

Bjrn Usadel

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

152
papers

39,705
citations

64
h-index

159
g-index

159
ext. papers

57,012
ext. citations

7.5
avg, IF

8.07
L-index

#	Paper	IF	Citations
152	Tomato leaves under stress: a comparison of stress response to mild abiotic stress between a cultivated and a wild tomato species. <i>Plant Molecular Biology</i> , 2021 , 107, 177-206	4.6	1
151	Plant PhysioSpace: a robust tool to compare stress response across plant species. <i>Plant Physiology</i> , 2021 , 187, 1795-1811	6.6	1
150	Seed hemicelluloses tailor mucilage properties and salt tolerance. <i>New Phytologist</i> , 2021 , 229, 1946-1954	4.8	4
149	Foliose Ulva Species Show Considerable Inter-Specific Genetic Diversity, Low Intra-Specific Genetic Variation, and the Rare Occurrence of Inter-Specific Hybrids in the Wild. <i>Journal of Phycology</i> , 2021 , 57, 219-233	3	9
148	Oxford Nanopore sequencing: new opportunities for plant genomics?. <i>Journal of Experimental Botany</i> , 2020 , 71, 5313-5322	7	20
147	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. <i>New Phytologist</i> , 2020 , 227, 260-273	9.8	42
146	Genetic and molecular characterization of multicomponent resistance of against allacin. <i>Life Science Alliance</i> , 2020 , 3,	5.8	8
145	Transcriptomic and proteomic data in developing tomato fruit. <i>Data in Brief</i> , 2020 , 28, 105015	1.2	7
144	Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. <i>Nature Communications</i> , 2020 , 11, 3719	17.4	41
143	Exploiting Natural Variation in Tomato to Define Pathway Structure and Metabolic Regulation of Fruit Polyphenolics in the Lycopersicum Complex. <i>Molecular Plant</i> , 2020 , 13, 1027-1046	14.4	23
142	Parallel Metabolomic and Transcriptomic Analysis Reveals Key Factors for Quality Improvement of Tea Plants. <i>Journal of Agricultural and Food Chemistry</i> , 2020 , 68, 5483-5495	5.7	2
141	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	9.8	8
140	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019 , 179, 1893-1907	6.6	21
139	Fluctuating Light Interacts with Time of Day and Leaf Development Stage to Reprogram Gene Expression. <i>Plant Physiology</i> , 2019 , 179, 1632-1657	6.6	36
138	Modeling Protein Destiny in Developing Fruit. <i>Plant Physiology</i> , 2019 , 180, 1709-1724	6.6	15
137	MapMan4: A Refined Protein Classification and Annotation Framework Applicable to Multi-Omics Data Analysis. <i>Molecular Plant</i> , 2019 , 12, 879-892	14.4	148
136	Cell type specific transcriptional reprogramming of maize leaves during <i>Ustilago maydis</i> induced tumor formation. <i>Scientific Reports</i> , 2019 , 9, 10227	4.9	7

135	Transcriptome Analysis of Durum Wheat Flag Leaves Provides New Insights Into the Regulatory Response to Elevated CO and High Temperature. <i>Frontiers in Plant Science</i> , 2019 , 10, 1605	6.2	16
134	Tomato@ 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	3.9	30
133	Isolation of Open Chromatin Identifies Regulators of Systemic Acquired Resistance. <i>Plant Physiology</i> , 2019 , 181, 817-833	6.6	13
132	TRM4 is essential for cellulose deposition in Arabidopsis seed mucilage by maintaining cortical microtubule organization and interacting with CESA3. <i>New Phytologist</i> , 2019 , 221, 881-895	9.8	14
131	Computational aspects underlying genome to phenome analysis in plants. <i>Plant Journal</i> , 2019 , 97, 182-188	10.8	33
130	Plant genome and transcriptome annotations: from misconceptions to simple solutions. <i>Briefings in Bioinformatics</i> , 2018 , 19, 437-449	13.4	40
129	Monitoring Polysaccharide Dynamics in the Plant Cell Wall. <i>Plant Physiology</i> , 2018 , 176, 2590-2600	6.6	61
128	The role of COBRA-LIKE 2 function, as part of the complex network of interacting pathways regulating Arabidopsis seed mucilage polysaccharide matrix organization. <i>Plant Journal</i> , 2018 , 94, 497-512	6.9	17
127	How to make a tumour: cell type specific dissection of Ustilago maydis-induced tumour development in maize leaves. <i>New Phytologist</i> , 2018 , 217, 1681-1695	9.8	31
126	The genetic architecture of photosynthesis and plant growth-related traits in tomato. <i>Plant, Cell and Environment</i> , 2018 , 41, 327-341	8.4	40
125	Footprints of parasitism in the genome of the parasitic flowering plant Cuscuta campestris. <i>Nature Communications</i> , 2018 , 9, 2515	17.4	79
124	RNAseq analysis of β -proteobacterium <i>Gluconobacter oxydans</i> 621H. <i>BMC Genomics</i> , 2018 , 19, 24	4.5	9
123	Monitoring of Plant Protein Post-translational Modifications Using Targeted Proteomics. <i>Frontiers in Plant Science</i> , 2018 , 9, 1168	6.2	32
122	The Multifaceted Role of Pectin Methylsterase Inhibitors (PMEIs). <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	69
121	Identification of Key Enzymes for Pectin Synthesis in Seed Mucilage. <i>Plant Physiology</i> , 2018 , 178, 1045-1064	10.6	31
120	One-Step Lignocellulose Fractionation by using 2,5-Furandicarboxylic Acid as a Biogenic and Recyclable Catalyst. <i>ChemSusChem</i> , 2018 , 11, 2051-2056	8.3	22
119	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	3.7	15
118	From plant genomes to phenotypes. <i>Journal of Biotechnology</i> , 2017 , 261, 46-52	3.7	22

117	Early metabolic and transcriptional variations in fruit of natural white-fruited <i>Fragaria vesca</i> genotypes. <i>Scientific Reports</i> , 2017 , 7, 45113	4.9	31
116	Insights into cell wall structure of <i>Sida hermaphrodita</i> and its influence on recalcitrance. <i>Carbohydrate Polymers</i> , 2017 , 168, 94-102	10.3	16
115	De Novo Assembly of a New Accession Using Nanopore Sequencing. <i>Plant Cell</i> , 2017 , 29, 2336-2348	11.6	138
114	A comparative analysis of nonhost resistance across the two Triticeae crop species wheat and barley. <i>BMC Plant Biology</i> , 2017 , 17, 232	5.3	16
113	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	3.7	8
112	Tomato facultative parthenocarpy results from SLAGAMOUS-LIKE 6 loss of function. <i>Plant Biotechnology Journal</i> , 2017 , 15, 634-647	11.6	147
111	Genetic architecture of plant stress resistance: multi-trait genome-wide association mapping. <i>New Phytologist</i> , 2017 , 213, 1346-1362	9.8	99
110	Metabolic Adaptation, a Specialized Leaf Organ Structure and Vascular Responses to Diurnal N Fixation by Sustain the Astonishing Productivity of Ferns without Nitrogen Fertilizer. <i>Frontiers in Plant Science</i> , 2017 , 8, 442	6.2	22
109	A Transcriptional and Metabolic Framework for Secondary Wall Formation in Arabidopsis. <i>Plant Physiology</i> , 2016 , 172, 1334-1351	6.6	31
108	<i>Streptomyces thermoautotrophicus</i> does not fix nitrogen. <i>Scientific Reports</i> , 2016 , 6, 20086	4.9	20
107	Identification of RNA-binding Proteins in Macrophages by Interactome Capture. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2699-714	7.6	49
106	Improving the utilization of lignocellulosic biomass by polysaccharide modification. <i>Process Biochemistry</i> , 2016 , 51, 288-296	4.8	15
105	Plant Pathway Databases. <i>Methods in Molecular Biology</i> , 2016 , 1374, 71-87	1.4	11
104	Extensive Natural Variation in Arabidopsis Seed Mucilage Structure. <i>Frontiers in Plant Science</i> , 2016 , 7, 803	6.2	20
103	Temporal kinetics of the transcriptional response to carbon depletion and sucrose readdition in Arabidopsis seedlings. <i>Plant, Cell and Environment</i> , 2016 , 39, 768-86	8.4	27
102	The Metabolic Signature of Biomass Formation in Barley. <i>Plant and Cell Physiology</i> , 2016 , 57, 1943-60	4.9	23
101	Measures for interoperability of phenotypic data: minimum information requirements and formatting. <i>Plant Methods</i> , 2016 , 12, 44	5.8	83
100	Genome-Wide Analysis of Yield in Europe: Allelic Effects Vary with Drought and Heat Scenarios. <i>Plant Physiology</i> , 2016 , 172, 749-764	6.6	72

99	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, 1556-73	4.9	43
98	Starting to gel: how Arabidopsis seed coat epidermal cells produce specialized secondary cell walls. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 3452-73	6.3	79
97	Cell wall modification in tobacco by differential targeting of recombinant endoglucanase from <i>Trichoderma reesei</i> . <i>BMC Plant Biology</i> , 2015 , 15, 54	5.3	25
96	Highly Branched Xylan Made by IRREGULAR XYLEM14 and MUCILAGE-RELATED21 Links Mucilage to Arabidopsis Seeds. <i>Plant Physiology</i> , 2015 , 169, 2481-95	6.6	55
95	MUCILAGE-RELATED10 Produces Galactoglucomannan That Maintains Pectin and Cellulose Architecture in Arabidopsis Seed Mucilage. <i>Plant Physiology</i> , 2015 , 169, 403-20	6.6	93
94	Genotype-phenotype modeling considering intermediate level of biological variation: a case study involving sensory traits, metabolites and QTLs in ripe tomatoes. <i>Molecular BioSystems</i> , 2015 , 11, 3101-10		12
93	De novo sequencing and analysis of the lily pollen transcriptome: an open access data source for an orphan plant species. <i>Plant Molecular Biology</i> , 2015 , 87, 69-80	4.6	20
92	Growing Near Net Shape Components from Renewable Materials. <i>Procedia CIRP</i> , 2015 , 29, 609-614	1.8	1
91	Towards recommendations for metadata and data handling in plant phenotyping. <i>Journal of Experimental Botany</i> , 2015 , 66, 5417-27	7	94
90	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. <i>Analytical Biochemistry</i> , 2014 , 448, 14-22	3.1	40
89	Mercator: a fast and simple web server for genome scale functional annotation of plant sequence data. <i>Plant, Cell and Environment</i> , 2014 , 37, 1250-8	8.4	373
88	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014 , 46, 1034-8	36.3	269
87	Trimmomatic: a flexible trimmer for Illumina sequence data. <i>Bioinformatics</i> , 2014 , 30, 2114-20	7.2	24714
86	GoMapMan: integration, consolidation and visualization of plant gene annotations within the MapMan ontology. <i>Nucleic Acids Research</i> , 2014 , 42, D1167-75	20.1	69
85	On the current status of <i>Phakopsora pachyrhizi</i> genome sequencing. <i>Frontiers in Plant Science</i> , 2014 , 5, 377	6.2	16
84	Plant genome sequencing - applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014 , 26, 31-7	11.4	128
83	Ethanol inducible expression of a mesophilic cellulase avoids adverse effects on plant development. <i>Biotechnology for Biofuels</i> , 2013 , 6, 53	7.8	28
82	Hochdurchsatz-Sequenzierung und dann?. <i>BioSpektrum</i> , 2013 , 19, 458-460	0.1	

81	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	11.5	260
80	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	4.5	30
79	Diurnal changes of polysome loading track sucrose content in the rosette of wild-type <i>Arabidopsis</i> and the starchless <i>pgm</i> mutant. <i>Plant Physiology</i> , 2013 , 162, 1246-65	6.6	106
78	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. <i>Briefings in Bioinformatics</i> , 2013 , 14, 548-55	13.4	7
77	Evolution of a complex locus for terpene biosynthesis in <i>Solanum</i> . <i>Plant Cell</i> , 2013 , 25, 2022-36	11.6	103
76	The plant transcriptome—from integrating observations to models. <i>Frontiers in Plant Science</i> , 2013 , 4, 48	6.2	6
75	Overexpression of a pectin methyltransferase 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	2.5	24
74	Demethylesterification of cell wall pectins in <i>Arabidopsis</i> plays a role in seed germination. <i>Plant Physiology</i> , 2013 , 161, 305-16	6.6	102
73	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	3.7	13
72	The art of growing plants for experimental purposes: a practical guide for the plant biologist. <i>Functional Plant Biology</i> , 2012 , 39, 821-838	2.7	144
71	LASSO modeling of the <i>Arabidopsis thaliana</i> seed/seedling transcriptome: a model case for detection of novel mucilage and pectin metabolism genes. <i>Molecular BioSystems</i> , 2012 , 8, 2566-74		24
70	The FRIABLE1 gene product affects cell adhesion in <i>Arabidopsis</i> . <i>PLoS ONE</i> , 2012 , 7, e42914	3.7	34
69	Klassifikation pflanzlicher Genome im Schnelldurchlauf. <i>BioSpektrum</i> , 2012 , 18, 277-279	0.1	
68	Reverse engineering: a key component of systems biology to unravel global abiotic stress cross-talk. <i>Frontiers in Plant Science</i> , 2012 , 3, 294	6.2	29
67	GabiPD - The GABI Primary Database integrates plant proteomic data with gene-centric information. <i>Frontiers in Plant Science</i> , 2012 , 3, 154	6.2	21
66	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	6.2	16
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, 2328-51	11.6	71
64	RobiNA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. <i>Nucleic Acids Research</i> , 2012 , 40, W622-7	20.1	614

63	The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. <i>Nucleic Acids Research</i> , 2012 , 40, D1313-7	20.1	32
62	Crystal structure and functional characterization of a glucosamine-6-phosphate N-acetyltransferase from <i>Arabidopsis thaliana</i> . <i>Biochemical Journal</i> , 2012 , 443, 427-37	3.8	7
61	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, 600-27	11.6	179
60	SLocX: Predicting Subcellular Localization of Arabidopsis Proteins Leveraging Gene Expression Data. <i>Frontiers in Plant Science</i> , 2011 , 2, 43	6.2	22
59	The interconversion of UDP-arabinopyranose and UDP-arabinofuranose is indispensable for plant development in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011 , 23, 1373-90	11.6	97
58	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, 2855-73	7	43
57	Identification of enzyme activity quantitative trait loci in a <i>Solanum lycopersicum</i> x <i>Solanum pennellii</i> introgression line population. <i>Plant Physiology</i> , 2011 , 157, 998-1014	6.6	31
56	HRE-type genes are regulated by growth-related changes in internal oxygen concentrations during the normal development of potato (<i>Solanum tuberosum</i>) tubers. <i>Plant and Cell Physiology</i> , 2011 , 52, 1957-72	4.9	23
55	Systems biology of tomato fruit development: combined transcript, protein, and metabolite analysis of tomato transcription factor (nor, rin) and ethylene receptor (Nr) mutants reveals novel regulatory interactions. <i>Plant Physiology</i> , 2011 , 157, 405-25	6.6	245
54	PlaNet: combined sequence and expression comparisons across plant networks derived from seven species. <i>Plant Cell</i> , 2011 , 23, 895-910	11.6	245
53	A topological map of the compartmentalized <i>Arabidopsis thaliana</i> leaf metabolome. <i>PLoS ONE</i> , 2011 , 6, e17806	3.7	84
52	De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant seg8. <i>Plant Journal</i> , 2010 , 64, 589-603	6.9	48
51	<i>Arabidopsis</i> and primary photosynthetic metabolism - more than the icing on the cake. <i>Plant Journal</i> , 2010 , 61, 1067-91	6.9	240
50	Structure and putative function of NFX1-like proteins in plants. <i>Plant Biology</i> , 2010 , 12, 381-94	3.7	13
49	Robin: an intuitive wizard application for R-based expression microarray quality assessment and analysis. <i>Plant Physiology</i> , 2010 , 153, 642-51	6.6	90
48	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, 2872-93	11.6	119
47	An orange ripening mutant links plastid NAD(P)H dehydrogenase complex activity to central and specialized metabolism during tomato fruit maturation. <i>Plant Cell</i> , 2010 , 22, 1977-97	11.6	53
46	Assembly of an interactive correlation network for the <i>Arabidopsis</i> genome using a novel heuristic clustering algorithm. <i>Plant Physiology</i> , 2010 , 152, 29-43	6.6	135

45	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. <i>Biochemical Journal</i> , 2010 , 427, 205-15	3.8	26
44	Quantitation in mass-spectrometry-based proteomics. <i>Annual Review of Plant Biology</i> , 2010 , 61, 491-516	30.7	257
43	Algorithm-driven artifacts in median polish summarization of microarray data. <i>BMC Bioinformatics</i> , 2010 , 11, 553	3.6	42
42	Visualisation of Transcriptomics Data in Metabolic Pathways 2010 , 335-342		
41	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, 10348-53	11.5	381
40	Transcriptional wiring of cell wall-related genes in Arabidopsis. <i>Molecular Plant</i> , 2009 , 2, 1015-24	14.4	35
39	Ribosome and transcript copy numbers, polysome occupancy and enzyme dynamics in Arabidopsis. <i>Molecular Systems Biology</i> , 2009 , 5, 314	12.2	229
38	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, 961-80	6.6	171
37	Regulatory features underlying pollination-dependent and -independent tomato fruit set revealed by transcript and primary metabolite profiling. <i>Plant Cell</i> , 2009 , 21, 1428-52	11.6	200
36	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	5.3	44
35	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, 1185-200	8.4	37
34	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, 1211-29	8.4	398
33	Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. <i>Plant, Cell and Environment</i> , 2009 , 32, 1633-51	8.4	373
32	An integrative genomics approach for deciphering the complex interactions between ascorbate metabolism and fruit growth and composition in tomato. <i>Comptes Rendus - Biologies</i> , 2009 , 332, 1007-21	11.4	30
31	RNA interference of LIN5 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, 1204-18	6.6	185
30	Large-scale phenotyping of transgenic tobacco plants (<i>Nicotiana tabacum</i>) to identify essential leaf functions. <i>Plant Biotechnology Journal</i> , 2008 , 6, 246-63	11.6	16
29	Multilevel genomic analysis of the response of transcripts, enzyme activities and metabolites in Arabidopsis rosettes to a progressive decrease of temperature in the non-freezing range. <i>Plant, Cell and Environment</i> , 2008 , 31, 518-47	8.4	162
28	A subtilisin-like serine protease essential for mucilage release from Arabidopsis seed coats. <i>Plant Journal</i> , 2008 , 54, 466-80	6.9	133

27	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	6.9	235
26	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	4.5	154
25	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, 1738-58	6.6	222
24	Metabolomics- and proteomics-assisted genome annotation and analysis of the draft metabolic network of <i>Chlamydomonas reinhardtii</i> . <i>Genetics</i> , 2008 , 179, 157-66	4	128
23	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, 1834-61	6.6	262
22	Interoperability with Moby 1.0—it's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008 , 9, 220-31	13.4	73
21	Detecting Inconsistencies in Large Biological Networks with Answer Set Programming. <i>Lecture Notes in Computer Science</i> , 2008 , 130-144	0.9	19
20	Adaptation of the MapMan ontology to biotic stress responses: application in solanaceous species. <i>Plant Methods</i> , 2007 , 3, 10	5.8	51
19	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	8.4	447
18	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, 1163-75	8.4	70
17	Temporal responses of transcripts, enzyme activities and metabolites after adding sucrose to carbon-deprived <i>Arabidopsis</i> seedlings. <i>Plant Journal</i> , 2007 , 49, 463-91	6.9	234
16	Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. <i>BMC Bioinformatics</i> , 2007 , 8, 165	3.6	10
15	The lipopolysaccharide of <i>Sinorhizobium meliloti</i> suppresses defense-associated gene expression in cell cultures of the host plant <i>Medicago truncatula</i> . <i>Plant Physiology</i> , 2007 , 143, 825-37	6.6	86
14	Reduced expression of succinyl-coenzyme A ligase can be compensated for by up-regulation of the gamma-aminobutyrate shunt in illuminated tomato leaves. <i>Plant Physiology</i> , 2007 , 145, 626-39	6.6	133
13	PageMan: an interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. <i>BMC Bioinformatics</i> , 2006 , 7, 535	3.6	276
12	Integration of metabolite with transcript and enzyme activity profiling during diurnal cycles in <i>Arabidopsis</i> rosettes. <i>Genome Biology</i> , 2006 , 7, R76	18.3	269
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, 1380-96	6.6	361
10	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, 773-92	4.6	110

9	GMD@CSB.DB: the Golm Metabolome Database. <i>Bioinformatics</i> , 2005 , 21, 1635-8	7.2	1064
8	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, 243-54	4.7	103
7	Sugars and circadian regulation make major contributions to the global regulation of diurnal gene expression in Arabidopsis. <i>Plant Cell</i> , 2005 , 17, 3257-81	11.6	521
6	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, 1195-204	6.6	514
5	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	11
4	CSB.DB: a comprehensive systems-biology database. <i>Bioinformatics</i> , 2004 , 20, 3647-51	7.2	145
3	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, 286-95	6.6	113
2	Identification and characterization of a UDP-D-glucuronate 4-epimerase in Arabidopsis. <i>FEBS Letters</i> , 2004 , 569, 327-31	3.8	39
1	Rapid structural phenotyping of plant cell wall mutants by enzymatic oligosaccharide fingerprinting. <i>Plant Physiology</i> , 2002 , 130, 1754-63	6.6	171