Joachim Kopka

List of Publications by Year in descending order

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232 papers 30,943 citations

7069 78 h-index 169 g-index

244 all docs 244 docs citations

times ranked

244

28725 citing authors

#	Article	IF	CITATIONS
1	Proposed minimum reporting standards for chemical analysis. Metabolomics, 2007, 3, 211-221.	1.4	3,589
2	Metabolite profiling for plant functional genomics. Nature Biotechnology, 2000, 18, 1157-1161.	9.4	1,936
3	Gas chromatography mass spectrometry–based metabolite profiling in plants. Nature Protocols, 2006, 1, 387-396.	5.5	1,808
4	GMD@CSB.DB: the Golm Metabolome Database. Bioinformatics, 2005, 21, 1635-1638.	1.8	1,247
5	Simultaneous analysis of metabolites in potato tuber by gas chromatography-mass spectrometry. Plant Journal, 2000, 23, 131-142.	2.8	1,058
6	Exploring the Temperature-Stress Metabolome of Arabidopsis. Plant Physiology, 2004, 136, 4159-4168.	2.3	943
7	Comprehensive metabolic profiling and phenotyping of interspecific introgression lines for tomato improvement. Nature Biotechnology, 2006, 24, 447-454.	9.4	707
8	Potential of metabolomics as a functional genomics tool. Trends in Plant Science, 2004, 9, 418-425.	4.3	685
9	GC-MS libraries for the rapid identification of metabolites in complex biological samples. FEBS Letters, 2005, 579, 1332-1337.	1.3	596
10	TagFinder for the quantitative analysis of gas chromatography—mass spectrometry (GC-MS)-based metabolite profiling experiments. Bioinformatics, 2008, 24, 732-737.	1.8	522
11	Identification of Uncommon Plant Metabolites Based on Calculation of Elemental Compositions Using Gas Chromatography and Quadrupole Mass Spectrometry. Analytical Chemistry, 2000, 72, 3573-3580.	3.2	520
12	Mass appeal: metabolite identification in mass spectrometry-focused untargeted metabolomics. Metabolomics, 2013, 9, 44-66.	1.4	452
13	Metabolomics of temperature stress. Physiologia Plantarum, 2008, 132, 220-235.	2.6	439
14	Transcript and metabolite profiling during cold acclimation of Arabidopsis reveals an intricate relationship of cold-regulated gene expression with modifications in metabolite content. Plant Journal, 2007, 50, 967-981.	2.8	419
15	Priming and memory of stress responses in organisms lacking a nervous system. Biological Reviews, 2016, 91, 1118-1133.	4.7	388
16	Systems Rebalancing of Metabolism in Response to Sulfur Deprivation, as Revealed by Metabolome Analysis of Arabidopsis Plants. Plant Physiology, 2005, 138, 304-318.	2.3	377
17	Downregulation of Cinnamoyl-Coenzyme A Reductase in Poplar: Multiple-Level Phenotyping Reveals Effects on Cell Wall Polymer Metabolism and Structure. Plant Cell, 2007, 19, 3669-3691.	3.1	352
18	Recommendations for Reporting Metabolite Data. Plant Cell, 2011, 23, 2477-2482.	3.1	326

#	Article	IF	CITATIONS
19	Parallel analysis of transcript and metabolic profiles: a new approach in systems biology. EMBO Reports, 2003, 4, 989-993.	2.0	308
20	Phosphorus Stress in Common Bean: Root Transcript and Metabolic Responses. Plant Physiology, 2007, 144, 752-767.	2.3	300
21	Decision tree supported substructure prediction of metabolites from GC-MS profiles. Metabolomics, 2010, 6, 322-333.	1.4	296
22	Global changes in transcription orchestrate metabolic differentiation during symbiotic nitrogen fixation inLotus japonicus. Plant Journal, 2004, 39, 487-512.	2.8	292
23	Plant metabolomics reveals conserved and divergent metabolic responses to salinity. Physiologia Plantarum, 2008, 132, 209-219.	2.6	290
24	Construction and application of a mass spectral and retention time index database generated from plant GC/EI-TOF-MS metabolite profiles. Phytochemistry, 2003, 62, 887-900.	1.4	285
25	A proposed framework for the description of plant metabolomics experiments and their results. Nature Biotechnology, 2004, 22, 1601-1606.	9.4	283
26	Comprehensive Dissection of Spatiotemporal Metabolic Shifts in Primary, Secondary, and Lipid Metabolism during Developmental Senescence in Arabidopsis Â. Plant Physiology, 2013, 162, 1290-1310.	2.3	278
27	DOF transcription factor AtDof1.1 (OBP2) is part of a regulatory network controlling glucosinolate biosynthesis in Arabidopsis. Plant Journal, 2006, 47, 10-24.	2.8	243
28	Metabolite profiling in plant biology: platforms and destinations. Genome Biology, 2004, 5, 109.	13.9	205
29	Integrative functional genomics of salt acclimatization in the model legume <i>Lotus japonicus</i> .		
	Plant Journal, 2008, 53, 973-987.	2.8	199
30	Plant Journal, 2008, 53, 973-987. Transcript and metabolite profiling of the adaptive response to mild decreases in oxygen concentration in the roots of arabidopsis plants. Annals of Botany, 2009, 103, 269-280.	2.8	199
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31	Plant Journal, 2008, 53, 973-987. Transcript and metabolite profiling of the adaptive response to mild decreases in oxygen concentration in the roots of arabidopsis plants. Annals of Botany, 2009, 103, 269-280. Lotus japonicus Metabolic Profiling. Development of Gas Chromatography-Mass Spectrometry Resources for the Study of Plant-Microbe Interactions. Plant Physiology, 2005, 137, 1302-1318. Identification of primary and secondary metabolites with phosphorus statusâ€dependent abundance in ⟨scp⟩⟨i⟩⟨a⟩⟨i⟩⟨i⟩⟨a⟩⟨i⟩⟨i⟩⟨a⟩⟨i⟩⟨i⟩⟨a⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩⟨i⟩	1.4 2.3	197
31	Plant Journal, 2008, 53, 973-987. Transcript and metabolite profiling of the adaptive response to mild decreases in oxygen concentration in the roots of arabidopsis plants. Annals of Botany, 2009, 103, 269-280. Lotus japonicus Metabolic Profiling. Development of Gas Chromatography-Mass Spectrometry Resources for the Study of Plant-Microbe Interactions. Plant Physiology, 2005, 137, 1302-1318. Identification of primary and secondary metabolites with phosphorus statusâ€dependent abundance in ⟨scp⟩⟨i⟩⟨a⟩⟨scp⟩⟨i⟩⟨abactor of metabolic changes during phosphorus limitation. Plant, Cell and Environment, 2015, 38, 172-187. Impact of soluble sugar concentrations on the acquisition of freezing tolerance in accessions of Arabidopsis thaliana with contrasting cold adaptation - evidence for a role of raffinose in cold	1.4 2.3 2.8	197 196 196
31 32 33	Plant Journal, 2008, 53, 973-987. Transcript and metabolite profiling of the adaptive response to mild decreases in oxygen concentration in the roots of arabidopsis plants. Annals of Botany, 2009, 103, 269-280. Lotus japonicus Metabolic Profiling. Development of Gas Chromatography-Mass Spectrometry Resources for the Study of Plant-Microbe Interactions. Plant Physiology, 2005, 137, 1302-1318. Identification of primary and secondary metabolites with phosphorus statusâ€dependent abundance in ⟨scp⟩⟨i⟩A⟨ i⟩⟨ scp⟩⟨i⟩rabidopsis⟨ i⟩, and of the transcription factor ⟨scp⟩PHR⟨ scp⟩1 as a major regulator of metabolic changes during phosphorus limitation. Plant, Cell and Environment, 2015, 38, 172-187. Impact of soluble sugar concentrations on the acquisition of freezing tolerance in accessions of Arabidopsis thaliana with contrasting cold adaptation - evidence for a role of raffinose in cold acclimation. Plant, Cell and Environment, 2004, 27, 1395-1404. Transgenic Arabidopsis plants can accumulate polyhydroxybutyrate to up to 4% of their fresh weight.	2.3 2.8 2.8	197 196 196

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37	Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies. Molecular Nutrition and Food Research, 2019, 63, e1800384.	1.5	173
38	Non-linear PCA: a missing data approach. Bioinformatics, 2005, 21, 3887-3895.	1.8	167
39	A Central Role of Abscisic Acid in Stress-Regulated Carbohydrate Metabolism. PLoS ONE, 2008, 3, e3935.	1.1	165
40	Metabolic and transcriptomic signatures of rice floral organs reveal sugar starvation as a factor in reproductive failure under heat and drought stress. Plant, Cell and Environment, 2015, 38, 2171-2192.	2.8	164
41	Global Changes in the Transcript and Metabolic Profiles during Symbiotic Nitrogen Fixation in Phosphorus-Stressed Common Bean Plants Â. Plant Physiology, 2009, 151, 1221-1238.	2.3	163
42	Molecular phenotyping of ligninâ€modified tobacco reveals associated changes in cellâ€wall metabolism, primary metabolism, stress metabolism and photorespiration. Plant Journal, 2007, 52, 263-285.	2.8	161
43	Inferring Hypotheses on Functional Relationships of Genes: Analysis of the Arabidopsis thaliana Subtilase Gene Family. PLoS Computational Biology, 2005, 1, e40.	1.5	157
44	Retention index thresholds for compound matching in GC–MS metabolite profiling. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2008, 871, 182-190.	1.2	157
45	CSB.DB: a comprehensive systems-biology database. Bioinformatics, 2004, 20, 3647-3651.	1.8	152
46	Metabolic profiling reveals local and systemic responses of host plants to nematode parasitism. Plant Journal, 2010, 62, 1058-1071.	2.8	152
47	Comprehensive chemical derivatization for gas chromatography–mass spectrometry-based multi-targeted profiling of the major phytohormones. Journal of Chromatography A, 2003, 993, 89-102.	1.8	150
48	Metabolome analysis: the potential of in vivo labeling with stable isotopes for metabolite profiling. Trends in Biotechnology, 2005, 23, 28-33.	4.9	149
49	Organization and Metabolism of Plastids and Mitochondria in Arbuscular Mycorrhizal Roots of Medicago truncatula Â. Plant Physiology, 2005, 139, 329-340.	2.3	148
50	A new synthetic biology approach allows transfer of an entire metabolic pathway from a medicinal plant to a biomass crop. ELife, 2016, 5, .	2.8	148
51	Transcriptome and metabolome reprogramming in Vitis vinifera cv. Trincadeira berries upon infection with Botrytis cinerea. Journal of Experimental Botany, 2015, 66, 1769-1785.	2.4	144
52	COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. Metabolomics, 2015, 11, 1587-1597.	1.4	140
53	Metabolic profiling of â€~Conference' pears under low oxygen stress. Postharvest Biology and Technology, 2009, 51, 123-130.	2.9	133
54	Phospholipase C is required for the control of stomatal aperture by ABA. Plant Journal, 2003, 34, 47-55.	2.8	130

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55	Comparative metabolomics of drought acclimation in model and forage legumes. Plant, Cell and Environment, 2012, 35, 136-149.	2.8	128
56	Profiling of diurnal patterns of metabolite and transcript abundance in potato (Solanum tuberosum) leaves. Planta, 2005, 221, 891-903.	1.6	127
57	Molecular and Enzymatic Characterization of Three Phosphoinositide-Specific Phospholipase C Isoforms from Potato1. Plant Physiology, 1998, 116, 239-250.	2.3	123
58	Systems Analysis of the Response of Photosynthesis, Metabolism, and Growth to an Increase in Irradiance in the Photosynthetic Model Organism $\langle i \rangle$ Chlamydomonas reinhardtii $\langle i \rangle$ Â Â Â. Plant Cell, 2014, 26, 2310-2350.	3.1	123
59	Comparative ionomics and metabolomics in extremophile and glycophytic <i>Lotus</i> species under salt stress challenge the metabolic preâ€adaptation hypothesis. Plant, Cell and Environment, 2011, 34, 605-617.	2.8	122
60	Increasing Sucrose Uptake Capacity of Wheat Grains Stimulates Storage Protein Synthesis Â. Plant Physiology, 2010, 152, 698-710.	2.3	121
61	Inter-laboratory reproducibility of fast gas chromatography–electron impact–time of flight mass spectrometry (GC–El–TOF/MS) based plant metabolomics. Metabolomics, 2009, 5, 479-496.	1.4	120
62	Predicting Arabidopsis Freezing Tolerance and Heterosis in Freezing Tolerance from Metabolite Composition. Molecular Plant, 2010, 3, 224-235.	3.9	120
63	Dissecting Rice Polyamine Metabolism under Controlled Long-Term Drought Stress. PLoS ONE, 2013, 8, e60325.	1.1	120
64	Identification of Drought Tolerance Markers in a Diverse Population of Rice Cultivars by Expression and Metabolite Profiling. PLoS ONE, 2013, 8, e63637.	1.1	119
65	Comparative Functional Genomics of Salt Stress in Related Model and Cultivated Plants Identifies and Overcomes Limitations to Translational Genomics. PLoS ONE, 2011, 6, e17094.	1.1	119
66	Nonsupervised Construction and Application of Mass Spectral and Retention Time Index Libraries From Time-of-Flight Gas Chromatography-Mass Spectrometry Metabolite Profiles. Methods in Molecular Biology, 2007, 358, 19-38.	0.4	116
67	Discovering plant metabolic biomarkers for phenotype prediction using an untargeted approach. Plant Biotechnology Journal, 2010, 8, 900-911.	4.1	113
68	Extensive metabolic crossâ€talk in melon fruit revealed by spatial and developmental combinatorial metabolomics. New Phytologist, 2011, 190, 683-696.	3.5	111
69	Systems-Wide Analysis of Acclimation Responses to Long-Term Heat Stress and Recovery in the Photosynthetic Model Organism <i>Chlamydomonas reinhardtii</i> AÂÂ. Plant Cell, 2014, 26, 4270-4297.	3.1	107
70	GC-EI-TOF-MS analysis of in vivo carbon-partitioning into soluble metabolite pools of higher plants by monitoring isotope dilution after 13CO2 labelling. Phytochemistry, 2007, 68, 2258-2272.	1.4	105
71	Metabolic contribution to salt stress in two maize hybrids with contrasting resistance. Plant Science, 2015, 233, 107-115.	1.7	102
72	Metabolic labeling of plant cell cultures with K(15)NO3 as a tool for quantitative analysis of proteins and metabolites. Plant Methods, 2006, 2, 14.	1.9	92

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73	Molecular signatures associated with increased freezing tolerance due to low temperature memory in <i>Arabidopsis</i> . Plant, Cell and Environment, 2019, 42, 854-873.	2.8	89
74	Metabolic Changes in Synechocystis PCC6803 upon Nitrogen-Starvation: Excess NADPH Sustains Polyhydroxybutyrate Accumulation. Metabolites, 2013, 3, 101-118.	1.3	87
75	High night temperature strongly impacts TCA cycle, amino acid and polyamine biosynthetic pathways in rice in a sensitivity-dependent manner. Journal of Experimental Botany, 2015, 66, 6385-6397.	2.4	86
76	Macromolecular recognition directs calcium ions to coccolith mineralization sites. Science, 2016, 353, 590-593.	6.0	86
77	Potato guard cells respond to drying soil by a complex change in the expression of genes related to carbon metabolism and turgor regulation. Plant Journal, 1997, 11, 871-882.	2.8	83
78	Metabolome Phenotyping of Inorganic Carbon Limitation in Cells of the Wild Type and Photorespiratory Mutants of the Cyanobacterium <i>Synechocystis</i> Physiology, 2008, 148, 2109-2120.	2.3	82
79	Modulation of the Major Paths of Carbon in Photorespiratory Mutants of Synechocystis. PLoS ONE, 2011, 6, e16278.	1.1	81
80	Metabolic and Transcriptomic Phenotyping of Inorganic Carbon Acclimation in the Cyanobacterium <i>Synechococcus elongatus</i> PCC 7942 Â. Plant Physiology, 2011, 155, 1640-1655.	2.3	81
81	The Golm Metabolome Database: aÂdatabase for GC-MS based metabolite profiling. Topics in Current Genetics, 2007, , 75-95.	0.7	79
82	Simultaneous Interaction of <i>Arabidopsis thaliana</i> with <i>Bradyrhizobium</i> Sp. Strain ORS278 and <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 Leads to Complex Transcriptome Changes. Molecular Plant-Microbe Interactions, 2008, 21, 244-259.	1.4	79
83	A rapid approach for phenotypeâ€screening and database independent detection of cSNP/protein polymorphism using mass accuracy precursor alignment. Proteomics, 2008, 8, 4214-4225.	1.3	78
84	Metabolome and water status phenotyping of <i>Arabidopsis</i> under abiotic stress cues reveals new insight into <i>ESK1</i> function. Plant, Cell and Environment, 2009, 32, 95-108.	2.8	78
85	Plant Metabolomics and Its Potential for Systems Biology Research. Methods in Enzymology, 2011, 500, 299-336.	0.4	78
86	TagFinder: Preprocessing Software for the Fingerprinting and the Profiling of Gas Chromatography–Mass Spectrometry Based Metabolome Analyses. Methods in Molecular Biology, 2011, 860, 255-286.	0.4	75
87	Characterization of leaf apoplastic peroxidases and metabolites in Vigna unguiculata in response to toxic manganese supply and silicon. Journal of Experimental Botany, 2009, 60, 1663-1678.	2.4	72
88	Photosynthesis and metabolism interact during acclimation of <i>Arabidopsis thaliana</i> to high irradiance and sulphur depletion. Plant, Cell and Environment, 2010, 33, 1974-1988.	2.8	71
89	A plastid-localized glycogen synthase kinase $\hat{a} \in f$ 3 modulates stress tolerance and carbohydrate metabolism. Plant Journal, 2007, 49, 1076-1090.	2.8	70
90	Search for Transcriptional and Metabolic Markers of Grape Pre-Ripening and Ripening and Insights into Specific Aroma Development in Three Portuguese Cultivars. PLoS ONE, 2013, 8, e60422.	1.1	69

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91	Rapid transcriptional and metabolic regulation of the deacclimation process in cold acclimated Arabidopsis thaliana. BMC Genomics, 2017, 18, 731.	1.2	68
92	Metabolite and transcript markers for the prediction of potato drought tolerance. Plant Biotechnology Journal, 2018, 16, 939-950.	4.1	68
93	The drought response of potato reference cultivars with contrasting tolerance. Plant, Cell and Environment, 2016, 39, 2370-2389.	2.8	66
94	<i>Polyamine oxidase 5</i> lossâ€ofâ€function mutations in <i>Arabidopsis thaliana</i> trigger metabolic and transcriptional reprogramming and promote salt stress tolerance. Plant, Cell and Environment, 2017, 40, 527-542.	2.8	66
95	Recent Applications of Metabolomics Toward Cyanobacteria. Metabolites, 2013, 3, 72-100.	1.3	65
96	Identification of brassinosteroid-related genes by means of transcript co-response analyses. Nucleic Acids Research, 2005, 33, 2685-2696.	6.5	64
97	Systems analysis of ethanol production in the genetically engineered cyanobacterium Synechococcus sp. PCC 7002. Biotechnology for Biofuels, 2017, 10, 56.	6.2	64
98	Primed primary metabolism in systemic leaves: a functional systems analysis. Scientific Reports, 2018, 8, 216.	1.6	64
99	Induced, Imprinted, and Primed Responses to Changing Environments: Does Metabolism Store and Process Information?. Frontiers in Plant Science, 2019, 10, 106.	1.7	63
100	An automated GCxGCâ€TOFâ€MS protocol for batchâ€wise extraction and alignment of mass isotopomer matrixes from differential ¹³ Câ€labelling experiments: a case study for photoautotrophicâ€mixotrophic grown <i>Chlamydomonas reinhardtii</i> cells. Journal of Basic Microbiology, 2009, 49, 82-91.	1.8	62
101	Metabolic profiling of Arabidopsis thaliana epidermal cells. Journal of Experimental Botany, 2010, 61, 1321-1335.	2.4	61
102	Modification of OsSUT1 gene expression modulates the salt response of rice Oryza sativa cv. Taipei 309. Plant Science, 2012, 182, 101-111.	1.7	60
103	Systematic Review of Plant Ribosome Heterogeneity and Specialization. Frontiers in Plant Science, 2020, 11, 948.	1.7	60
104	Ca2+/phospholipid-binding (C2) domain in multiple plant proteins: novel components of the calcium-sensing apparatus. Plant Molecular Biology, 1998, 36, 627-637.	2.0	59
105	Regulation of arbuscular mycorrhization by apoplastic invertases: enhanced invertase activity in the leaf apoplast affects the symbiotic interaction. Plant Journal, 2007, 51, 390-405.	2.8	59
106	Mining for robust transcriptional and metabolic responses to longâ€term salt stress: a case study on the model legume ⟨i⟩Lotus japonicus⟨li⟩. Plant, Cell and Environment, 2010, 33, 468-480.	2.8	57
107	Integrated Transcriptomic and Metabolomic Characterization of the Low-Carbon Response Using an <i>ndhR</i> Mutant of <i>Synechocystis</i> sp. PCC 6803. Plant Physiology, 2015, 169, 1540-1556.	2.3	57
108	Autoinducers Act as Biological Timers in Vibrio harveyi. PLoS ONE, 2012, 7, e48310.	1.1	57

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109	Cyanobacterial Lactate Oxidases Serve as Essential Partners in N ₂ Fixation and Evolved into Photorespiratory Glycolate Oxidases in Plants. Plant Cell, 2011, 23, 2978-2990.	3.1	56
110	Discovery of food identity markers by metabolomics and machine learning technology. Scientific Reports, 2019, 9, 9697.	1.6	56
111	Comparative Metabolome Analysis of the Salt Response in Breeding Cultivars of Rice., 2007,, 285-315.		54
112	Integrated analysis of rice transcriptomic and metabolomic responses to elevated night temperatures identifies sensitivity―and toleranceâ€related profiles. Plant, Cell and Environment, 2017, 40, 121-137.	2.8	54
113	Dynamic Transcriptional and Metabolic Responses in Yeast Adapting to Temperature Stress. OMICS A Journal of Integrative Biology, 2010, 14, 249-259.	1.0	53
114	Metabolic responses of rice cultivars with different tolerance to combined drought and heat stress under field conditions. GigaScience, 2019, 8, .	3.3	52
115	Both cold and sub-zero acclimation induce cell wall modification and changes in the extracellular proteome in Arabidopsis thaliana. Scientific Reports, 2019, 9, 2289.	1.6	51
116	Highly Resolved Systems Biology to Dissect the Etioplast-to-Chloroplast Transition in Tobacco Leaves. Plant Physiology, 2019, 180, 654-681.	2.3	51
117	Identification of Arabidopsis Mutants Impaired in the Systemic Regulation of Root Nitrate Uptake by the Nitrogen Status of the Plant Â. Plant Physiology, 2010, 153, 1250-1260.	2.3	50
118	Insights into isoprene production using the cyanobacterium Synechocystis sp. PCC 6803. Biotechnology for Biofuels, 2016, 9, 89.	6.2	49
119	Carbon flux through photosynthesis and central carbon metabolism show distinct patterns between algae, C3 and C4 plants. Nature Plants, 2022, 8, 78-91.	4.7	49
120	Physiologic and metabolic responses of wheat seedlings to elevated and super-elevated carbon dioxide. Advances in Space Research, 2008, 42, 1917-1928.	1.2	45
121	Isolation and characterization of three new PGPR and their effects on the growth of <i>Arabidopsis</i> and <i>Datura</i> plants. Journal of Plant Interactions, 2017, 12, 1-6.	1.0	45
122	Light modulated activity of root alkaline/neutral invertase involves the interaction with 14â€3â€3 proteins. Plant Journal, 2014, 80, 785-796.	2.8	43
123	Cell wall modification by the xyloglucan endotransglucosylase/hydrolase <scp>XTH19</scp> influences freezing tolerance after cold and subâ€zero acclimation. Plant, Cell and Environment, 2021, 44, 915-930.	2.8	43
124	Metabolite Profiling Reveals a Role for Atypical Cinnamyl Alcohol Dehydrogenase CAD1 in the Synthesis of Coniferyl Alcohol in Tobacco Xylem. Plant Molecular Biology, 2005, 59, 753-769.	2.0	42
125	Metabolic Pathway Relationships Revealed by an Integrative Analysis of the Transcriptional and Metabolic Temperature Stress-Response Dynamics in Yeast. OMICS A Journal of Integrative Biology, 2010, 14, 261-274.	1.0	42
126	Overexpression of Sinapine Esterase BnSCE3 in Oilseed Rape Seeds Triggers Global Changes in Seed Metabolism Â. Plant Physiology, 2011, 155, 1127-1145.	2.3	42

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127	Profiling Methods to Identify Cold-Regulated Primary Metabolites Using Gas Chromatography Coupled to Mass Spectrometry. Methods in Molecular Biology, 2014, 1166, 171-197.	0.4	42
128	Characterization of the Wheat Leaf Metabolome during Grain Filling and under Varied N-Supply. Frontiers in Plant Science, 2017, 8, 2048.	1.7	42
129	Global Metabolic Profiling of Arabidopsis Polyamine Oxidase 4 (AtPAO4) Loss-of-Function Mutants Exhibiting Delayed Dark-Induced Senescence. Frontiers in Plant Science, 2016, 7, 173.	1.7	41
130	Central metabolite and sterol profiling divides tobacco male gametophyte development and pollen tube growth into eight metabolic phases. Plant Journal, 2017, 92, 129-146.	2.8	40
131	PaVESy: Pathway Visualization and Editing System. Bioinformatics, 2004, 20, 2841-2844.	1.8	39
132	Plant metabolomics coming of age. Physiologia Plantarum, 2008, 132, 113-116.	2.6	39
133	Metabolite profiling reveals novel multi-level cold responses in the diploid model Fragaria vesca (woodland strawberry). Phytochemistry, 2012, 77, 99-109.	1.4	39
134	Arabidopsis thaliana Glyoxalase 2-1 Is Required during Abiotic Stress but Is Not Essential under Normal Plant Growth. PLoS ONE, 2014, 9, e95971.	1.1	39
135	Plant Temperature Acclimation and Growth Rely on Cytosolic Ribosome Biogenesis Factor Homologs. Plant Physiology, 2018, 176, 2251-2276.	2.3	39
136	CyAbrB2 Contributes to the Transcriptional Regulation of Low CO ₂ Acclimation in <i>Synechocystis</i> PCC 6803. Plant and Cell Physiology, 2016, 57, 2232-2243.	1.5	37
137	Genetic and genomic analysis of legume flowers and seeds. Current Opinion in Plant Biology, 2006, 9, 133-141.	3.5	35
138	Low-carbon acclimation in carboxysome-less and photorespiratory mutants of the cyanobacterium Synechocystis sp. strain PCC 6803. Microbiology (United Kingdom), 2012, 158, 398-413.	0.7	35
139	Metabolic and transcriptional transitions in barley glumes reveal a role as transitory resource buffers during endosperm filling. Journal of Experimental Botany, 2015, 66, 1397-1411.	2.4	35
140	Comparative Metabolomics and Molecular Phylogenetics of Melon (Cucumis melo, Cucurbitaceae) Biodiversity. Metabolites, 2020, 10, 121.	1.3	35
141	Hybrid weakness controlled by the dosageâ€dependent lethal (DL) gene system in common bean (<i>Phaseolus vulgaris</i>) is caused by a shootâ€derived inhibitory signal leading to salicylic acidâ€associated root death. New Phytologist, 2007, 176, 537-549.	3.5	34
142	Dissection of jasmonate functions in tomato stamen development by transcriptome and metabolome analyses. BMC Biology, 2015, 13, 28.	1.7	34
143	Metabolic Flexibility Underpins Growth Capabilities of the Fastest Growing Alga. Current Biology, 2017, 27, 2559-2567.e3.	1.8	34
144	Hypothesis-driven approach to predict transcriptional units from gene expression data. Bioinformatics, 2004, 20, 1928-1939.	1.8	33

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145	Selective induction and subcellular distribution of ACONITASE 3 reveal the importance of cytosolic citrate metabolism during lipid mobilization in <i>Arabidopsis</i> . Biochemical Journal, 2014, 463, 309-317.	1.7	33
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