

List of Publications by Year in descending order

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154
papers

66,145
citations

11651

70
h-index

7348

152
g-index

159
all docs

159
docs citations

159
times ranked

88679
citing authors

#	ARTICLE	IF	CITATIONS
1	Trimmomatic: a flexible trimmer for Illumina sequence data. <i>Bioinformatics</i> , 2014, 30, 2114-2120.	4.1	46,646
2	GMD@CSB.DB: the Golm Metabolome Database. <i>Bioinformatics</i> , 2005, 21, 1635-1638.	4.1	1,247
3	RobiNA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. <i>Nucleic Acids Research</i> , 2012, 40, W622-W627.	14.5	729
4	Sugars and Circadian Regulation Make Major Contributions to the Global Regulation of Diurnal Gene Expression in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2005, 17, 3257-3281.	6.6	608
5	Extension of the Visualization Tool MapMan to Allow Statistical Analysis of Arrays, Display of Corresponding Genes, and Comparison with Known Responses. <i>Plant Physiology</i> , 2005, 138, 1195-1204.	4.8	576
6	<sc>M</sc>erator: a fast and simple web server for genome scale functional annotation of plant sequence data. <i>Plant, Cell and Environment</i> , 2014, 37, 1250-1258.	5.7	575
7	A guide to using MapMan to visualize and compare Omics data in plants: a case study in the crop species, Maize. <i>Plant, Cell and Environment</i> , 2009, 32, 1211-1229.	5.7	561
8	Genome-wide reprogramming of metabolism and regulatory networks of <i>Arabidopsis</i> in response to phosphorus. <i>Plant, Cell and Environment</i> , 2007, 30, 85-112.	5.7	533
9	Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. <i>Plant, Cell and Environment</i> , 2009, 32, 1633-1651.	5.7	480
10	Starch as a major integrator in the regulation of plant growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10348-10353.	7.1	467
11	Integrated Analysis of Metabolite and Transcript Levels Reveals the Metabolic Shifts That Underlie Tomato Fruit Development and Highlight Regulatory Aspects of Metabolic Network Behavior. <i>Plant Physiology</i> , 2006, 142, 1380-1396.	4.8	432
12	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	21.4	391
13	MapMan4: A Refined Protein Classification and Annotation Framework Applicable to Multi-Omics Data Analysis. <i>Molecular Plant</i> , 2019, 12, 879-892.	8.3	353
14	Reprogramming a maize plant: transcriptional and metabolic changes induced by the fungal biotroph <i>Ustilago maydis</i> . <i>Plant Journal</i> , 2008, 56, 181-195.	5.7	328
15	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2655-62.	7.1	325
16	PageMan: An interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. <i>BMC Bioinformatics</i> , 2006, 7, 535.	2.6	309
17	Global Transcript Levels Respond to Small Changes of the Carbon Status during Progressive Exhaustion of Carbohydrates in <i>Arabidopsis</i> Rosettes. <i>Plant Physiology</i> , 2008, 146, 1834-1861.	4.8	306
18	Integration of metabolite with transcript and enzyme activity profiling during diurnal cycles in <i>Arabidopsis</i> rosettes. <i>Genome Biology</i> , 2006, 7, R76.	9.6	304

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19	Systems Biology of Tomato Fruit Development: Combined Transcript, Protein, and Metabolite Analysis of Tomato Transcription Factor (<i>nor, rin</i>) and Ethylene Receptor (<i>Nr</i>) Mutants Reveals Novel Regulatory Interactions. <i>Plant Physiology</i> , 2011, 157, 405-425.	4.8	303
20	Quantitation in Mass-Spectrometry-Based Proteomics. <i>Annual Review of Plant Biology</i> , 2010, 61, 491-516.	18.7	301
21	Arabidopsis and primary photosynthetic metabolism – more than the icing on the cake. <i>Plant Journal</i> , 2010, 61, 1067-1091.	5.7	300
22	PlaNet: Combined Sequence and Expression Comparisons across Plant Networks Derived from Seven Species. <i>Plant Cell</i> , 2011, 23, 895-910.	6.6	297
23	Ribosome and transcript copy numbers, polysome occupancy and enzyme dynamics in <i>Arabidopsis</i> . <i>Molecular Systems Biology</i> , 2009, 5, 314.	7.2	276
24	Temporal responses of transcripts, enzyme activities and metabolites after adding sucrose to carbon-deprived <i>Arabidopsis</i> seedlings. <i>Plant Journal</i> , 2007, 49, 463-491.	5.7	272
25	Regulatory Features Underlying Pollination-Dependent and -Independent Tomato Fruit Set Revealed by Transcript and Primary Metabolite Profiling. <i>Plant Cell</i> , 2009, 21, 1428-1452.	6.6	258
26	Barley Grain Maturation and Germination: Metabolic Pathway and Regulatory Network Commonalities and Differences Highlighted by New MapMan/PageMan Profiling Tools. <i>Plant Physiology</i> , 2008, 146, 1738-1758.	4.8	250
27	Tomato facultative parthenocarpy results from <i>SlAGAMOUS</i> – <i>LIKE</i> 6 loss of function. <i>Plant Biotechnology Journal</i> , 2017, 15, 634-647.	8.3	244
28	Mapping Metabolic and Transcript Temporal Switches during Germination in Rice Highlights Specific Transcription Factors and the Role of RNA Instability in the Germination Process. <i>Plant Physiology</i> , 2009, 149, 961-980.	4.8	236
29	RNA Interference of <i>LIN5</i> in Tomato Confirms Its Role in Controlling Brix Content, Uncovers the Influence of Sugars on the Levels of Fruit Hormones, and Demonstrates the Importance of Sucrose Cleavage for Normal Fruit Development and Fertility. <i>Plant Physiology</i> , 2009, 150, 1204-1218.	4.8	226
30	Antisense Inhibition of the Iron-Sulphur Subunit of Succinate Dehydrogenase Enhances Photosynthesis and Growth in Tomato via an Organic Acid-Mediated Effect on Stomatal Aperture. <i>Plant Cell</i> , 2011, 23, 600-627.	6.6	221
31	The art of growing plants for experimental purposes: a practical guide for the plant biologist. <i>Functional Plant Biology</i> , 2012, 39, 821.	2.1	217
32	De Novo Assembly of a New <i>Solanum pennellii</i> Accession Using Nanopore Sequencing. <i>Plant Cell</i> , 2017, 29, 2336-2348.	6.6	192
33	Multilevel genomic analysis of the response of transcripts, enzyme activities and metabolites in <i>Arabidopsis</i> rosettes to a progressive decrease of temperature in the non-freezing range. <i>Plant, Cell and Environment</i> , 2008, 31, 518-547.	5.7	191
34	Rapid Structural Phenotyping of Plant Cell Wall Mutants by Enzymatic Oligosaccharide Fingerprinting. <i>Plant Physiology</i> , 2002, 130, 1754-1763.	4.8	182
35	Analysis of expressed sequence tags from <i>Actinidia</i> : applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. <i>BMC Genomics</i> , 2008, 9, 351.	2.8	178
36	Assembly of an Interactive Correlation Network for the <i>Arabidopsis</i> Genome Using a Novel Heuristic Clustering Algorithm. <i>Plant Physiology</i> , 2009, 152, 29-43.	4.8	174

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37	Plant genome sequencing â€” applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	6.6	164
38	A subtilisinâ€”like serine protease essential for mucilage release from Arabidopsis seed coats. <i>Plant Journal</i> , 2008, 54, 466-480.	5.7	159
39	CSB.DB: a comprehensive systems-biology database. <i>Bioinformatics</i> , 2004, 20, 3647-3651.	4.1	152
40	Reduced Expression of Succinyl-Coenzyme A Ligase Can Be Compensated for by Up-Regulation of the <i>3</i> -Aminobutyrate Shunt in Illuminated Tomato Leaves. <i>Plant Physiology</i> , 2007, 145, 626-639.	4.8	151
41	The Multifaceted Role of Pectin Methyltransferase Inhibitors (PMEIs). <i>International Journal of Molecular Sciences</i> , 2018, 19, 2878.	4.1	148
42	Genetic architecture of plant stress resistance: multiâ€”trait genomeâ€”wide association mapping. <i>New Phytologist</i> , 2017, 213, 1346-1362.	7.3	144
43	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008, 179, 157-166.	2.9	141
44	Footprints of parasitism in the genome of the parasitic flowering plant <i>Cuscuta campestris</i> . <i>Nature Communications</i> , 2018, 9, 2515.	12.8	141
45	Genome-wide analysis of yield in Europe: allelic effects as functions of drought and heat scenarios. <i>Plant Physiology</i> , 2016, 172, pp.00621.2016.	4.8	140
46	The inositol oxygenase gene family of Arabidopsis is involved in the biosynthesis of nucleotide sugar precursors for cell-wall matrix polysaccharides. <i>Planta</i> , 2005, 221, 243-254.	3.2	135
47	The Interconversion of UDP-Arabinopyranose and UDP-Arabinofuranose Is Indispensable for Plant Development in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011, 23, 1373-1390.	6.6	134
48	Diurnal Changes of Polysome Loading Track Sucrose Content in the Rosette of Wild-Type Arabidopsis and the Starchless <i>pgm</i> Mutant. <i>Plant Physiology</i> , 2013, 162, 1246-1265.	4.8	133
49	Evolution of a Complex Locus for Terpene Biosynthesis in <i>Solanum</i> . <i>Plant Cell</i> , 2013, 25, 2022-2036.	6.6	132
50	Network Analysis of Enzyme Activities and Metabolite Levels and Their Relationship to Biomass in a Large Panel of <i>Arabidopsis</i> Accessions. <i>Plant Cell</i> , 2010, 22, 2872-2893.	6.6	131
51	RHM2 Is Involved in Mucilage Pectin Synthesis and Is Required for the Development of the Seed Coat in Arabidopsis. <i>Plant Physiology</i> , 2004, 134, 286-295.	4.8	127
52	MUCILAGE-RELATED10 Produces Galactoglucomannan That Maintains Pectin and Cellulose Architecture in Arabidopsis Seed Mucilage. <i>Plant Physiology</i> , 2015, 169, 403-420.	4.8	126
53	Demethylesterification of Cell Wall Pectins in Arabidopsis Plays a Role in Seed Germination. <i>Plant Physiology</i> , 2012, 161, 305-316.	4.8	124
54	Starting to Gel: How Arabidopsis Seed Coat Epidermal Cells Produce Specialized Secondary Cell Walls. <i>International Journal of Molecular Sciences</i> , 2015, 16, 3452-3473.	4.1	118

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55	Towards recommendations for metadata and data handling in plant phenotyping. <i>Journal of Experimental Botany</i> , 2015, 66, 5417-5427.	4.8	116
56	Conversion of MapMan to Allow the Analysis of Transcript Data from Solanaceous Species: Effects of Genetic and Environmental Alterations in Energy Metabolism in the Leaf. <i>Plant Molecular Biology</i> , 2006, 60, 773-792.	3.9	115
57	Measures for interoperability of phenotypic data: minimum information requirements and formatting. <i>Plant Methods</i> , 2016, 12, 44.	4.3	109
58	GoMapMan: integration, consolidation and visualization of plant gene annotations within the MapMan ontology. <i>Nucleic Acids Research</i> , 2014, 42, D1167-D1175.	14.5	108
59	Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. <i>Nature Communications</i> , 2020, 11, 3719.	12.8	108
60	A Topological Map of the Compartmentalized Arabidopsis thaliana Leaf Metabolome. <i>PLoS ONE</i> , 2011, 6, e17806.	2.5	101
61	The Lipopolysaccharide of Sinorhizobium meliloti Suppresses Defense-Associated Gene Expression in Cell Cultures of the Host Plant Medicago truncatula Å. <i>Plant Physiology</i> , 2007, 143, 825-837.	4.8	100
62	Monitoring Polysaccharide Dynamics in the Plant Cell Wall. <i>Plant Physiology</i> , 2018, 176, 2590-2600.	4.8	99
63	Robin: An Intuitive Wizard Application for R-Based Expression Microarray Quality Assessment and Analysis Å Å. <i>Plant Physiology</i> , 2010, 153, 642-651.	4.8	96
64	Interoperability with Moby 1.0-It's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008, 9, 220-231.	6.5	91
65	Antisense Inhibition of the 2-Oxoglutarate Dehydrogenase Complex in Tomato Demonstrates Its Importance for Plant Respiration and during Leaf Senescence and Fruit Maturation. <i>Plant Cell</i> , 2012, 24, 2328-2351.	6.6	88
66	Identification of RNA-binding Proteins in Macrophages by Interactome Capture. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2699-2714.	3.8	88
67	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020, 227, 260-273.	7.3	84
68	Description and applications of a rapid and sensitive non-radioactive microplate-based assay for maximum and initial activity of D-ribulose-1,5-bisphosphate carboxylase/oxygenase. <i>Plant, Cell and Environment</i> , 2007, 30, 1163-1175.	5.7	82
69	Highly Branched Xylan Made by IRX14 and MUC121 Links Mucilage to Arabidopsis Seeds. <i>Plant Physiology</i> , 2015, 169, pp.01441.2015.	4.8	82
70	Quantitative RT-PCR Platform to Measure Transcript Levels of C and N Metabolism-Related Genes in Durum Wheat: Transcript Profiles in Elevated [CO ₂] and High Temperature at Different Levels of N Supply. <i>Plant and Cell Physiology</i> , 2015, 56, 1556-1573.	3.1	76
71	Adaptation of the MapMan ontology to biotic stress responses: application in solanaceous species. <i>Plant Methods</i> , 2007, 3, 10.	4.3	74
72	The Metabolic Signature of Biomass Formation in Barley. <i>Plant and Cell Physiology</i> , 2016, 57, 1943-1960.	3.1	66

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73	Identification of Key Enzymes for Pectin Synthesis in Seed Mucilage. <i>Plant Physiology</i> , 2018, 178, 1045-1064.	4.8	63
74	Plant genome and transcriptome annotations: from misconceptions to simple solutions. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw135.	6.5	62
75	An <i>Orange Ripening</i> Mutant Links Plastid NAD(P)H Dehydrogenase Complex Activity to Central and Specialized Metabolism during Tomato Fruit Maturation. <i>Plant Cell</i> , 2010, 22, 1977-1997.	6.6	61
76	Identification and characterization of a UDP-d-glucuronate 4-epimerase in <i>Arabidopsis</i> . <i>FEBS Letters</i> , 2004, 569, 327-331.	2.8	60
77	Transcriptional Wiring of Cell Wall-Related Genes in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2009, 2, 1015-1024.	8.3	60
78	De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant <i>seg8</i> . <i>Plant Journal</i> , 2010, 64, 589-603.	5.7	59
79	The genetic architecture of photosynthesis and plant growth-related traits in tomato. <i>Plant, Cell and Environment</i> , 2018, 41, 327-341.	5.7	59
80	A Transcriptional and Metabolic Framework for Secondary Wall Formation in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2016, 172, pp.01100.2016.	4.8	57
81	Exploiting Natural Variation in Tomato to Define Pathway Structure and Metabolic Regulation of Fruit Polyphenolics in the <i>Lycopersicon</i> Complex. <i>Molecular Plant</i> , 2020, 13, 1027-1046.	8.3	56
82	Demethylation of oligogalacturonides by FaPE1 in the fruits of the wild strawberry <i>Fragaria vesca</i> triggers metabolic and transcriptional changes associated with defence and development of the fruit. <i>Journal of Experimental Botany</i> , 2011, 62, 2855-2873.	4.8	55
83	How to make a tumour: cell type specific dissection of <i>Ustilago maydis</i> induced tumour development in maize leaves. <i>New Phytologist</i> , 2018, 217, 1681-1695.	7.3	55
84	Fluctuating Light Interacts with Time of Day and Leaf Development Stage to Reprogram Gene Expression. <i>Plant Physiology</i> , 2019, 179, 1632-1657.	4.8	53
85	Gene expression profiling in susceptible interaction of grapevine with its fungal pathogen <i>Eutypa lata</i> : Extending MapMan ontology for grapevine. <i>BMC Plant Biology</i> , 2009, 9, 104.	3.6	51
86	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019, 97, 182-198.	5.7	50
87	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2014, 448, 14-22.	2.4	49
88	The FRIABLE1 Gene Product Affects Cell Adhesion in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2012, 7, e42914.	2.5	48
89	Algorithm-driven Artifacts in median polish summarization of Microarray data. <i>BMC Bioinformatics</i> , 2010, 11, 553.	2.6	47
90	Oxford Nanopore sequencing: new opportunities for plant genomics?. <i>Journal of Experimental Botany</i> , 2020, 71, 5313-5322.	4.8	46

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91	Early metabolic and transcriptional variations in fruit of natural white-fruited <i>Fragaria vesca</i> genotypes. <i>Scientific Reports</i> , 2017, 7, 45113.	3.3	44
92	Metabolic Adaptation, a Specialized Leaf Organ Structure and Vascular Responses to Diurnal N ₂ Fixation by <i>Nostoc azollae</i> Sustain the Astonishing Productivity of <i>Azolla</i> Ferns without Nitrogen Fertilizer. <i>Frontiers in Plant Science</i> , 2017, 8, 442.	3.6	43
93	Xeml Lab: a tool that supports the design of experiments at a graphical interface and generates computer-readable metadata files, which capture information about genotypes, growth conditions, environmental perturbations and sampling strategy. <i>Plant, Cell and Environment</i> , 2009, 32, 1185-1200.	5.7	42
94	Monitoring of Plant Protein Post-translational Modifications Using Targeted Proteomics. <i>Frontiers in Plant Science</i> , 2018, 9, 1168.	3.6	41
95	Tomato's Green Gold: Bioeconomy Potential of Residual Tomato Leaf Biomass as a Novel Source for the Secondary Metabolite Rutin. <i>ACS Omega</i> , 2019, 4, 19071-19080.	3.5	38
96	Transcriptome sequencing and microarray design for functional genomics in the extremophile <i>Arabidopsis</i> relative <i>Thellungiella salsuginea</i> (<i>Eutrema salsugineum</i>). <i>BMC Genomics</i> , 2013, 14, 793.	2.8	37
97	Overexpression of a pectin methylesterase inhibitor in <i>Arabidopsis thaliana</i> leads to altered growth morphology of the stem and defective organ separation. <i>Plant Signaling and Behavior</i> , 2013, 8, e26464.	2.4	37
98	Temporal kinetics of the transcriptional response to carbon depletion and sucrose readdition in <i>Arabidopsis</i> seedlings. <i>Plant, Cell and Environment</i> , 2016, 39, 768-786.	5.7	37
99	Identification of Enzyme Activity Quantitative Trait Loci in a <i>Solanum lycopersicum</i> – <i>Solanum pennellii</i> Introgression Line Population. <i>Plant Physiology</i> , 2011, 157, 998-1014.	4.8	36
100	The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. <i>Nucleic Acids Research</i> , 2012, 40, D1313-D1317.	14.5	35
101	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019, 179, 1893-1907.	4.8	34
102	Reverse Engineering: A Key Component of Systems Biology to Unravel Global Abiotic Stress Cross-Talk. <i>Frontiers in Plant Science</i> , 2012, 3, 294.	3.6	33
103	Modeling Protein Destiny in Developing Fruit. <i>Plant Physiology</i> , 2019, 180, 1709-1724.	4.8	33
104	SLoCX: predicting subcellular localization of <i>Arabidopsis</i> proteins leveraging gene expression data. <i>Frontiers in Plant Science</i> , 2011, 2, 43.	3.6	32
105	Ethanol inducible expression of a mesophilic cellulase avoids adverse effects on plant development. <i>Biotechnology for Biofuels</i> , 2013, 6, 53.	6.2	32
106	The role of COBRA-LIKE 2 function, as part of the complex network of interacting pathways regulating <i>Arabidopsis</i> seed mucilage polysaccharide matrix organization. <i>Plant Journal</i> , 2018, 94, 497-512.	5.7	32
107	One-Step Lignocellulose Fractionation by using 2,5-Furandicarboxylic Acid as a Biogenic and Recyclable Catalyst. <i>ChemSusChem</i> , 2018, 11, 2051-2056.	6.8	32
108	Extensive Natural Variation in <i>Arabidopsis</i> Seed Mucilage Structure. <i>Frontiers in Plant Science</i> , 2016, 7, 803.	3.6	31

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109	Streptomyces thermoautotrophicus does not fix nitrogen. Scientific Reports, 2016, 6, 20086.	3.3	31
110	An integrative genomics approach for deciphering the complex interactions between ascorbate metabolism and fruit growth and composition in tomato. Comptes Rendus - Biologies, 2009, 332, 1007-1021.	0.2	30
111	Chloroplast DnaJ-like proteins 3 and 4 (CDJ3/4) from <i>Chlamydomonas reinhardtii</i> contain redox-active Fe-S clusters and interact with stromal HSP70B. Biochemical Journal, 2010, 427, 205-215.	3.7	30
112	LASSO modeling of the Arabidopsis thaliana seed/seedling transcriptome: a model case for detection of novel mucilage and pectin metabolism genes. Molecular BioSystems, 2012, 8, 2566.	2.9	30
113	TRM 4 is essential for cellulose deposition in Arabidopsis seed mucilage by maintaining cortical microtubule organization and interacting with CESA 3. New Phytologist, 2019, 221, 881-895.	7.3	30
114	From plant genomes to phenotypes. Journal of Biotechnology, 2017, 261, 46-52.	3.8	29
115	A chromosome scale tomato genome built from complementary PacBio and Nanopore sequences alone reveals extensive linkage drag during breeding. Plant Journal, 2022, 110, 572-588.	5.7	29
116	Cell wall modification in tobacco by differential targeting of recombinant endoglucanase from Trichoderma reesei. BMC Plant Biology, 2015, 15, 54.	3.6	28
117	Improving the utilization of lignocellulosic biomass by polysaccharide modification. Process Biochemistry, 2016, 51, 288-296.	3.7	28
118	De Novo Transcriptome Analysis of Durum Wheat Flag Leaves Provides New Insights Into the Regulatory Response to Elevated CO2 and High Temperature. Frontiers in Plant Science, 2019, 10, 1605.	3.6	28
119	Isolation of Open Chromatin Identifies Regulators of Systemic Acquired Resistance. Plant Physiology, 2019, 181, 817-833.	4.8	28
120	HRE-Type Genes are Regulated by Growth-Related Changes in Internal Oxygen Concentrations During the Normal Development of Potato (Solanum tuberosum) Tubers. Plant and Cell Physiology, 2011, 52, 1957-1972.	3.1	25
121	Genotype-phenotype modeling considering intermediate level of biological variation: a case study involving sensory traits, metabolites and QTLs in ripe tomatoes. Molecular BioSystems, 2015, 11, 3101-3110.	2.9	25
122	Large-scale phenotyping of transgenic tobacco plants (<i>Nicotiana tabacum</i>) to identify essential leaf functions. Plant Biotechnology Journal, 2008, 6, 246-263.	8.3	24
123	Foliose <i>Ulva</i> Species Show Considerable Inter-specific Genetic Diversity, Low Intra-specific Genetic Variation, and the Rare Occurrence of Inter-specific Hybrids in the Wild. Journal of Phycology, 2021, 57, 219-233.	2.3	24
124	GabiPD - The GABI Primary Database integrates plant proteomic data with gene-centric information. Frontiers in Plant Science, 2012, 3, 154.	3.6	23
125	De novo sequencing and analysis of the lily pollen transcriptome: an open access data source for an orphan plant species. Plant Molecular Biology, 2015, 87, 69-80.	3.9	23
126	On the current status of Phakopsora pachyrhizi genome sequencing. Frontiers in Plant Science, 2014, 5, 377.	3.6	21

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127	Insights into cell wall structure of <i>Sida hermaphrodita</i> and its influence on recalcitrance. <i>Carbohydrate Polymers</i> , 2017, 168, 94-102.	10.2	21
128	A comparative analysis of nonhost resistance across the two Triticeae crop species wheat and barley. <i>BMC Plant Biology</i> , 2017, 17, 232.	3.6	21
129	Detecting Inconsistencies in Large Biological Networks with Answer Set Programming. <i>Lecture Notes in Computer Science</i> , 2008, , 130-144.	1.3	21
130	Structure and putative function of NFX1-like proteins in plants. <i>Plant Biology</i> , 2010, 12, 381-394.	3.8	20
131	The Plant Growth Promoting Substance, Lumichrome, Mimics Starch, and Ethylene-Associated Symbiotic Responses in Lotus and Tomato Roots. <i>Frontiers in Plant Science</i> , 2012, 3, 120.	3.6	20
132	Cell type specific transcriptional reprogramming of maize leaves during <i>Ustilago maydis</i> induced tumor formation. <i>Scientific Reports</i> , 2019, 9, 10227.	3.3	18
133	High precision genome sequencing of engineered <i>Gluconobacter oxydans</i> 621H by combining long nanopore and short accurate Illumina reads. <i>Journal of Biotechnology</i> , 2017, 258, 197-205.	3.8	17
134	Transcriptomic and proteomic data in developing tomato fruit. <i>Data in Brief</i> , 2020, 28, 105015.	1.0	17
135	RNAseq analysis of $\hat{\pm}$ -proteobacterium <i>Gluconobacter oxydans</i> 621H. <i>BMC Genomics</i> , 2018, 19, 24.	2.8	16
136	A <i>Solanum lycopersicoides</i> reference genome facilitates insights into tomato specialized metabolism and immunity. <i>Plant Journal</i> , 2022, 110, 1791-1810.	5.7	16
137	Plant Pathway Databases. <i>Methods in Molecular Biology</i> , 2016, 1374, 71-87.	0.9	15
138	Towards Positional Isolation of Three Quantitative Trait Loci Conferring Resistance to Powdery Mildew in Two Spanish Barley Landraces. <i>PLoS ONE</i> , 2013, 8, e67336.	2.5	14
139	Crystal structure and functional characterization of a glucosamine-6-phosphate N-acetyltransferase from <i>Arabidopsis thaliana</i> . <i>Biochemical Journal</i> , 2012, 443, 427-437.	3.7	13
140	Transcriptional co-response analysis as a tool to identify new components of the wall biosynthetic machinery. <i>Plant Biosystems</i> , 2005, 139, 69-73.	1.6	12
141	Bioinformatics in the plant genomic and phenomic domain: The German contribution to resources, services and perspectives. <i>Journal of Biotechnology</i> , 2017, 261, 37-45.	3.8	12
142	Seed hemicelluloses tailor mucilage properties and salt tolerance. <i>New Phytologist</i> , 2021, 229, 1946-1954.	7.3	12
143	Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. <i>BMC Bioinformatics</i> , 2007, 8, 165.	2.6	11
144	Smut infection of perennial hosts: the genome and the transcriptome of the Brassicaceae smut fungus <i>Thecaphora thlaspeos</i> reveal functionally conserved and novel effectors. <i>New Phytologist</i> , 2019, 222, 1474-1492.	7.3	11

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