Ute Roessner

List of Publications by Year in descending order

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Version: 2024-02-01

195 16,370 57 121 papers citations h-index g-index

214 214 214 18459
all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Modulators or facilitators? Roles of lipids in plant root–microbe interactions. Trends in Plant Science, 2022, 27, 180-190.	8.8	45
2	Root Growth and Architecture of Wheat and Brachypodium Vary in Response to Algal Fertilizer in Soil and Solution. Agronomy, 2022, 12, 285.	3.0	4
3	Functional Traits 2.0: The power of the metabolome for ecology. Journal of Ecology, 2022, 110, 4-20.	4.0	42
4	Low doses of the organic insecticide spinosad trigger lysosomal defects, elevated ROS, lipid dysregulation, and neurodegeneration in flies. ELife, 2022, 11 , .	6.0	16
5	Metabolomics as an emerging tool to study plant–microbe interactions. Emerging Topics in Life Sciences, 2022, 6, 175-183.	2.6	28
6	Salt stress alters membrane lipid content and lipid biosynthesis pathways in the plasma membrane and tonoplast. Plant Physiology, 2022, 189, 805-826.	4.8	25
7	Germline mutations in mitochondrial complex I reveal genetic and targetable vulnerability in IDH1-mutant acute myeloid leukaemia. Nature Communications, 2022, 13, 2614.	12.8	9
8	The Effect of Cold Stress on the Root-Specific Lipidome of Two Wheat Varieties with Contrasting Cold Tolerance. Plants, 2022, 11, 1364.	3 . 5	4
9	The metabolic significance of symbiont community composition in the coral-algal symbiosis. , 2022, , 211-229.		O
10	Exploring the coral bleaching tipping point with 13C metabolomics., 2022, , 199-209.		0
11	Alleviation of salinity stress in plants by endophytic plant-fungal symbiosis: Current knowledge, perspectives and future directions. Plant and Soil, 2021, 461, 219-244.	3.7	109
12	Time-resolution of the shoot and root growth of the model cereal Brachypodium in response to inoculation with Azospirillum bacteria at low phosphorus and temperature. Plant Growth Regulation, 2021, 93, 149-162.	3 . 4	10
13	Wheat Can Access Phosphorus From Algal Biomass as Quickly and Continuously as From Mineral Fertilizer. Frontiers in Plant Science, 2021, 12, 631314.	3.6	7
14	Arabidopsis REI-LIKE proteins activate ribosome biogenesis during cold acclimation. Scientific Reports, 2021, 11, 2410.	3.3	19
15	Membrane-Enriched Proteomics Link Ribosome Accumulation and Proteome Reprogramming With Cold Acclimation in Barley Root Meristems. Frontiers in Plant Science, 2021, 12, 656683.	3.6	15
16	An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. Plant Journal, 2021, 107, 287-302.	5.7	18
17	Evaluation of physiological and biochemical responses of pistachio plants (Pistacia vera L.) exposed to pesticides. Ecotoxicology, 2021, 30, 1084-1097.	2.4	10
18	The Metabolic Response of Brachypodium Roots to the Interaction with Beneficial Bacteria Is Affected by the Plant Nutritional Status. Metabolites, 2021, 11, 358.	2.9	8

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19	Spatially Enriched Paralog Rearrangements Argue Functionally Diverse Ribosomes Arise during Cold Acclimation in Arabidopsis. International Journal of Molecular Sciences, 2021, 22, 6160.	4.1	10
20	Inoculation of barley with <i>Trichoderma harzianum</i> T-22 modifies lipids and metabolites to improve salt tolerance. Journal of Experimental Botany, 2021, 72, 7229-7246.	4.8	13
21	Characterization of epidermal bladder cells in <scp><i>Chenopodium quinoa</i></scp> . Plant, Cell and Environment, 2021, 44, 3836-3852.	5.7	13
22	The metabolic environment of the developing embryo: A multidisciplinary approach on oilseed rapeseed. Journal of Plant Physiology, 2021, 265, 153505.	3.5	7
23	The state of the art in plant lipidomics. Molecular Omics, 2021, 17, 894-910.	2.8	16
24	Reproductive Stage Drought Tolerance in Wheat: Importance of Stomatal Conductance and Plant Growth Regulators. Genes, 2021, 12, 1742.	2.4	16
25	Effect of Spirotetramat Application on Salicylic Acid, Antioxidative Enzymes, Amino Acids, Mineral Elements, and Soluble Carbohydrates in Cucumber (Cucumis sativus L.)., 2021, 11,.		1
26	Comparative spatial lipidomics analysis reveals cellular lipid remodelling in different developmental zones of barley roots in response to salinity. Plant, Cell and Environment, 2020, 43, 327-343.	5.7	23
27	Insights Into Oxidized Lipid Modification in Barley Roots as an Adaptation Mechanism to Salinity Stress. Frontiers in Plant Science, 2020, 11, 1.	3.6	477
28	Comparative metabolomics implicates threitol as a fungal signal supporting colonization of <i>Armillaria luteobubalina</i> on eucalypt roots. Plant, Cell and Environment, 2020, 43, 374-386.	5.7	19
29	Antioxidant system status of cucumber plants under pesticides treatment. Acta Physiologiae Plantarum, 2020, 42, 1.	2.1	24
30	Low doses of the neonicotinoid insecticide imidacloprid induce ROS triggering neurological and metabolic impairments in <i>Drosophila</i> . Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 25840-25850.	7.1	85
31	Edaphic niche characterization of four Proteaceae reveals unique calcicole physiology linked to hyperâ€endemism of Grevillea thelemanniana. New Phytologist, 2020, 228, 869-883.	7.3	10
32	Metabolite pools of the reef building coral Montipora capitata are unaffected by Symbiodiniaceae community composition. Coral Reefs, 2020, 39, 1727-1737.	2.2	19
33	Evaluating modified diets and dietary supplement therapies for reducing muscle lipid accumulation and improving muscle function in neurofibromatosis type 1 (NF1). PLoS ONE, 2020, 15, e0237097.	2.5	5
34	A comprehensive comparison of four methods for extracting lipids from Arabidopsis tissues. Plant Methods, 2020, 16, 155.	4.3	15
35	Phenotyping the Chilling and Freezing Responses of Young Microspore Stage Wheat Spikes Using Targeted Metabolome and Lipidome Profiling. Cells, 2020, 9, 1309.	4.1	14
36	Integrative Multi-omics Analyses of Barley Rootzones under Salinity Stress Reveal Two Distinctive Salt Tolerance Mechanisms. Plant Communications, 2020, 1, 100031.	7.7	26

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37	Metabolome Analysis., 2019, , 396-409.		3
38	Genotypic Variation in the Root and Shoot Metabolite Profiles of Wheat (Triticum aestivum L.) Indicate Sustained, Preferential Carbon Allocation as a Potential Mechanism in Phosphorus Efficiency. Frontiers in Plant Science, 2019, 10, 995.	3.6	32
39	Morphological and metabolic responses to salt stress of rice (Oryza sativa L.) cultivars which differ in salinity tolerance. Plant Physiology and Biochemistry, 2019, 144, 427-435.	5.8	59
40	Phenotyping reproductive stage chilling and frost tolerance in wheat using targeted metabolome and lipidome profiling. Metabolomics, 2019, 15, 144.	3.0	31
41	Spatio-Temporal Metabolite and Elemental Profiling of Salt Stressed Barley Seeds During Initial Stages of Germination by MALDI-MSI and µ-XRF Spectrometry. Frontiers in Plant Science, 2019, 10, 1139.	3.6	46
42	Genome-wide association studies of 74 plasma metabolites of German shepherd dogs reveal two metabolites associated with genes encoding their enzymes. Metabolomics, 2019, 15, 123.	3.0	4
43	The changes in the release level of polyunsaturated fatty acids (ω-3 and ω-6) and lipids in the untreated and water-soaked chia seed. Food Research International, 2019, 126, 108665.	6.2	8
44	The Influence of Contrasting Microbial Lifestyles on the Pre-symbiotic Metabolite Responses of Eucalyptus grandis Roots. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	17
45	Opposite fates of the purine metabolite allantoin under water and nitrogen limitations in bread wheat. Plant Molecular Biology, 2019, 99, 477-497.	3.9	41
46	Phenotypic and metabolic plasticity shapes lifeâ€history strategies under combinations of abiotic stresses. Plant Direct, 2019, 3, e00113.	1.9	39
47	High-mass-resolution MALDI mass spectrometry imaging reveals detailed spatial distribution of metabolites and lipids in roots of barley seedlings in response to salinity stress. Metabolomics, 2018, 14, 63.	3.0	69
48	13C metabolomics reveals widespread change in carbon fate during coral bleaching. Metabolomics, 2018, 14, 12.	3.0	60
49	Dietary intervention rescues myopathy associated with neurofibromatosis type 1. Human Molecular Genetics, 2018, 27, 577-588.	2.9	21
50	Structural and functional measures of marine microbial communities: An experiment to assess implications for oil spill management. Marine Pollution Bulletin, 2018, 131, 525-529.	5.0	12
51	A high-resolution HPLC-QqTOF platform using parallel reaction monitoring for in-depth lipid discovery and rapid profiling. Analytica Chimica Acta, 2018, 1026, 87-100.	5.4	47
52	Identification of physiological changes and key metabolites coincident with postharvest internal browning of pineapple (Ananas comosus L.) fruit. Postharvest Biology and Technology, 2018, 137, 56-65.	6.0	23
53	Partner switching and metabolic flux in a model cnidarian–dinoflagellate symbiosis. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, .	2.6	72
54	RNA Catabolites Contribute to the Nitrogen Pool and Support Growth Recovery of Wheat. Frontiers in Plant Science, 2018, 9, 1539.	3.6	29

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55	A Golgi UDP-GlcNAc transporter delivers substrates for N-linked glycans and sphingolipids. Nature Plants, 2018, 4, 792-801.	9.3	27
56	Feeding the Walls: How Does Nutrient Availability Regulate Cell Wall Composition?. International Journal of Molecular Sciences, 2018, 19, 2691.	4.1	52
57	Extraction of Plant Lipids for LC-MS-Based Untargeted Plant Lipidomics. Methods in Molecular Biology, 2018, 1778, 125-135.	0.9	8
58	Single cellâ€type analysis of cellular lipid remodelling in response to salinity in the epidermal bladder cells of the model halophyte <scp><i>Mesembryanthemum crystallinum</i></scp> . Plant, Cell and Environment, 2018, 41, 2390-2403.	5.7	22
59	Quantification of Sugars and Organic Acids in Biological Matrices Using GC-QqQ-MS. Methods in Molecular Biology, 2018, 1778, 207-223.	0.9	5
60	Comparative metabolic and ionomic profiling of two cultivars of Stevia rebaudiana Bert. (Bertoni) grown under salinity stress. Plant Physiology and Biochemistry, 2018, 129, 56-70.	5.8	26
61	Systems-based approaches enable identification of gene targets which improve the flavour profile of low-ethanol wine yeast strains. Metabolic Engineering, 2018, 49, 178-191.	7.0	16
62	Water availability moderates N ₂ fixation benefit from elevated [CO ₂]: A 2â€year freeâ€air CO ₂ enrichment study on lentil (<i>Lens culinaris</i> MEDIK.) in a water limited agroecosystem. Plant, Cell and Environment, 2018, 41, 2418-2434.	5.7	24
63	Determination of amino acids in urine of patients with prostate cancer and benign prostate growth. European Journal of Cancer Prevention, 2017, 26, 131-134.	1.3	17
64	Mapping carbon fate during bleaching in a model cnidarian symbiosis: the application of ¹³ C metabolomics. New Phytologist, 2017, 214, 1551-1562.	7.3	53
65	MASTR-MS: a web-based collaborative laboratory information management system (LIMS) for metabolomics. Metabolomics, 2017, 13, 14.	3.0	16
66	The genome of Chenopodium quinoa. Nature, 2017, 542, 307-312.	27.8	569
67	Transition from a maternal to external nitrogen source in maize seedlings. Journal of Integrative Plant Biology, 2017, 59, 261-274.	8.5	11
68	Diurnal Changes in Transcript and Metabolite Levels during the Iron Deficiency Response of Rice. Rice, 2017, 10, 14.	4.0	25
69	From common to rare Zingiberaceae plants - A metabolomics study using GC-MS. Phytochemistry, 2017, 140, 141-150.	2.9	31
70	Epidermal bladder cells confer salinity stress tolerance in the halophyte quinoa and Atriplex species. Plant, Cell and Environment, 2017, 40, 1900-1915.	5.7	98
71	Optimal nutrient exchange and immune responses operate in partner specificity in the cnidarian-dinoflagellate symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13194-13199.	7.1	181
72	Prospection and identification of nematotoxic compounds from Canavalia ensiformis seeds effective in the control of the root knot nematode Meloidogyne incognita. Biotechnology Research and Innovation, 2017, 1, 87-100.	0.9	18

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73	Metabolite profiling of symbiont and host during thermal stress and bleaching in the coral Acropora aspera. Coral Reefs, 2017, 36, 105-118.	2.2	87
74	De novo transcriptome assembly and analysis of differentially expressed genes of two barley genotypes reveal root-zone-specific responses to salt exposure. Scientific Reports, 2016, 6, 31558.	3.3	33
75	Nitrogen assimilation system in maize is regulated by developmental and tissue-specific mechanisms. Plant Molecular Biology, 2016, 92, 293-312.	3.9	16
76	Cell-Type-Specific H ⁺ -ATPase Activity in Root Tissues Enables K ⁺ Retention and Mediates Acclimation of Barley (<i>Hordeum vulgare</i>) to Salinity Stress. Plant Physiology, 2016, 172, 2445-2458.	4.8	158
77	Elemental imaging of leaves from the metal hyperaccumulating plant Noccaea caerulescens shows different spatial distribution of Ni, Zn and Cd. RSC Advances, 2016, 6, 2337-2344.	3.6	42
78	Beta-glucan-depleted, glycopeptide-rich extracts from Brewer's and Baker's yeast (Saccharomyces) Tj ET Chemistry, 2016, 197, 761-768.	Qq0 0 0 r 8.2	gBT /Overlock 15
79	Root spatial metabolite profiling of two genotypes of barley <i>(Hordeum vulgare</i> L.) reveals differences in response to short-term salt stress. Journal of Experimental Botany, 2016, 67, 3731-3745.	4.8	137
80	Inactivation of Mitochondrial Complex I Induces the Expression of a Twin Cysteine Protein that Targets and Affects Cytosolic, Chloroplastidic and Mitochondrial Function. Molecular Plant, 2016, 9, 696-710.	8.3	28
81	Salt-stress induced alterations in the root lipidome of two barley genotypes with contrasting responses to salinity. Functional Plant Biology, 2016, 43, 207.	2.1	48
82	Mass spectrometry imaging for plant biology: a review. Phytochemistry Reviews, 2016, 15, 445-488.	6.5	210
83	A Quantitative Profiling Method of Phytohormones and Other Metabolites Applied to Barley Roots Subjected to Salinity Stress. Frontiers in Plant Science, 2016, 7, 2070.	3.6	63
84	2015: an eventful year for the Metabolomics Society. Metabolomics, 2015, 11, 1475-1477.	3.0	0
85	A new peak detection algorithm for MALDI mass spectrometry data based on a modified Asymmetric Pseudo-Voigt model. BMC Genomics, 2015, 16, S12.	2.8	7
86	One minute with the Metabolomics Society's Honorary Fellows 2015. Metabolomics, 2015, 11, 779-781.	3.0	0
87	Metabolomics, Standards, and Metabolic Modeling for Synthetic Biology in Plants. Frontiers in Bioengineering and Biotechnology, 2015, 3, 167.	4.1	15
88	EXIMS: an improved data analysis pipeline based on a new peak picking method for EXploring Imaging Mass Spectrometry data. Bioinformatics, 2015, 31, 3198-3206.	4.1	31
89	Detection of QTL for metabolic and agronomic traits in wheat with adjustments for variation at genetic loci that affect plant phenology. Plant Science, 2015, 233, 143-154.	3.6	72
90	Non-protein amino acids in Australian acacia seed: Implications for food security and recommended processing methods to reduce djenkolic acid. Food Chemistry, 2015, 179, 109-115.	8.2	10

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91	The international Metabolomics Society in 2015: the path forward to success. Metabolomics, 2015, 11, 1-2.	3.0	7
92	A tandem liquid chromatography–mass spectrometry (LC–MS) method for profiling small molecules in complex samples. Metabolomics, 2015, 11, 1552-1562.	3.0	12
93	Quantitative profiling of polar primary metabolites of two chickpea cultivars with contrasting responses to salinity. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2015, 1000, 1-13.	2.3	96
94	Metabolic profiling of a transgenic Caenorhabditis elegans Alzheimer model. Metabolomics, 2015, 11, 477-486.	3.0	33
95	Metabolomics Society's International Affiliations. Metabolomics, 2015, 11, 501-502.	3.0	0
96	The use of metabolomics in the study of metals in biological systems. Metallomics, 2015, 7, 29-38.	2.4	25
97	Flicker Light-Induced Retinal Vasodilation Is Unaffected by Inhibition of Epoxyeicosatrienoic Acids and Prostaglandins in Humans. Investigative Ophthalmology and Visual Science, 2014, 55, 7007-7013.	3.3	8
98	Proposed quantitative and alphanumeric metabolite identification metrics. Metabolomics, 2014, 10, 1047-1049.	3.0	91
99	The International Metabolomics Society forms affiliations with regional metabolomics initiatives: a reflection of 2013 and looking forward to 2014. Metabolomics, 2014, 10, 3-4.	3.0	0
100	Hyperaccumulation of zinc by Noccaea caerulescens results in a cascade of stress responses and changes in the elemental profile. Metallomics, 2014, 6, 1671-1682.	2.4	30
101	Metabolomics continues to flourish: highlights from the 2014 Metabolomics Society Conference. Metabolomics, 2014, 10, 772-774.	3.0	1
102	Metabolite profiling of wheat (Triticum aestivum L.) phloem exudate. Plant Methods, 2014, 10, 27.	4.3	31
103	The election process for the Board of Directors of the Metabolomics Society: call for nomination of new board directors. Metabolomics, 2014, 10, 349-349.	3.0	0
104	Metabolomic study reveals a selective accumulation of l-arginine in the d-ornithine treated tobacco cell suspension culture. Process Biochemistry, 2014, 49, 140-147.	3.7	12
105	Metabolomics of capsicum ripening reveals modification of the ethylene related-pathway and carbon metabolism. Postharvest Biology and Technology, 2014, 89, 19-31.	6.0	40
106	Unsupervised learning for exploring MALDI imaging mass spectrometry & amp; $\pm x2018$; omics & amp; $\pm x2019$; data., 2014,,.		8
107	LC-MS Profiling to Link Metabolic and Phenotypic Diversity in Plant Mapping Populations. Methods in Molecular Biology, 2014, 1198, 29-41.	0.9	9
108	Applications of metabolomics in the study of pathogenic microorganisms and their effects on human health, 2014, , 124-140.		1

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109	The response of the maize nitrate transport system to nitrogen demand and supply across the lifecycle. New Phytologist, 2013, 198, 82-94.	7.3	108
110	Rice suspension cultured cells are evaluated as a model system to study salt responsive networks in plants using a combined proteomic and metabolomic profiling approach. Proteomics, 2013, 13, 2046-2062.	2.2	55
111	Exploratory analysis of high-throughput metabolomic data. Metabolomics, 2013, 9, 1311-1320.	3.0	11
112	The election process for the Board of Directors of the Metabolomics Society. Metabolomics, 2013, 9, 753-754.	3.0	0
113	Genetic variation in the root growth response of barley genotypes to salinity stress. Functional Plant Biology, 2013, 40, 516.	2.1	53
114	Metabolomics Society Board Election 2013: introduction of new board members. Metabolomics, 2013, 9, 1132-1133.	3.0	0
115	Mechanisms associated with <scp>Fe</scp> â€deficiency tolerance and signaling in shoots of <i>Pisum sativum</i> . Physiologia Plantarum, 2013, 147, 381-395.	5.2	53
116	A SIEVE-RAFT HYPOTHESIS FOR THE REGULATION OF ENDOTHELIAL FENESTRATIONS. Computational and Structural Biotechnology Journal, 2013, 8, e201308003.	4.1	21
117	Insights into Lipidomic Perturbations in Zebrafish Tissues upon Exposure to Microcystin-LR and Microcystin-RR. Environmental Science & Environmental S	10.0	29
118	Whole-Genome Mapping of Agronomic and Metabolic Traits to Identify Novel Quantitative Trait Loci in Bread Wheat Grown in a Water-Limited Environment. Plant Physiology, 2013, 162, 1266-1281.	4.8	115
119	Advances in functional genomics for investigating salinity stress tolerance mechanisms in cereals. Frontiers in Plant Science, 2013, 4, 123.	3.6	62
120	Characterization of Ion Contents and Metabolic Responses to Salt Stress of Different Arabidopsis AtHKT1;1 Genotypes and Their Parental Strains. Molecular Plant, 2013, 6, 350-368.	8.3	61
121	Plant Tissue Extraction for Metabolomics. Methods in Molecular Biology, 2013, 1055, 21-28.	0.9	14
122	Cross-Platform Urine Metabolomics of Experimental Hyperglycemia in Type 2 Diabetes. Journal of Diabetes & Metabolism, 2013, 01, .	0.2	9
123	Drought Responses of Leaf Tissues from Wheat Cultivars of Differing Drought Tolerance at the Metabolite Level. Molecular Plant, 2012, 5, 418-429.	8.3	370
124	Elemental and metabolite profiling of nickel hyperaccumulators from New Caledonia. Phytochemistry, 2012, 81, 80-89.	2.9	38
125	Metabolomics for Salinity Research. , 2012, 913, 203-215.		4
126	PyMS: a Python toolkit for processing of gas chromatography-mass spectrometry (GC-MS) data. Application and comparative study of selected tools. BMC Bioinformatics, 2012, 13, 115.	2.6	63

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127	A Historical Overview of Natural Products in Drug Discovery. Metabolites, 2012, 2, 303-336.	2.9	1,254
128	Normalizing and Integrating Metabolomics Data. Analytical Chemistry, 2012, 84, 10768-10776.	6.5	183
129	Plant metabolomics., 2012,, 67-81.		23
130	Comprehensive Profiling and Quantitation of Amine Group Containing Metabolites. Analytical Chemistry, 2011, 83, 7523-7530.	6.5	107
131	Metabolomics and the move towards biology. Metabolomics, 2011, 7, 454-456.	3.0	4
132	Facile synthesis, stabilization, and anti-bacterial performance of discrete Ag nanoparticles using Medicago sativa seed exudates. Journal of Colloid and Interface Science, 2011, 353, 433-444.	9.4	251
133	Metabolomics – The Combination of Analytical Biochemistry, Biology, and Informatics. , 2011, , 447-459.		18
134	Characterisation of HvALMT1 function in transgenic barley plants. Functional Plant Biology, 2011, 38, 163.	2.1	35
135	Proteomic and Metabolic Profiling of Rice Suspension Culture Cells as a Model to Study Abscisic Acid Signaling Response Pathways in Plants. Journal of Proteome Research, 2010, 9, 6623-6634.	3.7	17
136	Shooting control by brassinosteroids: metabolomic analysis and effect of brassinazole on Malus prunifolia, the Marubakaido apple rootstock. Tree Physiology, 2009, 29, 607-620.	3.1	24
137	Profiling of polar metabolites in biological extracts using diamond hydrideâ€based aqueous normal phase chromatography. Journal of Separation Science, 2009, 32, 2273-2280.	2.5	63
138	Metabolic profiling of transgenic wheat over-expressing the high-molecular-weight Dx5 glutenin subunit. Metabolomics, 2009, 5, 239-252.	3.0	36
139	Metabolic responses to salt stress of barley (Hordeum vulgare L.) cultivars, Sahara and Clipper, which differ in salinity tolerance. Journal of Experimental Botany, 2009, 60, 4089-4103.	4.8	375
140	What is metabolomics all about?. BioTechniques, 2009, 46, 363-365.	1.8	160
141	Phylogenetic analysis and functional characterisation of strictosidine synthase-like genes in Arabidopsis thaliana. Functional Plant Biology, 2009, 36, 1098.	2.1	13
142	Metabolite Measurements., 2009,, 39-69.		23
143	Plant metabolomics reveals conserved and divergent metabolic responses to salinity. Physiologia Plantarum, 2008, 132, 209-219.	5.2	290
144	LC–MS and GC–MS metabolite profiling of nickel(II) complexes in the latex of the nickel-hyperaccumulating tree Sebertia acuminata and identification of methylated aldaric acid as a new nickel(II) ligand. Phytochemistry, 2008, 69, 240-251.	2.9	45

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145	Metabolite Profiling Reveals Distinct Changes in Carbon and Nitrogen Metabolism in Phosphate-Deficient Barley Plants (Hordeum vulgare L.). Plant and Cell Physiology, 2008, 49, 691-703.	3.1	169
146	Metabolomics: Enabling Systems-Level Phenotyping in Rice Functional Genomics. , 2007, , 91-107.		6
147	Changes in the Sugarcane Metabolome with Stem Development. Are They Related to Sucrose Accumulation?. Plant and Cell Physiology, 2007, 48, 573-584.	3.1	87
148	The importance of anatomy and physiology in plant metabolomics. Topics in Current Genetics, 2007, , 253-278.	0.7	4
149	Metabolite analysis for the comparison of irrigated and non-irrigated field grown tomato of varying genotype. Metabolomics, 2007, 3, 289-295.	3.0	72
150	The impact of constitutive heterologous expression of a moss Na+ transporter on the metabolomes of rice and barley. Metabolomics, 2007, 3, 307-317.	3.0	57
151	Minimum reporting standards for plant biology context information in metabolomic studies. Metabolomics, 2007, 3, 195-201.	3.0	116
152	ncovering the Plant Metabolome: Current and Future Challenges. , 2007, , 71-85.		3
153	Comprehensive metabolic profiling and phenotyping of interspecific introgression lines for tomato improvement. Nature Biotechnology, 2006, 24, 447-454.	17.5	707
154	Transcriptional and metabolic profiles of stress-induced, embryogenic tobacco microspores. Plant Molecular Biology, 2006, 63, 137-149.	3.9	31
155	An Investigation of Boron Toxicity in Barley Using Metabolomics. Plant Physiology, 2006, 142, 1087-1101.	4.8	174
156	Pyruvate Decarboxylase Provides Growing Pollen Tubes with a Competitive Advantage in Petunia. Plant Cell, 2005, 17, 2355-2368.	6.6	82
157	GC–MS libraries for the rapid identification of metabolites in complex biological samples. FEBS Letters, 2005, 579, 1332-1337.	2.8	596
158	Kinetics of labelling of organic and amino acids in potato tubers by gas chromatography-mass spectrometry following incubation in 13C labelled isotopes. Plant Journal, 2004, 39, 668-679.	5.7	118
159	A proposed framework for the description of plant metabolomics experiments and their results. Nature Biotechnology, 2004, 22, 1601-1606.	17.5	283
160	Potential of metabolomics as a functional genomics tool. Trends in Plant Science, 2004, 9, 418-425.	8.8	685
161	Overexpression of the sucrose transporter SoSUT1 in potato results in alterations in leaf carbon partitioning and in tuber metabolism but has little impact on tuber morphology. Planta, 2003, 217, 158-167.	3.2	101
162	Parallel analysis of transcript and metabolic profiles: a new approach in systems biology. EMBO Reports, 2003, 4, 989-993.	4.5	308

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163	The Sucrose Transporter StSUT1 Localizes to Sieve Elements in Potato Tuber Phloem and Influences Tuber Physiology and Development,. Plant Physiology, 2003, 131, 102-113.	4.8	134
164	Expression of a Bacterial Xylose Isomerase in Potato Tubers Results in an Altered Hexose Composition and a Consequent Induction of Metabolism. Plant and Cell Physiology, 2003, 44, 1359-1367.	3.1	18
165	Metabolic Profiling of Transgenic Tomato Plants Overexpressing Hexokinase Reveals That the Influence of Hexose Phosphorylation Diminishes during Fruit Development. Plant Physiology, 2003, 133, 84-99.	4.8	331
166	Enzymes of Glycolysis Are Functionally Associated with the Mitochondrion in Arabidopsis Cells. Plant Cell, 2003, 15, 2140-2151.	6.6	345
167	De Novo Amino Acid Biosynthesis in Potato Tubers Is Regulated by Sucrose Levels. Plant Physiology, 2003, 133, 683-692.	4.8	71
168	Metabolic profiling and biochemical phenotyping of plant systems. Plant Cell Reports, 2002, 21, 189-196.	5.6	66
169	Antisense repression of cytosolic phosphoglucomutase in potato (Solanum tuberosum) results in severe growth retardation, reduction in tuber number and altered carbon metabolism. Planta, 2002, 214, 510-520.	3.2	76
170	Increases of 3-phosphoglyceric acid in potato plants through antisense reduction of cytoplasmic phosphoglycerate mutase impairs photosynthesis and growth, but does not increase starch contents. Plant, Cell and Environment, 2002, 25, 1133-1143.	5.7	24
171	High-Resolution Metabolic Phenotyping of Genetically and Environmentally Diverse Potato Tuber Systems. Identification of Phenocopies. Plant Physiology, 2001, 127, 749-764.	4.8	24
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