

ePlant: Visualizing and Exploring Multiple Levels of Data Plant Biology

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Citation Report

#	ARTICLE	IF	CITATIONS
1	So Much Data, So Little Time: ePlant Steps into the Breach for Plant Researchers. <i>Plant Cell</i> , 2017, 29, 1797-1797.	3.1	0
2	Identification of regulatory modules in genome scale transcription regulatory networks. <i>BMC Systems Biology</i> , 2017, 11, 140.	3.0	14
3	Interactions between transcription factors and chromatin regulators in the control of flower development. <i>Journal of Experimental Botany</i> , 2018, 69, 2461-2471.	2.4	17
4	Biology in Bloom: A Primer on the <i>Arabidopsis thaliana</i> Model System. <i>Genetics</i> , 2018, 208, 1337-1349.	1.2	38
5	AgriSeqDB: an online RNA-Seq database for functional studies of agriculturally relevant plant species. <i>BMC Plant Biology</i> , 2018, 18, 200.	1.6	21
6	EBP1 nuclear accumulation negatively feeds back on FERONIA-mediated RALF1 signaling. <i>PLoS Biology</i> , 2018, 16, e2006340.	2.6	66
7	NMT1 and NMT3 N-Methyltransferase Activity Is Critical to Lipid Homeostasis, Morphogenesis, and Reproduction. <i>Plant Physiology</i> , 2018, 177, 1605-1628.	2.3	20
8	Lipid transport required to make lipids of photosynthetic membranes. <i>Photosynthesis Research</i> , 2018, 138, 345-360.	1.6	40
9	The Integration of Electrical Signals Originating in the Root of Vascular Plants. <i>Frontiers in Plant Science</i> , 2017, 8, 2173.	1.7	36
10	In Silico Methods to Predict Disease-Resistance Candidate Genes in Plants. , 2018, , 91-106.		0
11	Identification of Two Auxin-Regulated Potassium Transporters Involved in Seed Maturation. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2132.	1.8	21
12	Accelerating structure-function mapping using the ViVa webtool to mine natural variation. <i>Plant Direct</i> , 2019, 3, e00147.	0.8	5
13	A Co-Expression Network in Hexaploid Wheat Reveals Mostly Balanced Expression and Lack of Significant Gene Loss of Homeologous Meiotic Genes Upon Polyploidization. <i>Frontiers in Plant Science</i> , 2019, 10, 1325.	1.7	24
14	SilkDB 3.0: visualizing and exploring multiple levels of data for silkworm. <i>Nucleic Acids Research</i> , 2020, 48, D749-D755.	6.5	59
15	Gene Expression Maps in Plants: Current State and Prospects. <i>Plants</i> , 2019, 8, 309.	1.6	14
16	Atypical Myrosinase as a Mediator of Glucosinolate Functions in Plants. <i>Frontiers in Plant Science</i> , 2019, 10, 1008.	1.7	51
17	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019, 179, 1893-1907.	2.3	34
18	A host-pathogen interactome uncovers phytopathogenic strategies to manipulate plant ABA responses. <i>Plant Journal</i> , 2019, 100, 187-198.	2.8	34

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19	iPlant Systems Biology (iPSB): An International Network Hub in the Plant Community. <i>Molecular Plant</i> , 2019, 12, 727-730.	3.9	5
20	1-Aminocyclopropane-1-Carboxylic Acid Oxidase (ACO): The Enzyme That Makes the Plant Hormone Ethylene. <i>Frontiers in Plant Science</i> , 2019, 10, 695.	1.7	226
21	Plant Proteome Databases and Bioinformatic Tools: An Expert Review and Comparative Insights. <i>OMICS A Journal of Integrative Biology</i> , 2019, 23, 190-206.	1.0	17
22	Organ-specific genetic interactions between paralogues of the <i>PXY</i> and <i>ER</i> receptor kinases enforce radial patterning in <i>Arabidopsis</i> vascular tissue. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	23
23	Characterization of S40-like proteins and their roles in response to environmental cues and leaf senescence in rice. <i>BMC Plant Biology</i> , 2019, 19, 174.	1.6	13
24	AtSPX1-mediated transcriptional regulation during leaf senescence in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2019, 283, 238-246.	1.7	10
25	<i>MADS</i> box genes underground becoming mainstream: plant root developmental mechanisms. <i>New Phytologist</i> , 2019, 223, 1143-1158.	3.5	57
26	A Network-Guided Genetic Approach to Identify Novel Regulators of Adventitious Root Formation in <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 461.	1.7	15
27	Clade I TGACG-Motif Binding Basic Leucine Zipper Transcription Factors Mediate BLADE-ON-PETIOLE-Dependent Regulation of Development. <i>Plant Physiology</i> , 2019, 180, 937-951.	2.3	68
28	The mitochondrial oxidation resistance protein AtOXR2 increases plant biomass and tolerance to oxidative stress. <i>Journal of Experimental Botany</i> , 2019, 70, 3177-3195.	2.4	14
29	A genome-wide association study reveals a novel regulator of ovule number and fertility in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2019, 15, e1007934.	1.5	37
30	Towards Building a Plant Cell Atlas. <i>Trends in Plant Science</i> , 2019, 24, 303-310.	4.3	86
31	Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 145, 19-39.	1.4	15
32	On the origins of osmotically driven stomatal movements. <i>New Phytologist</i> , 2019, 222, 84-90.	3.5	27
33	Imbalance of tyrosine by modulating TyrA arogenate dehydrogenases impacts growth and development of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2019, 97, 901-922.	2.8	24
34	PlantPAN3.0: a new and updated resource for reconstructing transcriptional regulatory networks from ChIP-seq experiments in plants. <i>Nucleic Acids Research</i> , 2019, 47, D1155-D1163.	6.5	315
35	Cation Specificity of Vacuolar NHX-Type Cation/H ⁺ Antiporters. <i>Plant Physiology</i> , 2019, 179, 616-629.	2.3	119
36	In situ assessment of mitochondrial calcium transport in tobacco pollen tubes. <i>Protoplasma</i> , 2019, 256, 503-509.	1.0	7

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37	<i>Arabidopsis</i> ADC1 functions as an N ⁵ -acetylornithine decarboxylase. <i>Journal of Integrative Plant Biology</i> , 2020, 62, 601-613.	4.1	16
38	ZmDREB1A Regulates RAFFINOSE SYNTHASE Controlling Raffinose Accumulation and Plant Chilling Stress Tolerance in Maize. <i>Plant and Cell Physiology</i> , 2020, 61, 331-341.	1.5	38
39	Plant Regulomics: a data-driven interface for retrieving upstream regulators from plant multi-omics data. <i>Plant Journal</i> , 2020, 101, 237-248.	2.8	75
40	The RALF1-FERONIA Complex Phosphorylates eIF4E1 to Promote Protein Synthesis and Polar Root Hair Growth. <i>Molecular Plant</i> , 2020, 13, 698-716.	3.9	88
41	The role of P-type IIA and P-type IIB Ca ²⁺ -ATPases in plant development and growth. <i>Journal of Experimental Botany</i> , 2020, 71, 1239-1248.	2.4	39
42	RBR-Type E3 Ligases and the Ubiquitin-Conjugating Enzyme UBC26 Regulate Abscisic Acid Receptor Levels and Signaling. <i>Plant Physiology</i> , 2020, 182, 1723-1742.	2.3	33
43	The effector GpRbpa1 of <i>Globodera pallida</i> targets a nuclear HECT E3 ubiquitin ligase to modulate gene expression in the host. <i>Molecular Plant Pathology</i> , 2020, 21, 66-82.	2.0	13
44	Single-Cell Transcriptomics: A High-Resolution Avenue for Plant Functional Genomics. <i>Trends in Plant Science</i> , 2020, 25, 186-197.	4.3	128
45	Genome-wide phylogenetic and structural analysis reveals the molecular evolution of the ABA receptor gene family. <i>Journal of Experimental Botany</i> , 2020, 71, 1322-1336.	2.4	19
46	Dynamic regulation of Pep-induced immunity through post-translational control of defence transcript splicing. <i>Nature Plants</i> , 2020, 6, 1008-1019.	4.7	40
47	Regulation of Cell Type-Specific Immunity Networks in <i>Arabidopsis</i> Roots. <i>Plant Cell</i> , 2020, 32, 2742-2762.	3.1	59
48	Cell type-specific genome scans of DNA methylation divergence indicate an important role for transposable elements. <i>Genome Biology</i> , 2020, 21, 172.	3.8	6
49	In-silico Exploration of Channel Type and Efflux Silicon Transporters and Silicification Proteins in 80 Sequenced Viridiplantae Genomes. <i>Plants</i> , 2020, 9, 1612.	1.6	7
50	Comprehensive Genome-Wide Association Analysis Reveals the Genetic Basis of Root System Architecture in Soybean. <i>Frontiers in Plant Science</i> , 2020, 11, 590740.	1.7	17
51	Calcium Binding by Arabinogalactan Polysaccharides Is Important for Normal Plant Development. <i>Plant Cell</i> , 2020, 32, 3346-3369.	3.1	65
52	Laccases and Peroxidases Co-Localize in Lignified Secondary Cell Walls throughout Stem Development. <i>Plant Physiology</i> , 2020, 184, 806-822.	2.3	84
53	The sunflower TLDC-containing protein HaOXR2 confers tolerance to oxidative stress and waterlogging when expressed in maize plants. <i>Plant Science</i> , 2020, 300, 110626.	1.7	8
54	AtPPRT3, a novel E3 ubiquitin ligase, plays a positive role in ABA signaling. <i>Plant Cell Reports</i> , 2020, 39, 1467-1478.	2.8	7

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55	BrassicaEDB: A Gene Expression Database for Brassica Crops. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5831.	1.8	44
56	Coping with stress: role of Arabidopsis phytoglobins in defence against <i>Sclerotinia sclerotiorum</i> . <i>Journal of Plant Biochemistry and Biotechnology</i> , 2020, 29, 804-815.	0.9	0
57	Transit Peptides From Photosynthesis-Related Proteins Mediate Import of a Marker Protein Into Different Plastid Types and Within Different Species. <i>Frontiers in Plant Science</i> , 2020, 11, 560701.	1.7	6
58	Bridging the GAPS in plant reproduction: a comparison of plant and animal GPI-anchored proteins. <i>Plant Reproduction</i> , 2020, 33, 129-142.	1.3	15
59	Phylogenetic analysis of plant multi-domain SEC14-like phosphatidylinositol transfer proteins and structureâ€“function properties of PATELLIN2. <i>Plant Molecular Biology</i> , 2020, 104, 665-678.	2.0	14
60	A Review on the Beneficial Role of Silicon against Salinity in Non-Accumulator Crops: Tomato as a Model. <i>Biomolecules</i> , 2020, 10, 1284.	1.8	55
61	Classification and Computational Analysis of Arabidopsis thaliana Sperm Cell-Specific F-Box Protein Gene 3p.AtFBP113. <i>Frontiers in Genetics</i> , 2020, 11, 609668.	1.1	2
62	Plant TDP1 (Tyrosyl-DNA Phosphodiesterase 1): A Phylogenetic Perspective and Gene Expression Data Mining. <i>Genes</i> , 2020, 11, 1465.	1.0	2
63	Probing natural variation of IRE1 expression and endoplasmic reticulum stress responses in Arabidopsis accessions. <i>Scientific Reports</i> , 2020, 10, 19154.	1.6	8
64	Nitric Oxide Overproduction by cue1 Mutants Differs on Developmental Stages and Growth Conditions. <i>Plants</i> , 2020, 9, 1484.	1.6	7
65	VAPYRIN-like is required for development of the moss <i>Physcomitrella patens</i> . <i>Development (Cambridge)</i> , 2020, 147, .	1.2	7
66	Gene coexpression network analysis and tissue-specific profiling of gene expression in jute (<i>Corchorus capsularis</i> L.). <i>BMC Genomics</i> , 2020, 21, 406.	1.2	7
67	Test of Arabidopsis Space Transcriptome: A Discovery Environment to Explore Multiple Plant Biology Spaceflight Experiments. <i>Frontiers in Plant Science</i> , 2020, 11, 147.	1.7	23
68	Promoter and Terminator Optimization for DNA Methylation Targeting in Arabidopsis. <i>Epigenomes</i> , 2020, 4, 9.	0.8	3
69	MaizeCUBIC: a comprehensive variation database for a maize synthetic population. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	5
70	Late Embryogenesis Abundant Proteinâ€“Client Protein Interactions. <i>Plants</i> , 2020, 9, 814.	1.6	17
71	Crosstalk between heterotrimeric G protein-coupled signaling pathways and WRKY transcription factors modulating plant responses to suboptimal micronutrient conditions. <i>Journal of Experimental Botany</i> , 2020, 71, 3227-3239.	2.4	19
72	ARGONAUTE5 Represses Age-Dependent Induction of Flowering through Physical and Functional Interaction with miR156 in Arabidopsis. <i>Plant and Cell Physiology</i> , 2020, 61, 957-966.	1.5	29

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73	Genetic attenuation of alkaloids and nicotine content in tobacco (<i>Nicotiana tabacum</i>). <i>Planta</i> , 2020, 251, 92.	1.6	12
74	SCF ^{SNIPER7} controls protein turnover of unfoldase CDC48A to promote plant immunity. <i>New Phytologist</i> , 2021, 229, 2795-2811.	3.5	13
75	Abscisic acid-mediated induction of FLAVIN-CONTAINING MONOOXYGENASE 2 leads to reduced accumulation of methylthioalkyl glucosinolates in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2021, 303, 110764.	1.7	6
76	A new decade and new data at SoyBase, the USDA-ARS soybean genetics and genomics database. <i>Nucleic Acids Research</i> , 2021, 49, D1496-D1501.	6.5	49
77	<i>De novo</i> genome assembly of <i>Solanum sitiens</i> reveals structural variation associated with drought and salinity tolerance. <i>Bioinformatics</i> , 2021, 37, 1941-1945.	1.8	9
78	Computational Prediction of Protein-Protein Interactions in Plants Using Only Sequence Information. <i>Lecture Notes in Computer Science</i> , 2021, , 115-125.	1.0	1
80	Using Gene Expression to Study Specialized Metabolism—A Practical Guide. <i>Frontiers in Plant Science</i> , 2020, 11, 625035.	1.7	24
81	Role of plant Ca ²⁺ -ATPase in calcium homeostasis during development and stresses. , 2021, , 103-128.		2
82	Integrating Pan-Omics Data in a Systems Approach for Crop Improvement: Opportunities and Challenges. , 2021, , 215-246.		2
83	The <i>Arabidopsis</i> embryo as a quantifiable model for studying pattern formation. <i>Quantitative Plant Biology</i> , 2021, 2, .	0.8	5
84	The <i>Arabidopsis thaliana</i> Class II Formin FH13 Modulates Pollen Tube Growth. <i>Frontiers in Plant Science</i> , 2021, 12, 599961.	1.7	10
86	ADAP is a possible negative regulator of glucosinolate biosynthesis in <i>Arabidopsis thaliana</i> based on clustering and gene expression analyses. <i>Journal of Plant Research</i> , 2021, 134, 327-339.	1.2	9
87	Plant multiscale networks: charting plant connectivity by multi-level analysis and imaging techniques. <i>Science China Life Sciences</i> , 2021, 64, 1392-1422.	2.3	21
88	Physical mapping and candidate gene prediction of branch number on the main stem in soybean [<i>Glycine max</i> (L.) Merr.]. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2907-2921.	0.8	2
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93	Acyl-CoA desaturase ADS4.2 is involved in the formation of characteristic wax alkenes in young <i>Arabidopsis</i> leaves. <i>Plant Physiology</i> , 2021, 186, 1812-1831.	2.3	4
94	KnetMiner: a comprehensive approach for supporting evidence-based gene discovery and complex trait analysis across species. <i>Plant Biotechnology Journal</i> , 2021, 19, 1670-1678.	4.1	50
95	The Story of Auxin-Binding Protein 1 (ABP1). <i>Cold Spring Harbor Perspectives in Biology</i> , 2021, 13, a039909.	2.3	23

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98	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
99	ATHB2 is a negative regulator of germination in <i>Arabidopsis thaliana</i> seeds. <i>Scientific Reports</i> , 2021, 11, 9688.	1.6	4
101	Downregulation of GeBP-like $\hat{\iota}$ factor by MiR827 suggests their involvement in senescence and phosphate homeostasis. <i>BMC Biology</i> , 2021, 19, 90.	1.7	7
103	A G protein-coupled receptor-like module regulates cellulose synthase secretion from the endomembrane system in <i>Arabidopsis</i> . <i>Developmental Cell</i> , 2021, 56, 1484-1497.e7.	3.1	23
104	Genetic mapping of the early responses to salt stress in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2021, 107, 544-563.	2.8	22
105	The lncRNA APOLO interacts with the transcription factor WRKY42 to trigger root hair cell expansion in response to cold. <i>Molecular Plant</i> , 2021, 14, 937-948.	3.9	72
106	The mitochondrial pyruvate carrier (MPC) complex mediates one of three pyruvate-supplying pathways that sustain <i>Arabidopsis</i> respiratory metabolism. <i>Plant Cell</i> , 2021, 33, 2776-2793.	3.1	39
107	Guard cell redox proteomics reveals a role of lipid transfer protein in plant defense. <i>Journal of Proteomics</i> , 2021, 242, 104247.	1.2	10
108	Control of the Rhizobia Nitrogen-Fixing Symbiosis by Common Bean MADS-Domain/AGL Transcription Factors. <i>Frontiers in Plant Science</i> , 2021, 12, 679463.	1.7	7
109	A method to analyze time expression profiles demonstrated in a database of chili pepper fruit development. <i>Scientific Reports</i> , 2021, 11, 13181.	1.6	4
110	Advances in Cell Wall Matrix Research with a Focus on Mixed-Linkage Glucan. <i>Plant and Cell Physiology</i> , 2021, . .	1.5	6
111	Altered Root Growth, Auxin Metabolism and Distribution in <i>Arabidopsis thaliana</i> Exposed to Salt and Osmotic Stress. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7993.	1.8	28
113	A prion-like protein regulator of seed germination undergoes hydration-dependent phase separation. <i>Cell</i> , 2021, 184, 4284-4298.e27.	13.5	99
114	MtExpress, a Comprehensive and Curated RNAseq-based Gene Expression Atlas for the Model Legume <i>Medicago truncatula</i> . <i>Plant and Cell Physiology</i> , 2021, 62, 1494-1500.	1.5	48
116	Specific methylation of (11R)-carlactonic acid by an <i>Arabidopsis</i> SABATH methyltransferase. <i>Planta</i> , 2021, 254, 88.	1.6	18
117	Vision, challenges and opportunities for a Plant Cell Atlas. <i>ELife</i> , 2021, 10, .	2.8	31
118	GWAS identifies an ortholog of the rice D11 gene as a candidate gene for grain size in an international collection of hexaploid wheat. <i>Scientific Reports</i> , 2021, 11, 19483.	1.6	8
119	Plant Biology Research: What Is Next?. <i>Frontiers in Plant Science</i> , 2021, 12, 749104.	1.7	3

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121	Viral inosine triphosphatase: A mysterious enzyme with typical activity, but an atypical function. <i>Molecular Plant Pathology</i> , 2021, 22, 382-389.	2.0	10
122	Anno genominis XX: 20 years of Arabidopsis genomics. <i>Plant Cell</i> , 2021, 33, 832-845.	3.1	11
131	Silicon flow from root to shoot in pepper: a comprehensive in silico analysis reveals a potential linkage between gene expression and hormone signaling that stimulates plant growth and metabolism. <i>PeerJ</i> , 2020, 8, e10053.	0.9	11
132	MutRank: an R shiny web-application for exploratory targeted mutual rank-based coexpression analyses integrated with user-provided supporting information. <i>PeerJ</i> , 2020, 8, e10264.	0.9	7
133	Arabidopsis bioinformatics: tools and strategies. <i>Plant Journal</i> , 2021, 108, 1585-1596.	2.8	9
135	Characterization of BRASSINOSTEROID F-BOX Proteins BRFPs that Regulate BRASSINOSTEROID-INSENSITIVE 2 Kinase. <i>Journal of Plant Biology</i> , 2022, 65, 53-63.	0.9	3
142	Characterization of the "Oat-Like Rice"™ Caused by a Novel Allele OsMADS1Olr Reveals Vital Importance of OsMADS1 in Regulating Grain Shape in <i>Oryza sativa</i> L.. <i>Rice</i> , 2020, 13, 73.	1.7	6
144	Bioinformatic Tools in Arabidopsis Research. <i>Methods in Molecular Biology</i> , 2021, 2200, 25-89.	0.4	4
145	Bibenzyl synthesis in <i>Cannabis sativa</i> L. <i>Plant Journal</i> , 2021, , .	2.8	6
147	Elevated tyrosine results in the cytosolic retention of 3-deoxy- β -D-arabino-heptulosonate 7-phosphate synthase in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2022, 109, 789-803.	2.8	7
148	The CLASSY family controls tissue-specific DNA methylation patterns in Arabidopsis. <i>Nature Communications</i> , 2022, 13, 244.	5.8	35
149	Chlorophyll and Pheophytin Dephnylating Enzymes Required for Efficient Repair of PSII in <i>Synechococcus elongatus</i> PCC 7942. <i>Plant and Cell Physiology</i> , 2022, 63, 410-420.	1.5	4
151	Identification of new proteins in mature sieve elements. <i>Physiologia Plantarum</i> , 2022, 174, e13634.	2.6	3
152	Genome-Wide Characterization and Expression Analysis of KH Family Genes Response to ABA and SA in <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 511.	1.8	0
153	Evolution of Bcl-2 Anthogenes (BAG) as the Regulators of Cell Death in Wild and Cultivated <i>Oryza</i> Species. <i>Journal of Plant Growth Regulation</i> , 0, , 1.	2.8	3
154	Multiple haplotype-based analyses provide genetic and evolutionary insights into tomato fruit weight and composition. <i>Horticulture Research</i> , 2022, 9, .	2.9	14
155	A putative SUBTILISIN-LIKE SERINE PROTEASE 1 (SUBSRP1) regulates anther cuticle biosynthesis and panicle development in rice. <i>Journal of Advanced Research</i> , 2022, 42, 273-287.	4.4	19
157	Subcellular Proteomics as a Unified Approach of Experimental Localizations and Computed Prediction Data for Arabidopsis and Crop Plants. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 67-89.	0.8	2

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159	SEED LIPID DROPLET PROTEIN1, SEED LIPID DROPLET PROTEIN2, and LIPID DROPLET PLASMA MEMBRANE ADAPTOR mediate lipid dropletâ€“plasma membrane tethering. <i>Plant Cell</i> , 2022, 34, 2424-2448.	3.1	12
161	CYTOKININ RESPONSE FACTORâ€“2 is involved in modulating the salt stress response. <i>Plant Journal</i> , 2022, 110, 1097-1110.	2.8	10
162	Research progress of aldehyde oxidases in plants. <i>PeerJ</i> , 2022, 10, e13119.	0.9	8
163	Apoplastic class III peroxidases PRX62 and PRX69 promote Arabidopsis root hair growth at low temperature. <i>Nature Communications</i> , 2022, 13, 1310.	5.8	25
164	Differential Involvement of Arabidopsis Î²â€“COP Isoforms in Plant Development. <i>Cells</i> , 2022, 11, 938.	1.8	3
165	GXP: Analyze and Plot Plant Omics Data in Web Browsers. <i>Plants</i> , 2022, 11, 745.	1.6	1
166	<sc>KNOX II</sc> transcription factor <sc>HOS59</sc> functions in regulating rice grain size. <i>Plant Journal</i> , 2022, 110, 863-880.	2.8	11
167	A Comprehensive Analysis of Calmodulin-Like Proteins of Glycine max Indicates Their Role in Calcium Signaling and Plant Defense Against Insect Attack. <i>Frontiers in Plant Science</i> , 2022, 13, 817950.	1.7	16
168	The <sc>RNA</sc> binding protein <sc>OsLa</sc> influences grain and anther development in rice. <i>Plant Journal</i> , 2022, 110, 1397-1414.	2.8	4
169	Challenges in large-scale bioinformatics projects. <i>Humanities and Social Sciences Communications</i> , 2022, 9, .	1.3	4
170	Exploiting plant transcriptomic databases: Resources, tools, and approaches. <i>Plant Communications</i> , 2022, 3, 100323.	3.6	20
171	Deep roots and many branches: Origins of plant-specialized metabolic enzymes in general metabolism. <i>Current Opinion in Plant Biology</i> , 2022, 66, 102192.	3.5	8
172	Arabidopsis CAMTA3/SR1 is involved in drought stress tolerance and ABA signaling. <i>Plant Science</i> , 2022, 319, 111250.	1.7	11
173	Topology of the redox network during induction of photosynthesis as revealed by time-resolved proteomics in tobacco. <i>Science Advances</i> , 2021, 7, eabi8307.	4.7	27
174	<i>ZmERF21</i> directly regulates hormone signaling and stressâ€“responsive gene expression to influence drought tolerance in maize seedlings. <i>Plant, Cell and Environment</i> , 2022, 45, 312-328.	2.8	29
176	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. <i>Frontiers in Plant Science</i> , 2021, 12, 736797.	1.7	1
177	Identification and Characterization of SOG1 (Suppressor of Gamma Response 1) Homologues in Plants Using Data Mining Resources and Gene Expression Profiling. <i>Genes</i> , 2022, 13, 667.	1.0	4

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216	BUMPY STEM Is an Arabidopsis Choline/Ethanolamine Kinase Required for Normal Development and Chilling Responses. <i>Frontiers in Plant Science</i> , 2022, 13, 851960.	1.7	3
217	Ethylene Insensitive 3-Like 2 is a <i>Brassicaceae</i> -specific transcriptional regulator involved in fine-tuning ethylene responses in <i>Arabidopsis thaliana</i> . <i>Journal of Experimental Botany</i> , 2022, 73, 4793-4805.	2.4	3
218	A native promoter-gene fusion created by CRISPR/Cas9-mediated genomic deletion offers a transgene-free method to drive oil accumulation in leaves. <i>FEBS Letters</i> , 2022, 596, 1865-1870.	1.3	6
219	Sucrose synthases are not involved in starch synthesis in Arabidopsis leaves. <i>Nature Plants</i> , 2022, 8, 574-582.	4.7	21
220	REGENOMICS: A web-based application for plant REGENERation-associated transcriptOMICS analyses. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3234-3247.	1.9	2
221	Prediction and expression analysis of deleterious nonsynonymous SNPs of Arabidopsis ACD11 gene by combining computational algorithms and molecular docking approach. <i>PLoS Computational Biology</i> , 2022, 18, e1009539.	1.5	0
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