Björn Usadel

List of Publications by Year
in descending order

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	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
2	Capsicum Leaves under Stress: Using Multi-Omics Analysis to Detect Abiotic Stress Network of Secondary Metabolism in Two Species. Antioxidants, 2022, 11, 671.	5.1	8
3	A <i>Solanum lycopersicoides</i> reference genome facilitates insights into tomato specialized metabolism and immunity. Plant Journal, 2022, 110, 1791-1810.	5.7	16
4	Seed hemicelluloses tailor mucilage properties and salt tolerance. New Phytologist, 2021, 229, 1946-1954.	7.3	12
5	Foliose <i>Ulva</i> Species Show Considerable Interâ€Specific Genetic Diversity, Low Intraâ€Specific Genetic Variation, and the Rare Occurrence of Interâ€Specific Hybrids in the Wild. Journal of Phycology, 2021, 57, 219-233.	2.3	24
6	Plant PhysioSpace: a robust tool to compare stress response across plant species. Plant Physiology, 2021, 187, 1795-1811.	4.8	3
7	Tomato leaves under stress: a comparison of stress response to mild abiotic stress between a cultivated and a wild tomato species. Plant Molecular Biology, 2021, 107, 177-206.	3.9	11
8	Transcriptomic and proteomic data in developing tomato fruit. Data in Brief, 2020, 28, 105015.	1.0	17
9	Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. Nature Communications, 2020, 11, 3719.	12.8	108
10	Oxford Nanopore sequencing: new opportunities for plant genomics?. Journal of Experimental Botany, 2020, 71, 5313-5322.	4.8	46
11	Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytologist, 2020, 227, 260-273.	7.3	84
12	Exploiting Natural Variation in Tomato to Define Pathway Structure and Metabolic Regulation of Fruit Polyphenolics in the Lycopersicum Complex. Molecular Plant, 2020, 13, 1027-1046.	8.3	56
13	Parallel Metabolomic and Transcriptomic Analysis Reveals Key Factors for Quality Improvement of Tea Plants. Journal of Agricultural and Food Chemistry, 2020, 68, 5483-5495.	5.2	9
14	Genetic and molecular characterization of multicomponent resistance of <i>Pseudomonas</i> against allicin. Life Science Alliance, 2020, 3, e202000670.	2.8	11
15	Cell type specific transcriptional reprogramming of maize leaves during Ustilago maydis induced tumor formation. Scientific Reports, 2019, 9, 10227.	3.3	18
16	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. New Phytologist, 2019, 222, 1474-1492.	7.3	11
17	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. Plant Physiology, 2019, 179, 1893-1907.	4.8	34
18	Fluctuating Light Interacts with Time of Day and Leaf Development Stage to Reprogram Gene Expression. Plant Physiology, 2019, 179, 1632-1657.	4.8	53

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19	Modeling Protein Destiny in Developing Fruit. Plant Physiology, 2019, 180, 1709-1724.	4.8	33
20	MapMan4: A Refined Protein Classification and Annotation Framework Applicable to Multi-Omics Data Analysis. Molecular Plant, 2019, 12, 879-892.	8.3	353
21	De Novo Transcriptome Analysis of Durum Wheat Flag Leaves Provides New Insights Into the Regulatory Response to Elevated CO_2 and High Temperature. Frontiers in Plant Science, 2019, 10, 1605.	3.6	28
22	Tomatoâ€™s Green Gold: Bioeconomy Potential of Residual Tomato Leaf Biomass as a Novel Source for the Secondary Metabolite Rutin. ACS Omega, 2019, 4, 19071-19080.	3.5	38
23	Isolation of Open Chromatin Identifies Regulators of Systemic Acquired Resistance. Plant Physiology, 2019, 181, 817-833.	4.8	28
24	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
25	Computational aspects underlying genome to phenome analysis in plants. Plant Journal, 2019, 97, 182-198.	5.7	50
26	Plant genome and transcriptome annotations: from misconceptions to simple solutions. Briefings in Bioinformatics, 2018, 19, bbw135.	6.5	62
27	Monitoring Polysaccharide Dynamics in the Plant Cell Wall. Plant Physiology, 2018, 176, 2590-2600.	4.8	99
28	The role of <scp>COBRA</scp>â€<scp>LIKE</scp> 2 function, as part of the complex network of interacting pathways regulating <i>Arabidopsis</i> seed mucilage polysaccharide matrix organization. Plant Journal, 2018, 94, 497-512.	5.7	32
29	How to make a tumour: cell type specific dissection of <i>Ustilago maydisâ€</i>induced tumour development in maize leaves. New Phytologist, 2018, 217, 1681-1695.	7.3	55
30	The genetic architecture of photosynthesis and plant growthâ€related traits in tomato. Plant, Cell and Environment, 2018, 41, 327-341.	5.7	59
31	The Multifaceted Role of Pectin Methylesterase Inhibitors (PMEIs). International Journal of Molecular Sciences, 2018, 19, 2878.	4.1	148
32	Identification of Key Enzymes for Pectin Synthesis in Seed Mucilage. Plant Physiology, 2018, 178, 1045-1064.	4.8	63
33	Oneâ€Step Lignocellulose Fractionation by using 2,5â€Furandicarboxylic Acid as a Biogenic and Recyclable Catalyst. ChemSusChem, 2018, 11, 2051-2056.	6.8	32
34	Footprints of parasitism in the genome of the parasitic flowering plant Cuscuta campestris. Nature Communications, 2018, 9, 2515.	12.8	141
35	RNAseq analysis of Î±-proteobacterium Gluconobacter oxydans 621H. BMC Genomics, 2018, 19, 24.	2.8	16
36	Monitoring of Plant Protein Post-translational Modifications Using Targeted Proteomics. Frontiers in Plant Science, 2018, 9, 1168.	3.6	41

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37	High precision genome sequencing of engineered Gluconobacter oxydans 621H by combining long nanopore and short accurate Illumina reads. Journal of Biotechnology, 2017, 258, 197-205.	3.8	17
38	From plant genomes to phenotypes. Journal of Biotechnology, 2017, 261, 46-52.	3.8	29
39	Early metabolic and transcriptional variations in fruit of natural white-fruited Fragaria vesca genotypes. Scientific Reports, 2017, 7, 45113.	3.3	44
40	Insights into cell wall structure of Sida hermaphrodita and its influence on recalcitrance. Carbohydrate Polymers, 2017, 168, 94-102.	10.2	21
41	De Novo Assembly of a New *Solanum pennellii* Accession Using Nanopore Sequencing. Plant Cell, 2017, 29, 2336-2348.	6.6	192
42	Bioinformatics in the plant genomic and phenomic domain: The German contribution to resources, services and perspectives. Journal of Biotechnology, 2017, 261, 37-45.	3.8	12
43	Tomato facultative parthenocarpy results from Sl*AGAMOUS‐LIKE 6* loss of function. Plant Biotechnology Journal, 2017, 15, 634-647.	8.3	244
44	Genetic architecture of plant stress resistance: multi‐trait genome‐wide association mapping. New Phytologist, 2017, 213, 1346-1362.	7.3	144
45	Metabolic Adaptation, a Specialized Leaf Organ Structure and Vascular Responses to Diurnal N2 Fixation by Nostoc azollae Sustain the Astonishing Productivity of Azolla Ferns without Nitrogen Fertilizer. Frontiers in Plant Science, 2017, 8, 442.	3.6	43
46	A comparative analysis of nonhost resistance across the two Triticeae crop species wheat and barley. BMC Plant Biology, 2017, 17, 232.	3.6	21
47	Extensive Natural Variation in Arabidopsis Seed Mucilage Structure. Frontiers in Plant Science, 2016, 7, 803.	3.6	31
48	Temporal kinetics of the transcriptional response to carbon depletion and sucrose readdition in *Arabidopsis* seedlings. Plant, Cell and Environment, 2016, 39, 768-786.	5.7	37
49	The Metabolic Signature of Biomass Formation in Barley. Plant and Cell Physiology, 2016, 57, 1943-1960.	3.1	66
50	Measures for interoperability of phenotypic data: minimum information requirements and formatting. Plant Methods, 2016, 12, 44.	4.3	109
51	Genome-wide analysis of yield in Europe: allelic effects as functions of drought and heat scenarios. Plant Physiology, 2016, 172, pp.00621.2016.	4.8	140
52	A Transcriptional and Metabolic Framework for Secondary Wall Formation in Arabidopsis. Plant Physiology, 2016, 172, pp.01100.2016.	4.8	57
53	Streptomyces thermoautotrophicus does not fix nitrogen. Scientific Reports, 2016, 6, 20086.	3.3	31
54	Identification of RNA-binding Proteins in Macrophages by Interactome Capture. Molecular and Cellular Proteomics, 2016, 15, 2699-2714.	3.8	88

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55	Improving the utilization of lignocellulosic biomass by polysaccharide modification. Process Biochemistry, 2016, 51, 288-296.	3.7	28
56	Plant Pathway Databases. Methods in Molecular Biology, 2016, 1374, 71-87.	0.9	15
57	Growing Near Net Shape Components from Renewable Materials. Procedia CIRP, 2015, 29, 609-614.	1.9	1
58	Towards recommendations for metadata and data handling in plant phenotyping. Journal of Experimental Botany, 2015, 66, 5417-5427.	4.8	116
59	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. Plant and Cell Physiology, 2015, 56, 1556-1573.	3.1	76
60	Starting to Gel: How Arabidopsis Seed Coat Epidermal Cells Produce Specialized Secondary Cell Walls. International Journal of Molecular Sciences, 2015, 16, 3452-3473.	4.1	118
61	Cell wall modification in tobacco by differential targeting of recombinant endoglucanase from Trichoderma reesei. BMC Plant Biology, 2015, 15, 54.	3.6	28
62	Highly Branched Xylan Made by IRX14 and MUCI21 Links Mucilage to Arabidopsis Seeds. Plant Physiology, 2015, 169, pp.01441.2015.	4.8	82
63	MUCILAGE-RELATED10 Produces Galactoglucomannan That Maintains Pectin and Cellulose Architecture in Arabidopsis Seed Mucilage. Plant Physiology, 2015, 169, 403-420.	4.8	126
64	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
65	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
66	GoMapMan: integration, consolidation and visualization of plant gene annotations within the MapMan ontology. Nucleic Acids Research, 2014, 42, D1167-D1175.	14.5	108
67	On the current status of Phakopsora pachyrhizi genome sequencing. Frontiers in Plant Science, 2014, 5, 377.	3.6	21
68	Plant genome sequencing — applications for crop improvement. Current Opinion in Biotechnology, 2014, 26, 31-37.	6.6	164
69	Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. Analytical Biochemistry, 2014, 448, 14-22.	2.4	49
70	Mercator: a fast and simple web server for genome scale functional annotation of plant sequence data. Plant, Cell and Environment, 2014, 37, 1250-1258.	5.7	575
71	The genome of the stress-tolerant wild tomato species Solanum pennellii. Nature Genetics, 2014, 46, 1034-1038.	21.4	391
72	Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics, 2014, 30, 2114-2120.	4.1	46,646

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73	Ethanol inducible expression of a mesophilic cellulase avoids adverse effects on plant development. Biotechnology for Biofuels, 2013, 6, 53.	6.2	32
74	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2655-62.	7.1	325
75	Transcriptome sequencing and microarray design for functional genomics in the extremophile Arabidopsis relative Thellungiella salsuginea (Eutrema salsugineum). BMC Genomics, 2013, 14, 793.	2.8	37
76	Diurnal Changes of Polysome Loading Track Sucrose Content in the Rosette of Wild-Type Arabidopsis and the Starchless *pgm* Mutant Â Â. Plant Physiology, 2013, 162, 1246-1265.	4.8	133
77	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. Briefings in Bioinformatics, 2013, 14, 548-555.	6.5	8
78	Evolution of a Complex Locus for Terpene Biosynthesis in *Solanum* Â Â. Plant Cell, 2013, 25, 2022-2036.	6.6	132
79	The plant transcriptomeâ€"from integrating observations to models. Frontiers in Plant Science, 2013, 4, 48.	3.6	10
80	Overexpression of a pectin methylesterase inhibitor in *Arabidopsis thaliana* leads to altered growth morphology of the stem and defective organ separation. Plant Signaling and Behavior, 2013, 8, e26464.	2.4	37
81	Towards Positional Isolation of Three Quantitative Trait Loci Conferring Resistance to Powdery Mildew in Two Spanish Barley Landraces. PLoS ONE, 2013, 8, e67336.	2.5	14
82	Reverse Engineering: A Key Component of Systems Biology to Unravel Global Abiotic Stress Cross-Talk. Frontiers in Plant Science, 2012, 3, 294.	3.6	33
83	GabiPD â€" The GABI Primary Database integrates plant proteomic data with gene-centric information. Frontiers in Plant Science, 2012, 3, 154.	3.6	23
84	The Plant Growth Promoting Substance, Lumichrome, Mimics Starch, and Ethylene-Associated Symbiotic Responses in Lotus and Tomato Roots. Frontiers in Plant Science, 2012, 3, 120.	3.6	20
85	Antisense Inhibition of the 2-Oxoglutarate Dehydrogenase Complex in Tomato Demonstrates Its Importance for Plant Respiration and during Leaf Senescence and Fruit Maturation. Plant Cell, 2012, 24, 2328-2351.	6.6	88
86	RobiNA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. Nucleic Acids Research, 2012, 40, W622-W627.	14.5	729
87	The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. Nucleic Acids Research, 2012, 40, D1313-D1317.	14.5	35
88	Demethylesterification of Cell Wall Pectins in Arabidopsis Plays a Role in Seed Germination Â Â. Plant Physiology, 2012, 161, 305-316.	4.8	124
89	Crystal structure and functional characterization of a glucosamine-6-phosphate N-acetyltransferase from *Arabidopsis thaliana*. Biochemical Journal, 2012, 443, 427-437.	3.7	13
90	The art of growing plants for experimental purposes: a practical guide for the plant biologist. Functional Plant Biology, 2012, 39, 821.	2.1	217

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91	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
92	The FRIABLE1 Gene Product Affects Cell Adhesion in Arabidopsis. PLoS ONE, 2012, 7, e42914.	2.5	48
93	Visualizing large, high-throughput datasets based on the cognitive representation of biological pathways. Proceedings of SPIE, 2011, , .	0.8	0
94	Antisense Inhibition of the Iron-Sulphur Subunit of Succinate Dehydrogenase Enhances Photosynthesis and Growth in Tomato via an Organic Acidâ€"Mediated Effect on Stomatal Aperture Â. Plant Cell, 2011, 23, 600-627.	6.6	221
95	SLocX: predicting subcellular localization of Arabidopsis proteins leveraging gene expression data. Frontiers in Plant Science, 2011, 2, 43.	3.6	32
96	The Interconversion of UDP-Arabinopyranose and UDP-Arabinofuranose Is Indispensable for Plant Development in<i>Arabidopsis</i>Â Â Â. Plant Cell, 2011, 23, 1373-1390.	6.6	134
97	Demethylation of oligogalacturonides by FaPE1 in the fruits of the wild strawberry Fragaria vesca triggers metabolic and transcriptional changes associated with defence and development of the fruit. Journal of Experimental Botany, 2011, 62, 2855-2873.	4.8	55
98	Identification of Enzyme Activity Quantitative Trait Loci in a Solanum lycopersicum Ã— Solanum pennellii Introgression Line Population Â Â. Plant Physiology, 2011, 157, 998-1014.	4.8	36
99	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
100	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 Â Â. Plant Physiology, 2011, 157, 405-425.	4.8	303
101	PlaNet: Combined Sequence and Expression Comparisons across Plant Networks Derived from Seven Species Â. Plant Cell, 2011, 23, 895-910.	6.6	297
102	A Topological Map of the Compartmentalized Arabidopsis thaliana Leaf Metabolome. PLoS ONE, 2011, 6, e17806.	2.5	101
103	Chloroplast DnaJ-like proteins 3 and 4 (CDJ3/4) from <i>Chlamydomonas reinhardtii</i> contain redox-active Feâ€"S clusters and interact with stromal HSP70B. Biochemical Journal, 2010, 427, 205-215.	3.7	30
104	Quantitation in Mass-Spectrometry-Based Proteomics. Annual Review of Plant Biology, 2010, 61, 491-516.	18.7	301
105	Algorithm-driven Artifacts in median polish summarization of Microarray data. BMC Bioinformatics, 2010, 11, 553.	2.6	47
106	De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant seg8. Plant Journal, 2010, 64, 589-603.	5.7	59
107	Arabidopsis and primary photosynthetic metabolism â€" more than the icing on the cake. Plant Journal, 2010, 61, 1067-1091.	5.7	300
108	Structure and putative function of NFX1â€like proteins in plants. Plant Biology, 2010, 12, 381-394.	3.8	20

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109	Robin: An Intuitive Wizard Application for R-Based Expression Microarray Quality Assessment and Analysis Â Â. Plant Physiology, 2010, 153, 642-651.	4.8	96
110	Network Analysis of Enzyme Activities and Metabolite Levels and Their Relationship to Biomass in a Large Panel of <i>Arabidopsis</i> Accessions Â Â. Plant Cell, 2010, 22, 2872-2893.	6.6	131
111	An <i>Orange Ripening</i> Mutant Links Plastid NAD(P)H Dehydrogenase Complex Activity to Central and Specialized Metabolism during Tomato Fruit Maturation Â. Plant Cell, 2010, 22, 1977-1997.	6.6	61
112	VisualisationVISUALISATION of Transcriptomic TRANSCRIPTOMICS s Data in Metabolic Pathways. , 2010, , 335-342.		0
113	Assembly of an Interactive Correlation Network for the Arabidopsis Genome Using a Novel Heuristic Clustering Algorithm Â. Plant Physiology, 2009, 152, 29-43.	4.8	174
114	Starch as a major integrator in the regulation of plant growth. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 10348-10353.	7.1	467
115	Transcriptional Wiring of Cell Wall-Related Genes in Arabidopsis. Molecular Plant, 2009, 2, 1015-1024.	8.3	60
116	Ribosome and transcript copy numbers, polysome occupancy and enzyme dynamics in <i>Arabidopsis</i>. Molecular Systems Biology, 2009, 5, 314.	7.2	276
117	Mapping Metabolic and Transcript Temporal Switches during Germination in Rice Highlights Specific Transcription Factors and the Role of RNA Instability in the Germination Process Â Â. Plant Physiology, 2009, 149, 961-980.	4.8	236
118	Regulatory Features Underlying Pollination-Dependent and -Independent Tomato Fruit Set Revealed by Transcript and Primary Metabolite Profiling. Plant Cell, 2009, 21, 1428-1452.	6.6	258
119	Gene expression profiling in susceptible interaction of grapevine with its fungal pathogen Eutypa lata: Extending MapMan ontology for grapevine. BMC Plant Biology, 2009, 9, 104.	3.6	51
120	Xeml Lab: a tool that supports the design of experiments at a graphical interface and generates computerâ€readable metadata files, which capture information about genotypes, growth conditions, environmental perturbations and sampling strategy. Plant, Cell and Environment, 2009, 32, 1185-1200.	5.7	42
121	A guide to using MapMan to visualize and compare Omics data in plants: a case study in the crop species, Maize. Plant, Cell and Environment, 2009, 32, 1211-1229.	5.7	561
122	Coâ€expression tools for plant biology: opportunities for hypothesis generation and caveats. Plant, Cell and Environment, 2009, 32, 1633-1651.	5.7	480
123	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
124	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 Â Â. Plant Physiology, 2009, 150, 1204-1218.	4.8	226
125	Largeâ€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
126	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 nonâ€freezing range. Plant, Cell and Environment, 2008, 31, 518-547.	5.7	191

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127	A subtilisinâ€like serine protease essential for mucilage release from Arabidopsis seed coats. Plant Journal, 2008, 54, 466-480.	5.7	159
128	Reprogramming a maize plant: transcriptional and metabolic changes induced by the fungal biotroph *Ustilago maydis*. Plant Journal, 2008, 56, 181-195.	5.7	328
129	Analysis of expressed sequence tags from Actinidia: applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. BMC Genomics, 2008, 9, 351.	2.8	178
130	Barley Grain Maturation and Germination: Metabolic Pathway and Regulatory Network Commonalities and Differences Highlighted by New MapMan/PageMan Profiling Tools Â Â. Plant Physiology, 2008, 146, 1738-1758.	4.8	250
131	Metabolomics- and Proteomics-Assisted Genome Annotation and Analysis of the Draft Metabolic Network of *Chlamydomonas reinhardtii*. Genetics, 2008, 179, 157-166.	2.9	141
132	Global Transcript Levels Respond to Small Changes of the Carbon Status during Progressive Exhaustion of Carbohydrates in Arabidopsis Rosettes Â Â. Plant Physiology, 2008, 146, 1834-1861.	4.8	306
133	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	6.5	91
134	Detecting Inconsistencies in Large Biological Networks with Answer Set Programming. Lecture Notes in Computer Science, 2008, , 130-144.	1.3	21
135	The Lipopolysaccharide of Sinorhizobium meliloti Suppresses Defense-Associated Gene Expression in Cell Cultures of the Host Plant Medicago truncatula Â. Plant Physiology, 2007, 143, 825-837.	4.8	100
136	Reduced Expression of Succinyl-Coenzyme A Ligase Can Be Compensated for by Up-Regulation of the *Î³*-Aminobutyrate Shunt in Illuminated Tomato Leaves. Plant Physiology, 2007, 145, 626-639.	4.8	151
137	Adaptation of the MapMan ontology to biotic stress responses: application in solanaceous species. Plant Methods, 2007, 3, 10.	4.3	74
138	Genome-wide reprogramming of metabolism and regulatory networks of Arabidopsis in response to phosphorus. Plant, Cell and Environment, 2007, 30, 85-112.	5.7	533
139	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. Plant, Cell and Environment, 2007, 30, 1163-1175.	5.7	82
140	Temporal responses of transcripts, enzyme activities and metabolites after adding sucrose to carbon-deprived Arabidopsis seedlings. Plant Journal, 2007, 49, 463-491.	5.7	272
141	Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. BMC Bioinformatics, 2007, 8, 165.	2.6	11
142	Integration of metabolite with transcript and enzyme activity profiling during diurnal cycles in Arabidopsis rosettes. Genome Biology, 2006, 7, R76.	9.6	304
143	Integrated Analysis of Metabolite and Transcript Levels Reveals the Metabolic Shifts That Underlie Tomato Fruit Development and Highlight Regulatory Aspects of Metabolic Network Behavior. Plant Physiology, 2006, 142, 1380-1396.	4.8	432
144	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. Plant Molecular Biology, 2006, 60, 773-792.	3.9	115

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145	PageMan: An interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. BMC Bioinformatics, 2006, 7, 535.	2.6	309
146	The inositol oxygenase gene family of Arabidopsis is involved in the biosynthesis of nucleotide sugar precursors for cell-wall matrix polysaccharides. Planta, 2005, 221, 243-254.	3.2	135
147	Sugars and Circadian Regulation Make Major Contributions to the Global Regulation of Diurnal Gene Expression in Arabidopsis Â. Plant Cell, 2005, 17, 3257-3281.	6.6	608
148	Extension of the Visualization Tool MapMan to Allow Statistical Analysis of Arrays, Display of Coresponding Genes, and Comparison with Known Responses. Plant Physiology, 2005, 138, 1195-1204.	4.8	576
149	Transcriptional co-response analysis as a tool to identify new components of the wall biosynthetic machinery. Plant Biosystems, 2005, 139, 69-73.	1.6	12
150	GMD@CSB.DB: the Golm Metabolome Database. Bioinformatics, 2005, 21, 1635-1638.	4.1	1,247
151	CSB.DB: a comprehensive systems-biology database. Bioinformatics, 2004, 20, 3647-3651.	4.1	152
152	RHM2 Is Involved in Mucilage Pectin Synthesis and Is Required for the Development of the Seed Coat in Arabidopsis. Plant Physiology, 2004, 134, 286-295.	4.8	127
153	Identification and characterization of a UDP-d-glucuronate 4-epimerase inArabidopsis. FEBS Letters, 2004, 569, 327-331.	2.8	60
154	Rapid Structural Phenotyping of Plant Cell Wall Mutants by Enzymatic Oligosaccharide Fingerprinting. Plant Physiology, 2002, 130, 1754-1763.	4.8	182