Genome</i> , 2019, 62, 635-642.	0.9	12
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1302	Transcriptomic Responses to Water Deficit and Nematode Infection in Mycorrhizal Tomato Roots. <i>Frontiers in Microbiology</i> , 2019, 10, 1807.	1.5	39
1303	Transcriptomic data during seed maturation in dormant and non-dormant genotypes of wheat ( <i>Triticum aestivum</i> L.). <i>Data in Brief</i> , 2019, 25, 104254.	0.5	1
1304	A Role for PICKLE in the Regulation of Cold and Salt Stress Tolerance in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 900.	1.7	58
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1306	Genome-Wide Profiling of Polyadenylation Events in Maize Using High-Throughput Transcriptomic Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2749-2760.	0.8	5
1307	Long noncoding RNAs in <i>Brassica rapa</i> L. following vernalization. <i>Scientific Reports</i> , 2019, 9, 9302.	1.6	42
1308	Characterization of functional relationships of R-loops with gene transcription and epigenetic modifications in rice. <i>Genome Research</i> , 2019, 29, 1287-1297.	2.4	38
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1310	Genome-wide identification and comparative analysis of drought-related microRNAs in two maize inbred lines with contrasting drought tolerance by deep sequencing. <i>PLoS ONE</i> , 2019, 14, e0219176.	1.1	40
1311	Activation and Characterization of Cryptic Gene Cluster: Two Series of Aromatic Polyketides Biosynthesized by Divergent Pathways. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 18046-18054.	7.2	12
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1315	An Integrative Approach to Analyze Seed Germination in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 1342.	1.7	31
1316	Diffusible signal factor (DSF)-mediated quorum sensing modulates expression of diverse traits in <i>Xanthomonas citri</i> and responses of citrus plants to promote disease. <i>BMC Genomics</i> , 2019, 20, 55.	1.2	35



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1318	Insight into transketolase of <i>Pyropia haitanensis</i> under desiccation stress based on integrative analysis of omics and transformation. <i>BMC Plant Biology</i> , 2019, 19, 475.	1.6	17
1319	Activation and Characterization of Cryptic Gene Cluster: Two Series of Aromatic Polyketides Biosynthesized by Divergent Pathways. <i>Angewandte Chemie</i> , 2019, 131, 18214-18222.	1.6	0
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1322	QTL mapping for aluminum tolerance in RIL population of soybean ( <i>Glycine max</i> L.) by RAD sequencing. <i>PLoS ONE</i> , 2019, 14, e0223674.	1.1	16
1323	Transcriptome Analyses of FY Mutants Reveal Its Role in mRNA Alternative Polyadenylation. <i>Plant Cell</i> , 2019, 31, 2332-2352.	3.1	36
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1330	Ray Parenchymal Cells Contribute to Lignification of Tracheids in Developing Xylem of Norway Spruce. <i>Plant Physiology</i> , 2019, 181, 1552-1572.	2.3	37
1331	Transcriptome Profiles of Strawberry ( <i>Fragaria vesca</i> ) Fruit Interacting With <i>Botrytis cinerea</i> at Different Ripening Stages. <i>Frontiers in Plant Science</i> , 2019, 10, 1131.	1.7	54
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1333	Global Transcriptional Insights of Pollen-Pistil Interactions Commencing Self-Incompatibility and Fertilization in Tea [ <i>Camellia sinensis</i> (L.) O. Kuntze]. <i>International Journal of Molecular Sciences</i> , 2019, 20, 539.	1.8	34
1334	Comparative analysis of two sister <i>Erythrophleum</i> species (Leguminosae) reveal contrasting transcriptome-wide responses to early drought stress. <i>Gene</i> , 2019, 694, 50-62.	1.0	2

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1339	Rapid identification of a candidate nicosulfuron sensitivity gene (Nss) in maize ( <i>Zea mays</i> L.) via combining bulked segregant analysis and RNA-seq. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1351-1361.	1.8	30
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1343	RNA-seq reveals differentially expressed genes in rice ( <i>Oryza sativa</i> ) roots during interactions with plant-growth promoting bacteria, <i>Azospirillum brasilense</i> . <i>PLoS ONE</i> , 2019, 14, e0217309.	1.1	40
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1345	Dysfunction in the arbuscular mycorrhizal symbiosis has consistent but small effects on the establishment of the fungal microbiota in <i>Lotus japonicus</i> . <i>New Phytologist</i> , 2019, 224, 409-420.	3.5	16
1346	Lateral Root and Nodule Transcriptomes of Soybean. <i>Data</i> , 2019, 4, 64.	1.2	8
1347	Identification of microRNA-target modules from rice variety Pusa Basmati-1 under high temperature and salt stress. <i>Functional and Integrative Genomics</i> , 2019, 19, 867-888.	1.4	12
1348	Comparative RNA-Sequencing and DNA Methylation Analyses of Apple ( <i>Malus domestica</i> Borkh.) Buds with Diverse Flowering Capabilities Reveal Novel Insights into the Regulatory Mechanisms of Flower Bud Formation. <i>Plant and Cell Physiology</i> , 2019, 60, 1702-1721.	1.5	27
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1350	miRNome. <i>Compendium of Plant Genomes</i> , 2019, , 195-203.	0.3	0
1351	Comparative analysis of the transcriptomes of the calyx abscission zone of sweet orange insights into the huanglongbing-associated fruit abscission. <i>Horticulture Research</i> , 2019, 6, 71.	2.9	39
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1354	Trait ontology analysis based on association mapping studies bridges the gap between crop genomics and Phenomics. <i>BMC Genomics</i> , 2019, 20, 443.	1.2	8
1355	The Globe Artichoke Genome. <i>Compendium of Plant Genomes</i> , 2019, , .	0.3	1
1356	Secondary metabolites have more influence than morphophysiological traits on litter decomposability across genotypes of <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2019, 224, 1532-1543.	3.5	7
1357	Identification and Analysis of Micro-Exon Genes in the Rice Genome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2685.	1.8	6
1358	Analysis of miRNAs Targeted Storage Regulatory Genes during Soybean Seed Development Based on Transcriptome Sequencing. <i>Genes</i> , 2019, 10, 408.	1.0	14
1359	Gene Expression analysis associated with salt stress in a reciprocally crossed rice population. <i>Scientific Reports</i> , 2019, 9, 8249.	1.6	66
1360	New steps in mucilage biosynthesis revealed by analysis of the transcriptome of the UDP-rhamnose/UDP-galactose transporter 2 mutant. <i>Journal of Experimental Botany</i> , 2019, 70, 5071-5088.	2.4	14
1361	Cytological and transcriptome analysis reveal that interaction at Sb pollen sterility locus cause down-regulation of important meiosis-related genes associated with high pollen sterility in autotetraploid rice hybrids. <i>Plant Physiology and Biochemistry</i> , 2019, 141, 73-82.	2.8	9
1362	Transcriptional Regulatory Network of GA Floral Induction Pathway in LA Hybrid Lily. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2694.	1.8	13
1363	Transcriptome analysis of bolting in <i>A. tequilana</i> reveals roles for florigen, MADS, fructans and gibberellins. <i>BMC Genomics</i> , 2019, 20, 473.	1.2	17
1364	Deciphering the non-coding RNA-level response to arsenic stress in rice ( <i>Oryza sativa</i> ). <i>Plant Signaling and Behavior</i> , 2019, 14, 1629268.	1.2	22
1365	Construction and analysis of an interologous protein-protein interaction network of <i>Camellia sinensis</i> leaf (TeaLIPIN) from RNA-Seq data sets. <i>Plant Cell Reports</i> , 2019, 38, 1249-1262.	2.8	9
1366	Long-range interactions between proximal and distal regulatory regions in maize. <i>Nature Communications</i> , 2019, 10, 2633.	5.8	79
1367	Salt-Responsive Genes are Differentially Regulated at the Chromatin Levels Between Seedlings and Roots in Rice. <i>Plant and Cell Physiology</i> , 2019, 60, 1790-1803.	1.5	33
1368	Transcriptomic Response to Feeding and Starvation in a Herbivorous Dinoflagellate. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	7
1369	Meta-analysis of drought-tolerant genotypes in <i>Oryza sativa</i> : A network-based approach. <i>PLoS ONE</i> , 2019, 14, e0216068.	1.1	40
1370	Transcriptional profiling of contrasting genotypes revealed key candidates and nucleotide variations for drought dissection in <i>Camellia sinensis</i> (L.) O. Kuntze. <i>Scientific Reports</i> , 2019, 9, 7487.	1.6	32

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1372	RNA-Seq analysis and transcriptome assembly of raspberry fruit ( <i>Rubus idaeus</i> "Heritage") revealed several candidate genes involved in fruit development and ripening. <i>Scientia Horticulturae</i> , 2019, 254, 26-34.	1.7	15
1373	Dynamic Transcriptome Changes Related to Oil Accumulation in Developing Soybean Seeds. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2202.	1.8	26
1374	Cold stress activates disease resistance in <i>Arabidopsis thaliana</i> through a salicylic acid dependent pathway. <i>Plant, Cell and Environment</i> , 2019, 42, 2645-2663.	2.8	58
1375	Identification of miRNAs and Their Response to Cold Stress in <i>Astragalus Membranaceus</i> . <i>Biomolecules</i> , 2019, 9, 182.	1.8	51
1376	Charting oat ( <i>Avena sativa</i> ) embryo and endosperm transcription factor expression reveals differential expression of potential importance for seed development. <i>Molecular Genetics and Genomics</i> , 2019, 294, 1183-1197.	1.0	7
1377	Transcriptional regulation of <i>Lonicera japonica</i> Thunb. during flower development as revealed by comprehensive analysis of transcription factors. <i>BMC Plant Biology</i> , 2019, 19, 198.	1.6	26
1378	Global Transcriptomic Profile Analysis of Genes Involved in Lignin Biosynthesis and Accumulation Induced by Boron Deficiency in Poplar Roots. <i>Biomolecules</i> , 2019, 9, 156.	1.8	19
1379	Genome-Wide Analysis of Glycoside Hydrolase Family 1 $\beta$ -glucosidase Genes in <i>Brassica rapa</i> and Their Potential Role in Pollen Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1663.	1.8	24
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1381	Characterization of the Nicotianamine Exporter ENA1 in Rice. <i>Frontiers in Plant Science</i> , 2019, 10, 502.	1.7	21
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1383	Comparative transcriptomics analysis of compatible wild type and incompatible <i>l'laeA</i> mutant strains of <i>Epichloa festucae</i> in association with perennial ryegrass. <i>Data in Brief</i> , 2019, 24, 103843.	0.5	7
1384	Identification of genes preferentially expressed in wild strawberry receptacle fruit and demonstration of their promoter activities. <i>Horticulture Research</i> , 2019, 6, 50.	2.9	6
1385	Eggplant Domestication: Pervasive Gene Flow, Feralization, and Transcriptomic Divergence. <i>Molecular Biology and Evolution</i> , 2019, 36, 1359-1372.	3.5	47
1386	Draft genome of <i>Santalum album</i> L. provides genomic resources for accelerated trait improvement. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	15
1387	Transcriptome Profiling and Genome-Wide Association Studies Reveal GSTs and Other Defense Genes Involved in Multiple Signaling Pathways Induced by Herbicide Safener in Grain Sorghum. <i>Frontiers in Plant Science</i> , 2019, 10, 192.	1.7	24
1388	Transcriptomic analysis of contrasting inbred lines and F2 segregant of Chinese cabbage provides valuable information on leaf morphology. <i>Genes and Genomics</i> , 2019, 41, 811-829.	0.5	1

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1390	ABSCISIC ACID-INSENSITIVE 3 is involved in brassinosteroid-mediated regulation of flowering in plants. <i>Plant Physiology and Biochemistry</i> , 2019, 139, 207-214.	2.8	18
1391	Functional annotation and characterization of hypothetical protein involved in blister blight tolerance in tea ( <i>Camellia sinensis</i> (L) O. Kuntze). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 447-459.	0.9	6
1392	Genome of <i>Crucihimalaya himalaica</i> , a close relative of <i>Arabidopsis</i> , shows ecological adaptation to high altitude. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7137-7146.	3.3	108
1393	Transcriptomic dynamics provide an insight into the mechanism for silicon-mediated alleviation of salt stress in cucumber plants. <i>Ecotoxicology and Environmental Safety</i> , 2019, 174, 245-254.	2.9	60
1394	Metabolomic and transcriptomic changes underlying cold and anaerobic stresses after storage of table grapes. <i>Scientific Reports</i> , 2019, 9, 2917.	1.6	33
1395	Genome-wide analysis of long non-coding RNAs unveils the regulatory roles in the heat tolerance of Chinese cabbage ( <i>Brassica rapa</i> ssp. <i>chinensis</i> ). <i>Scientific Reports</i> , 2019, 9, 5002.	1.6	95
1396	Maize glossy6 is involved in cuticular wax deposition and drought tolerance. <i>Journal of Experimental Botany</i> , 2019, 70, 3089-3099.	2.4	62
1397	The Chromatin-Associated Protein PWO1 Interacts with Plant Nuclear Lamin-like Components to Regulate Nuclear Size. <i>Plant Cell</i> , 2019, 31, 1141-1154.	3.1	56
1398	A <i>Phytophthora capsici</i> Effector Targets ACD11 Binding Partners that Regulate ROS-Mediated Defense Response in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2019, 12, 565-581.	3.9	95
1399	Transcriptome analysis of a rice cultivar reveals the differentially expressed genes in response to wild and mutant strains of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> . <i>Scientific Reports</i> , 2019, 9, 3757.	1.6	19
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1401	Identification of phloem-associated transcriptome alterations during leaf development in <i>Prunus domestica</i> L. <i>Horticulture Research</i> , 2019, 6, 16.	2.9	10
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1403	Key Maize Drought-Responsive Genes and Pathways Revealed by Comparative Transcriptome and Physiological Analyses of Contrasting Inbred Lines. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1268.	1.8	78
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1409	Identification and characterization of dwarf mistletoe responding genes in Ziarat juniper tree ( <i>Juniperus excelsa</i> M.Bieb) through suppression subtractive hybridization and deep sequencing. <i>Trees - Structure and Function</i> , 2019, 33, 1027-1039.	0.9	1
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1414	Spatio-Temporal Transcriptional Dynamics of Maize Long Non-Coding RNAs Responsive to Drought Stress. <i>Genes</i> , 2019, 10, 138.	1.0	41
1415	Transcriptome Analysis of Chinese Chestnut ( <i>Castanea mollissima</i> Blume) in Response to <i>Dryocosmus kuriphilus</i> Yasumatsu Infestation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 855.	1.8	19
1416	RNA Binding Motif Protein 48 Is Required for U12 Splicing and Maize Endosperm Differentiation. <i>Plant Cell</i> , 2019, 31, 715-733.	3.1	27
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1467	<i>Gb</i> CYP86A1 from <i>Gossypium barbadense</i> positively regulates defence against <i>Verticillium dahliae</i> by cell wall modification and activation of immune pathways. <i>Plant Biotechnology Journal</i> , 2020, 18, 222-238.	4.1	37
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1474	Ethephon-regulated maize internode elongation associated with modulating auxin and gibberellin signal to alter cell wall biosynthesis and modification. <i>Plant Science</i> , 2020, 290, 110196.	1.7	35
1475	A role for Arabidopsis growth-regulating factors 1 and 3 in growth-stress antagonism. <i>Journal of Experimental Botany</i> , 2020, 71, 1402-1417.	2.4	32
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1487	Genetic regulatory networks for salt-alkali stress in <i>Gossypium hirsutum</i> with differing morphological characteristics. <i>BMC Genomics</i> , 2020, 21, 15.	1.2	33
1488	Favorable haplotypes and associated genes for flowering time and photoperiod sensitivity identified by comparative selective signature analysis and GWAS in temperate and tropical maize. <i>Crop Journal</i> , 2020, 8, 227-242.	2.3	6
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1520	Technical benefit on apple fruit of controlled atmosphere influenced by 1-MCP at molecular levels. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1443-1457.	1.0	1
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1539	Differential Gene Expression Analysis of Wheat Breeding Lines Reveal Molecular Insights in Yellow Rust Resistance under Field Conditions. <i>Agronomy</i> , 2020, 10, 1888.	1.3	8
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1542	Temperature differentially modulates the transcriptome response in <i>Oryza sativa</i> to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> infection. <i>Genomics</i> , 2020, 112, 4842-4852.	1.3	11
1543	Global mRNA and microRNA expression dynamics in response to anthracnose infection in sorghum. <i>BMC Genomics</i> , 2020, 21, 760.	1.2	20
1544	Potential Molecular Mechanisms of Plantain in the Treatment of Gout and Hyperuricemia Based on Network Pharmacology. <i>Evidence-based Complementary and Alternative Medicine</i> , 2020, 2020, 1-20.	0.5	20
1545	Transcriptomic data-driven discovery of global regulatory features of rice seeds developing under heat stress. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2556-2567.	1.9	7
1546	Transcriptomic profiling of purple broccoli reveals light-induced anthocyanin biosynthetic signaling and structural genes. <i>PeerJ</i> , 2020, 8, e8870.	0.9	19
1547	The draft genome sequence of an upland wild rice species, <i>Oryza granulata</i> . <i>Scientific Data</i> , 2020, 7, 131.	2.4	21
1548	Bioinformatics Resources for Plant Abiotic Stress Responses: State of the Art and Opportunities in the Fast Evolving -Omics Era. <i>Plants</i> , 2020, 9, 591.	1.6	25
1549	Exploring dynamic protein-protein interactions in cassava through the integrative interactome network. <i>Scientific Reports</i> , 2020, 10, 6510.	1.6	15
1550	De novo transcriptome sequence of <i>Senna tora</i> provides insights into anthraquinone biosynthesis. <i>PLoS ONE</i> , 2020, 15, e0225564.	1.1	14
1551	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
1552	Transcriptional dynamics of Zn-accumulation in developing kernels of maize reveals important Zn-uptake mechanisms. <i>Genomics</i> , 2020, 112, 3435-3447.	1.3	9

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1553	Draft genomes of two outcrossing wild rice, <i>Oryza rufipogon</i> and <i>O. longistaminata</i> , reveal genomic features associated with mating system evolution. <i>Plant Direct</i> , 2020, 4, e00232.	0.8	9
1554	Cell-type-dependent histone demethylase specificity promotes meiotic chromosome condensation in <i>Arabidopsis</i> . <i>Nature Plants</i> , 2020, 6, 823-837.	4.7	13
1555	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
1556	Transcriptome analyses suggest that changes in fungal endophyte lifestyle could be involved in grapevine bud necrosis. <i>Scientific Reports</i> , 2020, 10, 9514.	1.6	14
1557	Functional characterization of <i>Arabidopsis</i> ARGONAUTE 3 in reproductive tissues. <i>Plant Journal</i> , 2020, 103, 1796-1809.	2.8	22
1559	RNA-seq Reveals Differentially Expressed Genes between Two indica Inbred Rice Genotypes Associated with Drought-Yield QTLs. <i>Agronomy</i> , 2020, 10, 621.	1.3	21
1560	Comparative Transcriptome Analysis of Two Contrasting Soybean Varieties in Response to Aluminum Toxicity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4316.	1.8	16
1561	<i>ENO1</i> regulates tomato fruit size through the floral meristem development network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8187-8195.	3.3	108
1562	miR159 Represses a Constitutive Pathogen Defense Response in Tobacco. <i>Plant Physiology</i> , 2020, 182, 2182-2198.	2.3	30
1564	The zoospores of the thraustochytrid <i>Aurantiochytrium limacinum</i> : Transcriptional reprogramming and lipid metabolism associated to their specific functions. <i>Environmental Microbiology</i> , 2020, 22, 1901-1916.	1.8	9
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1566	Seasonal nitrogen remobilization and the role of auxin transport in poplar trees. <i>Journal of Experimental Botany</i> , 2020, 71, 4512-4530.	2.4	14
1567	Mapping and validation of a fiber length QTL on chromosome D11 using two independent F2 populations of upland cotton. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	6
1568	Melatonin improves rice salinity stress tolerance by NADPH oxidase-dependent control of the plasma membrane K <sup>+</sup> transporters and K <sup>+</sup> homeostasis. <i>Plant, Cell and Environment</i> , 2020, 43, 2591-2605.	2.8	93
1569	Water lily ( <i>Nymphaea thermarum</i> ) genome reveals variable genomic signatures of ancient vascular cambium losses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8649-8656.	3.3	33
1570	Epigenomic Regulatory Mechanism in Vegetative Phase Transition of <i>Malus hupehensis</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 4812-4829.	2.4	10
1571	The Role of Gibberellins in Regulation of Nitrogen Uptake and Physiological Traits in Maize Responding to Nitrogen Availability. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1824.	1.8	23
1572	Identification of introduced and stably inherited DNA methylation variants in soybean associated with soybean cyst nematode parasitism. <i>New Phytologist</i> , 2020, 227, 168-184.	3.5	27

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1574	Genomic variation between PRSV resistant transgenic SunUp and its progenitor cultivar Sunset. <i>BMC Genomics</i> , 2020, 21, 398.	1.2	3
1575	Characterization of microRNA genes from Pigeonpea ( <i>Cajanus cajan</i> L.) and understanding their involvement in drought stress. <i>Journal of Biotechnology</i> , 2020, 321, 23-34.	1.9	10
1576	Genetic architecture, demographic history, and genomic differentiation of <i>Populus davidiana</i> revealed by whole-genome resequencing. <i>Evolutionary Applications</i> , 2020, 13, 2582-2596.	1.5	10
1577	Generation of High Yielding and Fragrant Rice ( <i>Oryza sativa</i> L.) Lines by CRISPR/Cas9 Targeted Mutagenesis of Three Homoeologs of Cytochrome P450 Gene Family and OsBADH2 and Transcriptome and Proteome Profiling of Revealed Changes Triggered by Mutations. <i>Plants</i> , 2020, 9, 788.	1.6	57
1578	Genomic identification of salt induced microRNAs in niger ( <i>Guizotia abyssinica</i> Cass.). <i>Plant Gene</i> , 2020, 23, 100242.	1.4	5
1579	Morphological and metabolic profiling of a tropical-adapted potato association panel subjected to water recovery treatment reveals new insights into plant vigor. <i>Plant Journal</i> , 2020, 103, 2193-2210.	2.8	10
1580	PHYTOCHROME-INTERACTING FACTOR-LIKE14 and SLENDER RICE1 Interaction Controls Seedling Growth under Salt Stress. <i>Plant Physiology</i> , 2020, 184, 506-517.	2.3	60
1581	Identification and characterization of differentially expressed genes in the rice root following exogenous application of spermidine during salt stress. <i>Genomics</i> , 2020, 112, 4125-4136.	1.3	2
1582	Comparative transcriptomics reveals candidate transcription factors involved in costunolide biosynthesis in medicinal plant-Saussurea lappa. <i>International Journal of Biological Macromolecules</i> , 2020, 150, 52-67.	3.6	13
1583	Comparative transcriptome provides molecular insight into defense-associated mechanisms against spider mite in resistant and susceptible common bean cultivars. <i>PLoS ONE</i> , 2020, 15, e0228680.	1.1	15
1584	TGF $\beta$ 2 Signaling Plays a Pivotal Role During Developmental Biliary Atresia in Sea Lamprey ( <i>Petromyzon</i> ) Tj ETQq1 1.0.784314 rgBT /Ov	2.0	6
1585	Spatial transcriptional dynamics of geographically separated genotypes revealed key regulators of podophyllotoxin biosynthesis in <i>Podophyllum hexandrum</i> . <i>Industrial Crops and Products</i> , 2020, 147, 112247.	2.5	11
1587	Genome-wide identification and comparative analysis of drought related genes in roots of two maize inbred lines with contrasting drought tolerance by RNA sequencing. <i>Journal of Integrative Agriculture</i> , 2020, 19, 449-464.	1.7	17
1588	PIF4 and HOOKLESS1 Impinge on Common Transcriptome and Isoform Regulation in Thermomorphogenesis. <i>Plant Communications</i> , 2020, 1, 100034.	3.6	28
1589	Global identification and analysis revealed differentially expressed lncRNAs associated with meiosis and low fertility in autotetraploid rice. <i>BMC Plant Biology</i> , 2020, 20, 82.	1.6	28
1590	Dual Transcriptome and Metabolic Analysis of <i>Vitis vinifera</i> cv. Pinot Noir Berry and <i>Botrytis cinerea</i> During Quiescence and Egressed Infection. <i>Frontiers in Plant Science</i> , 2019, 10, 1704.	1.7	26
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1593	An endophyte from salt-adapted Pokkali rice confers salt-tolerance to a salt-sensitive rice variety and targets a unique pattern of genes in its new host. <i>Scientific Reports</i> , 2020, 10, 3237.	1.6	58
1594	Rice pyramided line IRBB67 (Xa4/Xa7) homeostasis under combined stress of high temperature and bacterial blight. <i>Scientific Reports</i> , 2020, 10, 683.	1.6	27
1595	Differential Expression of Genes at Panicle Initiation and Grain Filling Stages Implied in Heterosis of Rice Hybrids. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1080.	1.8	12
1596	Host and symbiont genetic determinants of nutritional phenotype in a natural population of the pea aphid. <i>Molecular Ecology</i> , 2020, 29, 848-858.	2.0	15
1597	Molecular and genetic bases of heat stress responses in crop plants and breeding for increased resilience and productivity. <i>Journal of Experimental Botany</i> , 2020, 71, 3780-3802.	2.4	186
1598	Quantitative trait loci analysis of seed oil content and composition of wild and cultivated soybean. <i>BMC Plant Biology</i> , 2020, 20, 51.	1.6	36
1599	Dissection of Dynamic Transcriptome Landscape of Leaf, Bract, and Lupulin Gland in Hop ( <i>Humulus lupulifera</i> ) Tj ETQq1 1 0.784314 rgBT /Overl... 1.8 19	1.8	19
1600	Monitoring rice anther proteome expression patterns during pollen development. <i>Plant Biotechnology Reports</i> , 2020, 14, 293-300.	0.9	1
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1603	Ascorbate oxidation activates systemic defence against root-knot nematode <i>Meloidogyne graminicola</i> in rice. <i>Journal of Experimental Botany</i> , 2020, 71, 4271-4284.	2.4	26
1604	Large-scale identification of expression quantitative trait loci in <i>Arabidopsis</i> reveals novel candidate regulators of immune responses and other processes. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 1469-1484.	4.1	7
1605	In <i>Arabidopsis thaliana</i> Heterosis Level Varies among Individuals in an F1 Hybrid Population. <i>Plants</i> , 2020, 9, 414.	1.6	2
1606	The Spread and Transmission of Sweet Potato Virus Disease (SPVD) and Its Effect on the Gene Expression Profile in Sweet Potato. <i>Plants</i> , 2020, 9, 492.	1.6	17
1607	mGWAS Uncovers Gln-Glucosinolate Seed-Specific Interaction and its Role in Metabolic Homeostasis. <i>Plant Physiology</i> , 2020, 183, 483-500.	2.3	24
1608	WRKY15 Suppresses Tracheary Element Differentiation Upstream of VND7 During Xylem Formation. <i>Plant Cell</i> , 2020, 32, 2307-2324.	3.1	36
1609	Epigenomic regulation of OTU5 in <i>Arabidopsis thaliana</i> . <i>Genomics</i> , 2020, 112, 3549-3559.	1.3	7

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1611	Root system architecture, physiological analysis and dynamic transcriptomics unravel the drought-responsive traits in rice genotypes. <i>Ecotoxicology and Environmental Safety</i> , 2021, 207, 111252.	2.9	39
1612	LAZY1 Controls Tiller Angle and Shoot Gravitropism by Regulating the Expression of Auxin Transporters and Signaling Factors in Rice. <i>Plant and Cell Physiology</i> , 2021, 61, 2111-2125.	1.5	27
1613	Transcriptome analysis reveals rice MADS13 as an important repressor of the carpel development pathway in ovules. <i>Journal of Experimental Botany</i> , 2021, 72, 398-414.	2.4	7
1614	Proteomic investigation of Zn-challenged rice roots reveals adverse effects and root physiological adaptation. <i>Plant and Soil</i> , 2021, 460, 69-88.	1.8	9
1615	TCP5 controls leaf margin development by regulating KNOX and BEL-like transcription factors in Arabidopsis. <i>Journal of Experimental Botany</i> , 2021, 72, 1809-1821.	2.4	26
1616	Comparative RNA-Seq analysis of the root revealed transcriptional regulation system for aluminum tolerance in contrasting indica rice of North East India. <i>Protoplasma</i> , 2021, 258, 517-528.	1.0	6
1617	Multiple-genotypes transcriptional analysis revealed candidate genes and nucleotide variants for improvement of quality characteristics in tea ( <i>Camellia sinensis</i> (L.) O. Kuntze). <i>Genomics</i> , 2021, 113, 305-316.	1.3	10
1618	TOA: A software package for automated functional annotation in non-model plant species. <i>Molecular Ecology Resources</i> , 2021, 21, 621-636.	2.2	10
1619	The transcriptional response to salicylic acid plays a role in Fusarium yellows resistance in Brassica rapa L. <i>Plant Cell Reports</i> , 2021, 40, 605-619.	2.8	7
1620	Candidatus Liberibacter asiaticus manipulates the expression of vitellogenin, cytoskeleton, and endocytotic pathway-related genes to become circulative in its vector, Diaphorina citri (Hemiptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5		
1621	Arabidopsis REI-LIKE proteins activate ribosome biogenesis during cold acclimation. <i>Scientific Reports</i> , 2021, 11, 2410.	1.6	19
1622	Profiling of MicroRNAs and Their Targets in Roots and Shoots Reveals a Potential MiRNA-Mediated Interaction Network in Response to Phosphate Deficiency in the Forestry Tree <i>Betula luminifera</i> . <i>Frontiers in Genetics</i> , 2021, 12, 552454.	1.1	10
1623	Auxin is involved in arbuscular mycorrhizal fungi-promoted tomato growth and NADP-malic enzymes expression in continuous cropping substrates. <i>BMC Plant Biology</i> , 2021, 21, 48.	1.6	22
1624	Transcriptome and degradome sequencing reveals changes in <i>Populus alba</i> caused by its allelopathic response to p-hydroxybenzoic acid. <i>Journal of Forestry Research</i> , 2021, 32, 2155-2168.	1.7	3
1625	Microarray analysis of <i>Arabidopsis thaliana</i> exposed to single and mixed infections with Cucumber mosaic virus and turnip viruses. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 11-27.	1.4	2
1626	Silencing of an Ubiquitin Ligase Increases Grain Width and Weight in indica Rice. <i>Frontiers in Genetics</i> , 2020, 11, 600378.	1.1	10
1627	Selection of transcripts related to low-temperature tolerance using RNA sequencing from F2 plants between japonica and indica rice ( <i>Oryza sativa</i> L.) cultivars. <i>Functional Plant Biology</i> , 2021, 48, 984.	1.1	3

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1629	Linkage analysis, GWAS, transcriptome analysis to identify candidate genes for rice seedlings in response to high temperature stress. <i>BMC Plant Biology</i> , 2021, 21, 85.	1.6	23
1631	<i>Rickettsia</i> increases its infection and spread in whitefly populations by manipulating the defense patterns of the host plant. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	8
1633	Comparative transcriptome analysis of <i>Rheum australe</i> , an endangered medicinal herb, growing in its natural habitat and those grown in controlled growth chambers. <i>Scientific Reports</i> , 2021, 11, 3702.	1.6	11
1634	Transcriptome analysis of the role of autophagy in plant response to heat stress. <i>PLoS ONE</i> , 2021, 16, e0247783.	1.1	5
1635	An epigenetic pathway in rice connects genetic variation to anaerobic germination and seedling establishment. <i>Plant Physiology</i> , 2021, 186, 1042-1059.	2.3	12
1636	Transcriptome Changes Reveal the Molecular Mechanisms of Humic Acid-Induced Salt Stress Tolerance in <i>Arabidopsis</i> . <i>Molecules</i> , 2021, 26, 782.	1.7	9
1637	The <i>Arabidopsis</i> condensin CAP $\epsilon$ subunits arrange interphase chromatin. <i>New Phytologist</i> , 2021, 230, 972-987.	3.5	9
1638	Natural population re-sequencing detects the genetic basis of local adaptation to low temperature in a woody plant. <i>Plant Molecular Biology</i> , 2021, 105, 585-599.	2.0	9
1639	Manipulating <i>ZmEXPA4</i> expression ameliorates the drought-induced prolonged anthesis and silking interval in maize. <i>Plant Cell</i> , 2021, 33, 2058-2071.	3.1	33
1640	RNAseq Reveals Differential Gene Expression Contributing to <i>Phytophthora nicotianae</i> Adaptation to Partial Resistance in Tobacco. <i>Agronomy</i> , 2021, 11, 656.	1.3	1
1641	Proteomic analysis reveals how pairing of a Mycorrhizal fungus with plant growth-promoting bacteria modulates growth and defense in wheat. <i>Plant, Cell and Environment</i> , 2021, 44, 1946-1960.	2.8	26
1642	Resequencing and SNP discovery of <i>Amur ide</i> ( <i>Leuciscus waleckii</i> ) provides insights into local adaptations to extreme environments. <i>Scientific Reports</i> , 2021, 11, 5064.	1.6	15
1643	Development of genic KASP SNP markers from RNA-Seq data for map-based cloning and marker-assisted selection in maize. <i>BMC Plant Biology</i> , 2021, 21, 157.	1.6	14
1645	Identification of virulence associated miRNAs and their bidirectional targets in <i>Rhizoctonia solani</i> and maize during infection. <i>BMC Plant Biology</i> , 2021, 21, 155.	1.6	7
1646	Bacterial effector targeting of a plant iron sensor facilitates iron acquisition and pathogen colonization. <i>Plant Cell</i> , 2021, 33, 2015-2031.	3.1	40
1647	Genome-wide analysis of long noncoding RNAs, 24-nt siRNAs, DNA methylation and H3K27me3 marks in <i>Brassica rapa</i> . <i>PLoS ONE</i> , 2021, 16, e0242530.	1.1	8
1648	MicroRNAs modulate ethylene induced retrograde signal for rice endosperm starch biosynthesis by default expression of transcriptome. <i>Scientific Reports</i> , 2021, 11, 5573.	1.6	8



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1650	Comparative transcriptome analysis reveals key insights into male sterility in <i>Salvia miltiorrhiza</i> Bunge. <i>PeerJ</i> , 2021, 9, e11326.	0.9	10
1651	Distinct morpho-physiological and biochemical features of arid and hyper-arid ecotypes of <i>Ziziphus nummularia</i> under drought suggest its higher tolerance compared with semi-arid ecotype. <i>Tree Physiology</i> , 2021, 41, 2063-2081.	1.4	2
1652	MP3RNA-seq: Massively parallel 3' end RNA sequencing for high-throughput gene expression profiling and genotyping. <i>Journal of Integrative Plant Biology</i> , 2021, 63, 1227-1239.	4.1	4
1653	Metatranscriptomic Comparison of Endophytic and Pathogenic <i>Fusarium</i> – <i>Arabidopsis</i> Interactions Reveals Plant Transcriptional Plasticity. <i>Molecular Plant-Microbe Interactions</i> , 2021, 34, 1071-1083.	1.4	25
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1655	Global Analysis of RNA-Dependent RNA Polymerase-Dependent Small RNAs Reveals New Substrates and Functions for These Proteins and SGS3 in <i>Arabidopsis</i> . <i>Non-coding RNA</i> , 2021, 7, 28.	1.3	10
1657	Comparative transcriptome analyses revealed different heat stress responses in pigeonpea ( <i>Cajanus</i> ) Tj ETQq1 1 0.784314 rgBT /Over	2.8	6
1658	Comparative Analyses Reveal Peroxidases Play Important Roles in Soybean Tolerance to Aluminum Toxicity. <i>Agronomy</i> , 2021, 11, 670.	1.3	6
1659	Comparative Analysis Based on Transcriptomics and Metabolomics Data Reveal Differences between Emmer and Durum Wheat in Response to Nitrogen Starvation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4790.	1.8	5
1662	Transcriptome analysis reveals genes expression pattern of seed response to heat stress in <i>Brassica napus</i> L.. <i>Oil Crop Science</i> , 2021, 6, 87-96.	0.9	14
1663	Comparative Transcriptome Analysis of Rice Resistant and Susceptible Genotypes to <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Identifies Novel Genes to Control Bacterial Leaf Blight. <i>Molecular Biotechnology</i> , 2021, 63, 719-731.	1.3	12
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1667	Assessing Physiological and Genetic Evidence for Evolution of Shared Weedy Rice Traits at the Vegetative Growth Stage. <i>Frontiers in Agronomy</i> , 2021, 3, .	1.5	3
1670	Whole-Genome Doubling Affects Pre-miRNA Expression in Plants. <i>Plants</i> , 2021, 10, 1004.	1.6	1
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1673	Cleaning the Medicago Microarray Database to Improve Gene Function Analysis. <i>Plants</i> , 2021, 10, 1240.	1.6	1
1674	Functional interplay of histone lysine 2-hydroxyisobutyrylation and acetylation in Arabidopsis under dark-induced starvation. <i>Nucleic Acids Research</i> , 2021, 49, 7347-7360.	6.5	12
1675	Comparative analysis of sRNAs, degradome and transcriptomics in sweet sorghum reveals the regulatory roles of miRNAs in Cd accumulation and tolerance. <i>Planta</i> , 2021, 254, 16.	1.6	6
1676	Molecular signatures of silencing suppression degeneracy from a complex RNA virus. <i>PLoS Computational Biology</i> , 2021, 17, e1009166.	1.5	3
1677	Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. <i>Genome Biology</i> , 2021, 22, 185.	3.8	47
1678	H3K27me3 demethylases alter HSP22 and HSP17.6C expression in response to recurring heat in Arabidopsis. <i>Nature Communications</i> , 2021, 12, 3480.	5.8	68
1679	Agrobacterium VirE2 Protein Modulates Plant Gene Expression and Mediates Transformation From Its Location Outside the Nucleus. <i>Frontiers in Plant Science</i> , 2021, 12, 684192.	1.7	8
1681	Transcriptome profiling of developing leaf and shoot apices to reveal the molecular mechanism and co-expression genes responsible for the wheat heading date. <i>BMC Genomics</i> , 2021, 22, 468.	1.2	11
1682	Identifying Genomic Regions Targeted During Eggplant Domestication Using Transcriptome Data. <i>Journal of Heredity</i> , 2021, 112, 519-525.	1.0	3
1683	mRNA-seq and miRNA-seq profiling analyses reveal molecular mechanisms regulating induction of fruiting body in <i>Ophiocordyceps sinensis</i> . <i>Scientific Reports</i> , 2021, 11, 12944.	1.6	5
1684	Genome-wide transcriptional analysis unveils the molecular basis of organ-specific expression of isosteroidal alkaloids biosynthesis in critically endangered <i>Fritillaria roylei</i> Hook. <i>Phytochemistry</i> , 2021, 187, 112772.	1.4	20
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1686	Divergence among rice cultivars reveals roles for transposition and epimutation in ongoing evolution of genomic imprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
1687	Potential evidence for transgenerational epigenetic memory in Arabidopsis thaliana following spaceflight. <i>Communications Biology</i> , 2021, 4, 835.	2.0	17
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1689	The Induction of the Isoflavone Biosynthesis Pathway Is Associated with Resistance to Common Bacterial Blight in <i>Phaseolus vulgaris</i> L. <i>Metabolites</i> , 2021, 11, 433.	1.3	3
1690	Sex biased expression of hormone related genes at early stage of sex differentiation in papaya flowers. <i>Horticulture Research</i> , 2021, 8, 147.	2.9	12

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1888	Positively Selected Orthologous Genes Identified in Sesame (<i>Sesamum indicum</i>) by Deep Resequencing. <i>Plant Breeding and Biotechnology</i> , 2019, 7, 24-33.	0.3	0
1893	De novo transcriptome analysis of peduncle necking in cut <i>Rosa hybrida</i> cultivar â€˜H30â€™. <i>Acta Horticulturae</i> , 2019, , 351-358.	0.1	1
1899	Genome-wide association study uncovers major genetic loci associated with seed flooding tolerance in soybean. <i>BMC Plant Biology</i> , 2021, 21, 497.	1.6	13
1901	Combined Transcriptome and Proteome Analysis to Elucidate Salt Tolerance Strategies of the Halophyte <i>Panicum antidotale</i> Retz. <i>Frontiers in Plant Science</i> , 2021, 12, 760589.	1.7	4

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1902	Comparative Transcriptomic Analysis of Two Rice ( <i>Oryza sativa</i> L.) Male Sterile Line Seed Embryos Under Accelerated Aging. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 282-293.	1.0	4
1903	Improving Maize Trait through Modifying Combination of Genes. <i>Emerging Topics in Statistics and Biostatistics</i> , 2020, , 173-196.	0.1	0
1904	Early transcriptional response to gravistimulation in poplar without phototropic confounding factors. <i>AoB PLANTS</i> , 2021, 13, plaa071.	1.2	6
1905	Examination of the usability of leaf chlorophyll content and gene expression analyses as nitrogen status biomarkers in <i>Sorghum bicolor</i> . <i>Journal of Plant Nutrition</i> , 2021, 44, 773-790.	0.9	3
1906	Variation of biomolecules in plant species. , 2022, , 81-99.		2
1908	Identification of quantitative trait loci associated with upper temperature tolerance in turbot, <i>Scophthalmus maximus</i> . <i>Scientific Reports</i> , 2021, 11, 21920.	1.6	12
1909	The Elite Alleles of OsSPL4 Regulate Grain Size and Increase Grain Yield in Rice. <i>Rice</i> , 2021, 14, 90.	1.7	23
1910	Leaf Apoplast of Field-Grown Potato Analyzed by Quantitative Proteomics and Activity-Based Protein Profiling. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12033.	1.8	1
1911	Atherosclerosis prediction by microarray-based DNA methylation analysis. <i>Experimental and Therapeutic Medicine</i> , 2020, 20, 2863-2869.	0.8	3
1912	Transcriptome-wide identification of MAPKKK genes in bermudagrass ( <i>Cynodon dactylon</i> L.) and their potential roles in low temperature stress responses. <i>PeerJ</i> , 2020, 8, e10159.	0.9	3
1914	Transcriptomic analysis of seed germination improvement of <i>Andrographis paniculata</i> responding to air plasma treatment. <i>PLoS ONE</i> , 2020, 15, e0240939.	1.1	4
1917	Sugar modulation of anaerobic-response networks in maize root tips. <i>Plant Physiology</i> , 2021, 185, 295-317.	2.3	7
1918	RNA-seq for revealing the function of the transcriptome. , 2022, , 105-129.		3
1920	Genome-wide identification and functional prediction of salt- stress related long non-coding RNAs (lncRNAs) in chickpea ( <i>Cicer arietinum</i> L.). <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 2605-2619.	1.4	12
1921	Transcriptome profiling based on Illumina- and SMRT-based RNA-seq reveals circadian regulation of key pathways in flower bud development in walnut. <i>PLoS ONE</i> , 2021, 16, e0260017.	1.1	1
1922	Flavonoids Modulate the Accumulation of Toxins From <i>Aspergillus flavus</i> in Maize Kernels. <i>Frontiers in Plant Science</i> , 2021, 12, 761446.	1.7	5
1924	PNET2 is a component of the plant nuclear lamina and is required for proper genome organization and activity. <i>Developmental Cell</i> , 2022, 57, 19-31.e6.	3.1	22
1926	Transcriptomic Analysis of Quinoa Reveals a Group of Germin-Like Proteins Induced by <i>Trichoderma</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	3

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1929	Population Evolution, Genetic Diversity and Structure of the Medicinal Legume, <i>Glycyrrhiza uralensis</i> and the Effects of Geographical Distribution on Leaves Nutrient Elements and Photosynthesis. Frontiers in Plant Science, 2021, 12, 708709.	1.7	3
1930	Phenotypic Diversity and Association Mapping of Ascorbic Acid Content in Spinach. Frontiers in Genetics, 2021, 12, 752313.	1.1	4
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1932	Systems scale characterization of circadian rhythm pathway in <i>Camellia sinensis</i> . Computational and Structural Biotechnology Journal, 2022, 20, 598-607.	1.9	5
1933	De novo transcriptome analysis of bamboo in vitro shoots for identification of genes differentiating juvenile and aged plants. Industrial Crops and Products, 2022, 176, 114353.	2.5	3
1934	Transcriptome and hormone analyses reveals differences in physiological age of 'Hass' avocado fruit. Postharvest Biology and Technology, 2022, 185, 111806.	2.9	8
1935	Genome-wide expression and variation in nucleotide sequences lead to differential response of <i>Arabidopsis thaliana</i> ecotypes towards arsenic stress under sulfur limiting condition. Environmental and Experimental Botany, 2022, 195, 104764.	2.0	5
1937	Salt Stress Modulates the Landscape of Transcriptome and Alternative Splicing in Date Palm ( <i>Phoenix</i> ) Tj ETQq1 1 0.784314 rgBT /Over	1.7	4
1938	Genome-wide Identification and Expression Analysis of CaM/CML Gene Family in Sacred Lotus ( <i>Nelumbo</i> ) Tj ETQq0 0.0 rgBT /Overlock 10	1.0	5
1939	Genome-Wide Association Study Reveals Complex Genetic Architecture of Cadmium and Mercury Accumulation and Tolerance Traits in <i>Medicago truncatula</i> . Frontiers in Plant Science, 2021, 12, 806949.	1.7	10
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1941	Broad-spectrum fungal resistance in sorghum is conferred through the complex regulation of an immune receptor gene embedded in a natural antisense transcript. Plant Cell, 2022, 34, 1641-1665.	3.1	17
1942	Conserved and distinct roles of H3K27me3 demethylases regulating flowering time in <i>Brassica rapa</i> . Plant, Cell and Environment, 2022, 45, 1428-1441.	2.8	3
1943	Regulation of ammonium acquisition and use in <i>Oryza longistaminata</i> ramets under nitrogen source heterogeneity. Plant Physiology, 2022, 188, 2364-2376.	2.3	7
1944	Identification of Molecular Subgroups in Liver Cirrhosis by Gene Expression Profiles. Hepatitis Monthly, 2022, 21, .	0.1	0
1945	SKIP Regulates ABA Signaling through Alternative Splicing in Arabidopsis. Plant and Cell Physiology, 2022, 63, 494-507.	1.5	7



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1947	Identification of genes associated with kernel size in almond [ <i>Prunus dulcis</i> (Mill.) D.A. Webb] using RNA-Seq. <i>Plant Growth Regulation</i> , 2022, 97, 357-373.	1.8	4
1948	Accumulation of somatic mutations leads to genetic mosaicism in cannabis. <i>Plant Genome</i> , 2022, 15, e20169.	1.6	16
1949	Loss-of-function alleles of ZmPLD3 cause haploid induction in maize. <i>Nature Plants</i> , 2021, 7, 1579-1588.	4.7	52
1950	Transcriptional Landscape of Cotton Fiber Development and Its Alliance With Fiber-Associated Traits. <i>Frontiers in Plant Science</i> , 2022, 13, 811655.	1.7	5
1952	Meta-Analysis of Common and Differential Transcriptomic Responses to Biotic and Abiotic Stresses in <i>Arabidopsis thaliana</i> . <i>Plants</i> , 2022, 11, 502.	1.6	8
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1954	Identification of One Major QTL and a Novel Gene OsIAA17q5 Associated with Tiller Number in Rice Using QTL Analysis. <i>Plants</i> , 2022, 11, 538.	1.6	12
1955	Global analysis of switchgrass ( <i>Panicum virgatum</i> L.) transcriptomes in response to interactive effects of drought and heat stresses. <i>BMC Plant Biology</i> , 2022, 22, 107.	1.6	4
1957	Uncovering the Gene Regulatory Network of Maize Hybrid ZD309 under Heat Stress by Transcriptomic and Metabolomic Analysis. <i>Plants</i> , 2022, 11, 677.	1.6	11
1959	ChENODL6 Isoforms from the Phycocyanin Gene Family Regulated Verticillium Wilt Resistance in Cotton. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2913.	1.8	12
1961	Genome-wide SNP and InDel analysis of three Philippine mango species inferred from whole-genome sequencing. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 46.	1.5	5
1963	The Nitrate Transporter MtNPF6.8 Is a Master Sensor of Nitrate Signal in the Primary Root Tip of <i>Medicago truncatula</i> . <i>Frontiers in Plant Science</i> , 2022, 13, 832246.	1.7	4
1964	Genome-Wide Expression and Physiological Profiling of Pearl Millet Genotype Reveal the Biological Pathways and Various Gene Clusters Underlying Salt Resistance. <i>Frontiers in Plant Science</i> , 2022, 13, 849618.	1.7	15
1965	A Proteome-Level Investigation Into <i>Plasmodiophora brassicae</i> Resistance in <i>Brassica napus</i> Canola. <i>Frontiers in Plant Science</i> , 2022, 13, 860393.	1.7	8
1966	Transcriptome expression profiles reveal response mechanisms to drought and drought-stress mitigation mechanisms by exogenous glycine betaine in maize. <i>Biotechnology Letters</i> , 2022, 44, 367-386.	1.1	13
1967	GC-MS/LC-MS and transcriptome analyses revealed the metabolisms of fatty acid and flavonoid in olive fruits ( <i>Olea europaea</i> L.). <i>Scientia Horticulturae</i> , 2022, 299, 111017.	1.7	8
1968	Proteomics and metabolomics reveal the mechanism underlying differential antioxidant activity among the organs of two base plants of Shiliang tea ( <i>Chimonanthus salicifolius</i> and <i>Chimonanthus</i> ) Tj ETQq1 1 0.784314 rg50 /Overl		

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1969	Evidence for thermosensitivity of the cotton ( <i>Gossypium hirsutum</i> L.) immature fiber (im) mutant via hypersensitive stomatal activity. <i>PLoS ONE</i> , 2021, 16, e0259562.	1.1	3
1970	Nonadditive gene expression is correlated with nonadditive phenotypic expression in interspecific triploid hybrids of willow ( <i>Salix</i> spp.). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	3
1972	UV-B Irradiation Results in Inhibition of Hypocotyl Elongation, Cell Cycle Arrest, and Decreased Endoreduplication Mediated by miR5642. <i>Photochemistry and Photobiology</i> , 2022, 98, 1084-1099.	1.3	4
1973	Identification of DIR1-Dependant Cellular Responses in Guard Cell Systemic Acquired Resistance. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 746523.	1.6	0
1974	<i>ZmERF21</i> directly regulates hormone signaling and stress-responsive gene expression to influence drought tolerance in maize seedlings. <i>Plant, Cell and Environment</i> , 2022, 45, 312-328.	2.8	29
1976	TimesVector-Web: A Web Service for Analysing Time Course Transcriptome Data with Multiple Conditions. <i>Genes</i> , 2022, 13, 73.	1.0	2
1977	Diverse Effect of Two Cytokinins, Kinetin and Benzyladenine, on Plant Development, Biotic Stress Tolerance, and Gene Expression. <i>Life</i> , 2021, 11, 1404.	1.1	3
1978	Transcriptome analysis reveals the regulatory mechanism by which <i>MdWOX11</i> suppresses adventitious shoot formation in apple. <i>Horticulture Research</i> , 2022, 9, .	2.9	5
1979	Systemic Regulation of Iron Acquisition by <i>Arabidopsis</i> in Environments with Heterogeneous Iron Distributions. <i>Plant and Cell Physiology</i> , 2022, 63, 842-854.	1.5	10
1980	<i>Verticillium dahliae</i> Secretes Small RNA to Target Host MIR157d and Retard Plant Floral Transition During Infection. <i>Frontiers in Plant Science</i> , 2022, 13, 847086.	1.7	8
2111	Expression analysis of transcription factors in sugarcane during cold stress. <i>Brazilian Journal of Biology</i> , 2021, 83, e242603.	0.4	3
2112	Comparative Proteomic Analysis of Plasma Membrane Proteins in Rice Leaves Reveals a Vesicle Trafficking Network in Plant Immunity That Is Provoked by Blast Fungi. <i>Frontiers in Plant Science</i> , 2022, 13, 853195.	1.7	2
2113	GmPIN1-mediated auxin asymmetry regulates leaf petiole angle and plant architecture in soybean. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 1325-1338.	4.1	20
2114	Overexpression of NDR1 leads to pathogen resistance at elevated temperatures. <i>New Phytologist</i> , 2022, 235, 1146-1162.	3.5	8
2116	Heterologous Expression of Arabidopsis AtARA6 in Soybean Enhances Salt Tolerance. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	2
2117	QKI-6 Suppresses Cell Proliferation, Migration, and EMT in Non-Small Cell Lung Cancer. <i>Frontiers in Oncology</i> , 2022, 12, .	1.3	3
2118	The tomato yellow leaf curl virus C4 protein alters the expression of plant developmental genes correlating to leaf upward cupping phenotype in tomato. <i>PLoS ONE</i> , 2022, 17, e0257936.	1.1	7
2119	Identification of a Major QTL and Validation of Related Genes for Tiller Angle in Rice Based on QTL Analysis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5192.	1.8	4

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2121	Integration of the transcriptome and proteome provides insights into the mechanism calcium regulated of <i>Ulva prolifera</i> in response to high-temperature stress. <i>Aquaculture</i> , 2022, 557, 738344.	1.7	6
2122	A Putative Plasma Membrane Na <sup>+</sup> /H <sup>+</sup> Antiporter GmSOS1 Is Critical for Salt Stress Tolerance in <i>Glycine max</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	19
2123	miR778 mediates gene expression, histone modification, and DNA methylation during cyst nematode parasitism. <i>Plant Physiology</i> , 2022, 189, 2432-2453.	2.3	4
2124	Transcriptomic and genomic analysis provides new insights in molecular and genetic processes involved in zucchini ZYMV tolerance. <i>BMC Genomics</i> , 2022, 23, 371.	1.2	4
2125	Enhanced reactive oxygen detoxification occurs in salt-stressed soybean roots expressing <i>GmSALT3</i> . <i>Physiologia Plantarum</i> , 2022, 174, e13709.	2.6	13
2126	Genome-Wide Association Analysis for Candidate Genes Contributing to Kernel-Related Traits in Maize. <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	6
2127	Common gene expression patterns are observed in rice roots during associations with plant growth-promoting bacteria, <i>Herbaspirillum seropedicae</i> and <i>Azospirillum brasilense</i> . <i>Scientific Reports</i> , 2022, 12, .	1.6	11
2128	Host genomic influence on bacterial composition in the switchgrass rhizosphere. <i>Molecular Ecology</i> , 2022, 31, 3934-3950.	2.0	13
2129	Secondary metabolite pathway of SDG (secoisolariciresinol) was observed to trigger ROS scavenging system in response to Ca <sup>2+</sup> stress in cotton. <i>Genomics</i> , 2022, 114, 110398.	1.3	5
2135	Time-resolved multiomics analysis of the genetic regulation of maize kernel moisture. <i>Crop Journal</i> , 2023, 11, 247-257.	2.3	8
2136	Analysis of the <i>Arabidopsis coilin</i> mutant reveals a positive role of AtCOILIN in plant immunity. <i>Plant Physiology</i> , 2022, 190, 745-761.	2.3	6
2137	Comparative proteomic analysis on chloroplast proteins provides new insights into the effects of low temperature in sugar beet. , 2022, 63, .		0
2138	Genomic Differentiation and Demographic Histories of Two Closely Related Salicaceae Species. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
2139	Transgenic Soybeans Expressing Phosphatidylinositol-3-Phosphate-Binding Proteins Show Enhanced Resistance Against the Oomycete Pathogen <i>Phytophthora sojae</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
2140	Multi-Omics Analysis Reveals a Regulatory Network of ZmCCT During Maize Resistance to <i>Gibberella</i> Stalk Rot at the Early Stage. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
2141	A Calcineurin Regulator MoRCN1 Is Important for Asexual Development, Stress Response, and Plant Infection of <i>Magnaporthe oryzae</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
2142	MicroSugar: A database of comprehensive miRNA target prediction framework for sugarcane ( <i>Saccharum officinarum</i> L.). <i>Genomics</i> , 2022, , 110420.	1.3	1

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2143	Analysis of TCP Transcription Factors Revealed Potential Roles in Plant Growth and Fusarium oxysporum f.sp. cubense Resistance in Banana (cv. Rasthali). <i>Applied Biochemistry and Biotechnology</i> , 2022, 194, 5456-5473.	1.4	5
2144	Refining bulk segregant analyses: ontology-mediated discovery of flowering time genes in Brassica oleracea. <i>Plant Methods</i> , 2022, 18, .	1.9	1
2145	Evolutionary fates of gene-body methylation and its divergent association with gene expression in pigeonpea. <i>Plant Genome</i> , 2022, 15, .	1.6	1
2146	Simultaneous Ozone and High Light Treatments Reveal an Important Role for the Chloroplast in Co-ordination of Defense Signaling. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
2147	Multiple compensatory mutations contribute to the de-domestication of Iberian weedy rice. <i>Plants People Planet</i> , 2022, 4, 499-510.	1.6	4
2148	Blue light increases anthocyanin content and delays fruit ripening in purple pepper fruit. <i>Postharvest Biology and Technology</i> , 2022, 192, 112024.	2.9	23
2149	Active components and molecular mechanism of <i>Syringa oblata</i> Lindl. in the treatment of endometritis based on pharmacology network prediction. <i>Frontiers in Veterinary Science</i> , 0, 9, .	0.9	0
2150	Functional characterization of ZmBHLH121, a bHLH transcription factor, focusing on Zea mays kernel development. <i>Gene Reports</i> , 2022, , 101645.	0.4	2
2151	GWAS and RNA-seq analysis uncover candidate genes associated with alkaline stress tolerance in maize ( <i>Zea mays</i> L.) seedlings. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
2152	C1QTNF6 regulated by miR-29a-3p promotes proliferation and migration in stage I lung adenocarcinoma. <i>BMC Pulmonary Medicine</i> , 2022, 22, .	0.8	3
2153	Stable sorghum grain quality QTL were identified using SC35 × RTx430 mapping population. <i>Plant Genome</i> , 0, , .	1.6	2
2154	Comprehensive evaluation of the response to aluminum stress in olive tree ( <i>Olea europaea</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
2155	New insights into defense responses against <i>Verticillium dahliae</i> infection revealed by a quantitative proteomic analysis in <i>Arabidopsis thaliana</i> . <i>Functional Plant Biology</i> , 2022, , .	1.1	1
2157	Complex developmental and transcriptional dynamics underlie pollinator-driven evolutionary transitions in nectar spur morphology in <i>Aquilegia</i> (columbine). <i>American Journal of Botany</i> , 2022, 109, 1360-1381.	0.8	1
2158	Mining of publicly available RNA-seq data to reveal phenotypic differences between Landsberg erecta-0 and Columbia-0 ecotypes in <i>Arabidopsis thaliana</i> . <i>Plant Growth Regulation</i> , 0, , .	1.8	0
2160	The START domain mediates <i>Arabidopsis</i> GLABRA2 dimerization and turnover independently of homeodomain DNA binding. <i>Plant Physiology</i> , 2022, 190, 2315-2334.	2.3	7
2161	Transcriptome Meta-Analysis Identifies Candidate Hub Genes and Pathways of Pathogen Stress Responses in <i>Arabidopsis thaliana</i> . <i>Biology</i> , 2022, 11, 1155.	1.3	3
2162	The BBX gene <i>CmBBX22</i> negatively regulates drought stress tolerance in chrysanthemum. <i>Horticulture Research</i> , 2022, 9, .	2.9	5

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2163	Positive selection and heat response transcriptomes reveal adaptive features of the Brassicaceae desert model, <i>Anastatica hierochuntica</i> . <i>New Phytologist</i> , 2022, 236, 1006-1026.	3.5	6
2164	CisCross: A gene list enrichment analysis to predict upstream regulators in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
2165	Role of a ZF-HD Transcription Factor in miR157-Mediated Feed-Forward Regulatory Module That Determines Plant Architecture in <i>Arabidopsis</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 8665.	1.8	4
2166	Transcriptomic analysis of CO <sub>2</sub> -treated strawberries ( <i>Fragaria vesca</i> ) with enhanced resistance to softening and oxidative stress at consumption. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
2168	Comparative Transcriptome Analysis of Salt-Stress-Responsive Genes in Rice Roots. <i>Phyton</i> , 2023, 92, 237-250.	0.4	1
2169	An Integrative Transcriptional Network Revealed Spatial Molecular Interplay Underlying Alantolactone and Inulin Biosynthesis in <i>Inula racemosa</i> Hook f.. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11213.	1.8	1
2170	Transcriptome Analysis of Berries of Spine Grape ( <i>Vitis davidii</i> FÃ¶rster) Infected by <i>Colletotrichum viniferum</i> during Symptom Development. <i>Horticulturae</i> , 2022, 8, 843.	1.2	4
2171	Multi-omic characterization of bifunctional peroxidase 4-coumarate 3-hydroxylase knockdown in <i>Brachypodium distachyon</i> provides insights into lignin modification-associated pleiotropic effects. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
2172	Genetic factors underlying anaerobic germination in rice: Genome-wide association study and transcriptomic analysis. <i>Plant Genome</i> , 0, , .	1.6	7
2173	Genetic variation underlying differential ammonium and nitrate responses in <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2022, 34, 4696-4713.	3.1	10
2174	Spatial Genomic Resource Reveals Molecular Insights into Key Bioactive-Metabolite Biosynthesis in Endangered <i>Angelica glauca</i> Edgew. <i>International Journal of Molecular Sciences</i> , 2022, 23, 11064.	1.8	1
2175	Identification and characterization of genes for drought tolerance in upland rice cultivar 'Banglami'™ of North East India. <i>Molecular Biology Reports</i> , 2022, 49, 11547-11555.	1.0	2
2176	Exogenous strigolactones enhance tolerance in soybean seedlings in response to alkaline stress. <i>Physiologia Plantarum</i> , 2022, 174, .	2.6	5
2177	Identification and characterization of putative targets of VEGETATIVE1/FULc, a key regulator of development of the compound inflorescence in pea and related legumes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
2178	Glutathione imparts stress tolerance against <i>Alternaria brassicicola</i> infection via miRNA mediated gene regulation. <i>Plant Signaling and Behavior</i> , 2022, 17, .	1.2	5
2179	Acta Agronomica Sinica(China), 2022, 48, 304-309.		
2180	The Perennial Horse Gram ( <i>Macrotyloma axillare</i> ) Genome, Phylogeny, and Selection Across the Fabaceae. <i>Compendium of Plant Genomes</i> , 2022, , 255-279.	0.3	2
2181	Utility of Network Biology Approaches to Understand the Aluminum Stress Responses in Soybean. , 2022, , 109-124.		0

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2182	Transcriptomic Analysis to Unravel Potential Pathways and Genes Involved in Pecan ( <i>Carya</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 747 To 2022, 23, 11621.	1.8	4
2183	Histone methyltransferases SDG33 and SDG34 regulate organ-specific nitrogen responses in tomato. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
2184	Molecular basis of genetic plasticity to varying environmental conditions on growing rice by dry/direct-sowing and exposure to drought stress: Insights for DSR varietal development. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	8
2185	Insight into the regulatory networks underlying the high lipid perennial ryegrass growth under different irradiances. <i>PLoS ONE</i> , 2022, 17, e0275503.	1.1	1
2186	Heat production and volatile biosynthesis are linked via alternative respiration in <i>Magnolia denudata</i> during floral thermogenesis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
2187	RNA G-quadruplex structure contributes to cold adaptation in plants. <i>Nature Communications</i> , 2022, 13, .	5.8	15
2188	Plant microProteins: Small but powerful modulators of plant development. <i>IScience</i> , 2022, 25, 105400.	1.9	5
2189	Identification of Potential Zinc Deficiency Responsive Genes and Regulatory Pathways in Rice by Weighted Gene Co-expression Network Analysis. <i>Rice Science</i> , 2022, 29, 545-558.	1.7	1
2190	Effect of prior drought and heat stress on <i>Camellia sinensis</i> transcriptome changes to <i>Ectropis oblique</i> (Lepidoptera: Geometridae) resistance. <i>Genomics</i> , 2022, 114, 110506.	1.3	3
2191	Time Course RNA-seq Reveals Soybean Responses against Root-Lesion Nematode and Resistance Players. <i>Plants</i> , 2022, 11, 2983.	1.6	1
2192	Identification of Genetic Variations and Candidate Genes Responsible for Stalk Sugar Content and Agronomic Traits in Fresh Corn via GWAS across Multiple Environments. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13490.	1.8	3
2193	Low-Density Reference Fingerprinting SNP Dataset of CIMMYT Maize Lines for Quality Control and Genetic Diversity Analyses. <i>Plants</i> , 2022, 11, 3092.	1.6	1
2194	Comprehensive Analysis of <i>Phaseolus vulgaris</i> SnRK Gene Family and Their Expression during Rhizobial and Mycorrhizal Symbiosis. <i>Genes</i> , 2022, 13, 2107.	1.0	1
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2202	Detection of Hub QTLs Underlying the Genetic Basis of Three Modules Covering Nine Agronomic Traits in an F2 Soybean Population. <i>Agronomy</i> , 2022, 12, 3135.	1.3	0
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2209	A binary interaction map between turnip mosaic virus and <i>Arabidopsis thaliana</i> proteomes. <i>Communications Biology</i> , 2023, 6, .	2.0	8
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2213	Specific suppression of long terminal repeat retrotransposon mobilization in plants. <i>Plant Physiology</i> , 2023, 191, 2245-2255.	2.3	2
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