Ute Roessner

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.

191 papers	12,469 citations	52 h-index	109 g-index
213 ext. papers	14,559 ext. citations	6.6 avg, IF	6.29 L-index

#	Paper	IF	Citations
191	Root Growth and Architecture of Wheat and Brachypodium Vary in Response to Algal Fertilizer in Soil and Solution. *Agronomy*, **2022**, 12, 285	3.6	0
190	Functional Traits 2.0: The power of the metabolome for ecology. *Journal of Ecology*, **2022**, 110, 4-20	6	5
189	Low doses of the organic insecticide spinosad trigger lysosomal defects, elevated ROS, lipid dysregulation, and neurodegeneration in flies.. *ELife*, **2022**, 11,	8.9	4
188	Metabolomics as an emerging tool to study plant-microbe interactions.. *Emerging Topics in Life Sciences*, **2022**,	3.5	3
187	Germline mutations in mitochondrial complex I reveal genetic and targetable vulnerability in IDH1-mutant acute myeloid leukaemia.. *Nature Communications*, **2022**, 13, 2614	17.4	0
186	The Effect of Cold Stress on the Root-Specific Lipidome of Two Wheat Varieties with Contrasting Cold Tolerance. *Plants*, **2022**, 11, 1364	4.5	0
185	The metabolic significance of symbiont community composition in the coral-algal symbiosis **2022**, 211-229		
184	Exploring the coral bleaching tipping point with 13C metabolomics **2022**, 199-209		
183	The state of the art in plant lipidomics. *Molecular Omics*, **2021**, 17, 894-910	4.4	3
182	Modulators or facilitators? Roles of lipids in plant root-microbe interactions. *Trends in Plant Science*, **2021**,	13.1	1
181	Reproductive Stage Drought Tolerance in Wheat: Importance of Stomatal Conductance and Plant Growth Regulators. *Genes*, **2021**, 12,	4.2	2
180	Membrane-Enriched Proteomics Link Ribosome Accumulation and Proteome Reprogramming With Cold Acclimation in Barley Root Meristems. *Frontiers in Plant Science*, **2021**, 12, 656683	6.2	4
179	An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. *Plant Journal*, **2021**, 107, 287-302	6.9	9
178	Evaluation of physiological and biochemical responses of pistachio plants (Pistacia vera L.) exposed to pesticides. *Ecotoxicology*, **2021**, 30, 1084-1097	2.9	2
177	The Metabolic Response of Brachypodium Roots to the Interaction with Beneficial Bacteria Is Affected by the Plant Nutritional Status. *Metabolites*, **2021**, 11,	5.6	5
176	Spatially Enriched Paralog Rearrangements Argue Functionally Diverse Ribosomes Arise during Cold Acclimation in Arabidopsis. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	1
175	Alleviation of salinity stress in plants by endophytic plant-fungal symbiosis: Current knowledge, perspectives and future directions. *Plant and Soil*, **2021**, 461, 219-244	4.2	40

174	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	3.2	4
173	Wheat Can Access Phosphorus From Algal Biomass as Quickly and Continuously as From Mineral Fertilizer. *Frontiers in Plant Science*, **2021**, 12, 631314	6.2	4
172	Arabidopsis REI-LIKE proteins activate ribosome biogenesis during cold acclimation. *Scientific Reports*, **2021**, 11, 2410	4.9	9
171	Inoculation of barley with Trichoderma harzianum T-22 modifies lipids and metabolites to improve salt tolerance. *Journal of Experimental Botany*, **2021**, 72, 7229-7246	7	1
170	Characterization of epidermal bladder cells in Chenopodium quinoa. *Plant, Cell and Environment*, **2021**, 44, 3606-3622	8.4	1
169	The metabolic environment of the developing embryo: A multidisciplinary approach on oilseed rapeseed. *Journal of Plant Physiology*, **2021**, 265, 153505	3.6	1
168	A comprehensive comparison of four methods for extracting lipids from Arabidopsis tissues. *Plant Methods*, **2020**, 16, 155	5.8	5
167	Phenotyping the Chilling and Freezing Responses of Young Microspore Stage Wheat Spikes Using Targeted Metabolome and Lipidome Profiling. *Cells*, **2020**, 9,	7.9	6
166	Integrative Multi-omics Analyses of Barley Rootzones under Salinity Stress Reveal Two Distinctive Salt Tolerance Mechanisms. *Plant Communications*, **2020**, 1, 100031	9	13
165	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	8.4	10
164	Insights Into Oxidized Lipid Modification in Barley Roots as an Adaptation Mechanism to Salinity Stress. *Frontiers in Plant Science*, **2020**, 11, 1	6.2	153
163	Comparative metabolomics implicates threitol as a fungal signal supporting colonization of Armillaria luteobubalina on eucalypt roots. *Plant, Cell and Environment*, **2020**, 43, 374-386	8.4	7
162	Antioxidant system status of cucumber plants under pesticides treatment. *Acta Physiologiae Plantarum*, **2020**, 42, 1	2.6	9
161	Low doses of the neonicotinoid insecticide imidacloprid induce ROS triggering neurological and metabolic impairments in. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 25840-25850	11.5	30
160	Edaphic niche characterization of four Proteaceae reveals unique calcicole physiology linked to hyper-endemism of Grevillea thelemanniana. *New Phytologist*, **2020**, 228, 869-883	9.8	5
159	Metabolite pools of the reef building coral Montipora capitata are unaffected by Symbiodiniaceae community composition. *Coral Reefs*, **2020**, 39, 1727-1737	4.2	6
158	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	3.7	2
157	Phenotyping reproductive stage chilling and frost tolerance in wheat using targeted metabolome and lipidome profiling. *Metabolomics*, **2019**, 15, 144	4.7	17

156	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	6.2	15
155	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	4.7	3
154	The changes in the release level of polyunsaturated fatty acids (ω3 and ω6) and lipids in the untreated and water-soaked chia seed. *Food Research International*, **2019**, 126, 108665	7	4
153	The Influence of Contrasting Microbial Lifestyles on the Pre-symbiotic Metabolite Responses of Eucalyptus grandis Roots. *Frontiers in Ecology and Evolution*, **2019**, 7,	3.7	7
152	Opposite fates of the purine metabolite allantoin under water and nitrogen limitations in bread wheat. *Plant Molecular Biology*, **2019**, 99, 477-497	4.6	22
151	Metabolome Analysis **2019**, 396-409		0
150	Genotypic Variation in the Root and Shoot Metabolite Profiles of Wheat (L.) Indicate Sustained, Preferential Carbon Allocation as a Potential Mechanism in Phosphorus Efficiency. *Frontiers in Plant Science*, **2019**, 10, 995	6.2	17
149	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	5.4	26
148	Phenotypic and metabolic plasticity shapes life-history strategies under combinations of abiotic stresses. *Plant Direct*, **2019**, 3, e00113	3.3	17
147	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	4.7	36
146	Dietary intervention rescues myopathy associated with neurofibromatosis type 1. *Human Molecular Genetics*, **2018**, 27, 577-588	5.6	11
145	Structural and functional measures of marine microbial communities: An experiment to assess implications for oil spill management. *Marine Pollution Bulletin*, **2018**, 131, 525-529	6.7	7
144	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	6.6	27
143	Abiotic Stress and Metabolomics **2018**, 61-85		12
142	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	5.4	19
141	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	9.7	13
140	Water availability moderates N fixation benefit from elevated [CO]: A 2-year free-air CO enrichment study on lentil (Lens culinaris MEDIK.) in a water limited agroecosystem. *Plant, Cell and Environment*, **2018**, 41, 2418-2434	8.4	17
139	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	6.2	15

138	Advances of Metabolite Profiling of Plants in Challenging Environments **2018**, 629-674		4
137	Partner switching and metabolic flux in a model cnidarian-dinoflagellate symbiosis. *Proceedings of the Royal Society B: Biological Sciences*, **2018**, 285,	4.4	43
136	RNA Catabolites Contribute to the Nitrogen Pool and Support Growth Recovery of Wheat. *Frontiers in Plant Science*, **2018**, 9, 1539	6.2	14
135	A Golgi UDP-GlcNAc transporter delivers substrates for N-linked glycans and sphingolipids. *Nature Plants*, **2018**, 4, 792-801	11.5	14
134	Feeding the Walls: How Does Nutrient Availability Regulate Cell Wall Composition?. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	26
133	Extraction of Plant Lipids for LC-MS-Based Untargeted Plant Lipidomics. *Methods in Molecular Biology*, **2018**, 1778, 125-135	1.4	7
132	Single cell-type analysis of cellular lipid remodelling in response to salinity in the epidermal bladder cells of the model halophyte Mesembryanthemum crystallinum. *Plant, Cell and Environment*, **2018**, 41, 2390-2403	8.4	11
131	Quantification of Sugars and Organic Acids in Biological Matrices Using GC-QqQ-MS. *Methods in Molecular Biology*, **2018**, 1778, 207-223	1.4	4
130	Determination of amino acids in urine of patients with prostate cancer and benign prostate growth. *European Journal of Cancer Prevention*, **2017**, 26, 131-134	2	12
129	Mapping carbon fate during bleaching in a model cnidarian symbiosis: the application of C metabolomics. *New Phytologist*, **2017**, 214, 1551-1562	9.8	37
128	MASTR-MS: a web-based collaborative laboratory information management system (LIMS) for metabolomics. *Metabolomics*, **2017**, 13, 14	4.7	12
127	The genome of Chenopodium quinoa. *Nature*, **2017**, 542, 307-312	50.4	345
126	Transition from a maternal to external nitrogen source in maize seedlings. *Journal of Integrative Plant Biology*, **2017**, 59, 261-274	8.3	6
125	Diurnal Changes in Transcript and Metabolite Levels during the Iron Deficiency Response of Rice. *Rice*, **2017**, 10, 14	5.8	11
124	From common to rare Zingiberaceae plants - A metabolomics study using GC-MS. *Phytochemistry*, **2017**, 140, 141-150	4	14
123	Epidermal bladder cells confer salinity stress tolerance in the halophyte quinoa and Atriplex species. *Plant, Cell and Environment*, **2017**, 40, 1900-1915	8.4	61
122	C metabolomics reveals widespread change in carbon fate during coral bleaching. *Metabolomics*, **2017**, 14, 12	4.7	26
121	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	11.5	103

120	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	10.1	9
119	Metabolite profiling of symbiont and host during thermal stress and bleaching in the coral Acropora aspera. *Coral Reefs*, **2017**, 36, 105-118	4.2	48
118	Mass spectrometry imaging for plant biology: a review. *Phytochemistry Reviews*, **2016**, 15, 445-488	7.7	149
117	Cell-Type-Specific H+-ATPase Activity in Root Tissues Enables K+ Retention and Mediates Acclimation of Barley (Hordeum vulgare) to Salinity Stress. *Plant Physiology*, **2016**, 172, 2445-2458	6.6	99
116	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	3.7	36
115	Beta-glucan-depleted, glycopeptide-rich extracts from Brewer's and Baker's yeast (Saccharomyces cerevisiae) lower interferon-gamma production by stimulated human blood cells in vitro. *Food Chemistry*, **2016**, 197, 761-8	8.5	10
114	Root spatial metabolite profiling of two genotypes of barley (Hordeum vulgare L.) reveals differences in response to short-term salt stress. *Journal of Experimental Botany*, **2016**, 67, 3731-45	7	74
113	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	14.4	21
112	Salt-stress induced alterations in the root lipidome of two barley genotypes with contrasting responses to salinity. *Functional Plant Biology*, **2016**, 43, 207-219	2.7	29
111	A Quantitative Profiling Method of Phytohormones and Other Metabolites Applied to Barley Roots Subjected to Salinity Stress. *Frontiers in Plant Science*, **2016**, 7, 2070	6.2	34
110	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	4.9	27
109	Nitrogen assimilation system in maize is regulated by developmental and tissue-specific mechanisms. *Plant Molecular Biology*, **2016**, 92, 293-312	4.6	11
108	A tandem liquid chromatography–mass spectrometry (LC–MS) method for profiling small molecules in complex samples. *Metabolomics*, **2015**, 11, 1552-1562	4.7	11
107	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	3.2	71
106	Metabolic profiling of a transgenic Alzheimer model. *Metabolomics*, **2015**, 11, 477-486	4.7	27
105	Advances in high-throughput untargeted LC–MS analysis for plant metabolomics **2015**, 58-71		8
104	The use of metabolomics in the study of metals in biological systems. *Metallomics*, **2015**, 7, 29-38	4.5	22
103	2015: an eventful year for the Metabolomics Society. *Metabolomics*, **2015**, 11, 1475-1477	4.7	

102	A new peak detection algorithm for MALDI mass spectrometry data based on a modified Asymmetric Pseudo-Voigt model. *BMC Genomics*, **2015**, 16 Suppl 12, S12	4.5	3
101	Metabolomics, Standards, and Metabolic Modeling for Synthetic Biology in Plants. *Frontiers in Bioengineering and Biotechnology*, **2015**, 3, 167	5.8	13
100	EXIMS: an improved data analysis pipeline based on a new peak picking method for EXploring Imaging Mass Spectrometry data. *Bioinformatics*, **2015**, 31, 3198-206	7.2	22
99	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	5.3	60
98	Non-protein amino acids in Australian acacia seed: implications for food security and recommended processing methods to reduce djenkolic acid. *Food Chemistry*, **2015**, 179, 109-15	8.5	4
97	Hyperaccumulation of zinc by Noccaea caerulescens results in a cascade of stress responses and changes in the elemental profile. *Metallomics*, **2014**, 6, 1671-82	4.5	15
96	Metabolite profiling of wheat (Triticum aestivum L.) phloem exudate. *Plant Methods*, **2014**, 10, 27	5.8	24
95	Metabolomic study reveals a selective accumulation of l-arginine in the d-ornithine treated tobacco cell suspension culture. *Process Biochemistry*, **2014**, 49, 140-147	4.8	6
94	Metabolomics of capsicum ripening reveals modification of the ethylene related-pathway and carbon metabolism. *Postharvest Biology and Technology*, **2014**, 89, 19-31	6.2	30
93	Unsupervised learning for exploring MALDI imaging mass spectrometry □mics□data **2014**,		7
92	Flicker light-induced retinal vasodilation is unaffected by inhibition of epoxyeicosatrienoic acids and prostaglandins in humans. *Investigative Ophthalmology and Visual Science*, **2014**, 55, 7007-13		8
91	Proposed quantitative and alphanumeric metabolite identification metrics. *Metabolomics*, **2014**, 10, 1047-1049	4.7	70
90	LC-MS profiling to link metabolic and phenotypic diversity in plant mapping populations. *Methods in Molecular Biology*, **2014**, 1198, 29-41	1.4	6
89	Applications of metabolomics in the study of pathogenic microorganisms and their effects on human health. **2014**, 124-140		1
88	The response of the maize nitrate transport system to nitrogen demand and supply across the lifecycle. *New Phytologist*, **2013**, 198, 82-94	9.8	85
87	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, 2046-62	4.8	46
86	Metabolomics Tools for Natural Product Discovery. *Methods in Molecular Biology*, **2013**,	1.4	12
85	Exploratory analysis of high-throughput metabolomic data. *Metabolomics*, **2013**, 9, 1311-1320	4.7	9

84	Genetic variation in the root growth response of barley genotypes to salinity stress. *Functional Plant Biology*, **2013**, 40, 516-530	2.7	30
83	Mechanisms associated with Fe-deficiency tolerance and signaling in shoots of Pisum sativum. *Physiologia Plantarum*, **2013**, 147, 381-95	4.6	41
82	Metabolic Profiling of Plants by GC-MS **2013**, 1-23		11
81	A Sieve-Raft Hypothesis for the regulation of endothelial fenestrations. *Computational and Structural Biotechnology Journal*, **2013**, 8, e201308003	6.8	15
80	Insights into lipidomic perturbations in zebrafish tissues upon exposure to microcystin-LR and microcystin-RR. *Environmental Science & Technology*, **2013**, 47, 14376-84	10.3	22
79	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, 1266-81	6.6	86
78	Advances in functional genomics for investigating salinity stress tolerance mechanisms in cereals. *Frontiers in Plant Science*, **2013**, 4, 123	6.2	52
77	Characterization of ion contents and metabolic responses to salt stress of different Arabidopsis AtHKT1;1 genotypes and their parental strains. *Molecular Plant*, **2013**, 6, 350-68	14.4	45
76	Cross-Platform Urine Metabolomics of Experimental Hyperglycemia in Type 2 Diabetes. *Journal of Diabetes & Metabolism*, **2013**, 01,	0	7
75	Plant tissue extraction for metabolomics. *Methods in Molecular Biology*, **2013**, 1055, 21-8	1.4	12
74	Drought responses of leaf tissues from wheat cultivars of differing drought tolerance at the metabolite level. *Molecular Plant*, **2012**, 5, 418-29	14.4	282
73	Elemental and metabolite profiling of nickel hyperaccumulators from New Caledonia. *Phytochemistry*, **2012**, 81, 80-9	4	37
72	Metabolomics for salinity research. *Methods in Molecular Biology*, **2012**, 913, 203-15	1.4	3
71	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	3.6	48
70	A historical overview of natural products in drug discovery. *Metabolites*, **2012**, 2, 303-36	5.6	887
69	Normalizing and integrating metabolomics data. *Analytical Chemistry*, **2012**, 84, 10768-76	7.8	148
68	Plant metabolomics: Applications and opportunities for agricultural biotechnology **2012**, 67-81		17
67	Abiotic Stress and Metabolomics **2011**, 61-85		9

66	Comprehensive profiling and quantitation of amine group containing metabolites. *Analytical Chemistry*, **2011**, 83, 7523-30	7.8	92
65	Facile synthesis, stabilization, and anti-bacterial performance of discrete Ag nanoparticles using Medicago sativa seed exudates. *Journal of Colloid and Interface Science*, **2011**, 353, 433-44	9.3	213
64	Metabolomics The Combination of Analytical Biochemistry, Biology, and Informatics **2011**, 447-459		13
63	Characterisation of HvALMT1 function in transgenic barley plants. *Functional Plant Biology*, **2011**, 38, 163-175	2.7	33
62	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, 6623-34	5.6	16
61	Phylogenetic analysis and functional characterisation of strictosidine synthase-like genes in Arabidopsis thaliana. *Functional Plant Biology*, **2010**, 36, 1098-1109	2.7	7
60	Shooting control by brassinosteroids: metabolomic analysis and effect of brassinazole on Malus prunifolia, the Marubakaido apple rootstock. *Tree Physiology*, **2009**, 29, 607-20	4.2	24
59	Profiling of polar metabolites in biological extracts using diamond hydride-based aqueous normal phase chromatography. *Journal of Separation Science*, **2009**, 32, 2273-80	3.4	60
58	Metabolic profiling of transgenic wheat over-expressing the high-molecular-weight Dx5 glutenin subunit. *Metabolomics*, **2009**, 5, 239-252	4.7	32
57	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, 4089-103	7	318
56	What is metabolomics all about?. *BioTechniques*, **2009**, 46, 363-5	2.5	120
55	Metabolite Measurements **2009**, 39-69		21
54	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	4.9	130
53	Plant metabolomics reveals conserved and divergent metabolic responses to salinity. *Physiologia Plantarum*, **2008**, 132, 209-19	4.6	201
52	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, 240-51	4	41
51	The importance of anatomy and physiology in plant metabolomics. *Topics in Current Genetics*, **2007**, 253-278		3
50	**2007**,		85
49	Metabolite analysis for the comparison of irrigated and non-irrigated field grown tomato of varying genotype. *Metabolomics*, **2007**, 3, 289-295	4.7	66

48	The impact of constitutive heterologous expression of a moss Na+ transporter on the metabolomes of rice and barley. *Metabolomics*, **2007**, 3, 307-317	4.7	53
47	Minimum reporting standards for plant biology context information in metabolomic studies. *Metabolomics*, **2007**, 3, 195-201	4.7	96
46	Metabolomics: Enabling Systems-Level Phenotyping in Rice Functional Genomics **2007**, 91-107		6
45	Changes in the sugarcane metabolome with stem development. Are they related to sucrose accumulation?. *Plant and Cell Physiology*, **2007**, 48, 573-84	4.9	68
44	Transcriptional and metabolic profiles of stress-induced, embryogenic tobacco microspores. *Plant Molecular Biology*, **2007**, 63, 137-49	4.6	27
43	ncovering the Plant Metabolome: Current and Future Challenges **2007**, 71-85		3
42	An investigation of boron toxicity in barley using metabolomics. *Plant Physiology*, **2006**, 142, 1087-101	6.6	158
41	Comprehensive metabolic profiling and phenotyping of interspecific introgression lines for tomato improvement. *Nature Biotechnology*, **2006**, 24, 447-54	44.5	619
40	GC-MS libraries for the rapid identification of metabolites in complex biological samples. *FEBS Letters*, **2005**, 579, 1332-7	3.8	504
39	Pyruvate decarboxylase provides growing pollen tubes with a competitive advantage in petunia. *Plant Cell*, **2005**, 17, 2355-68	11.6	70
38	Kinetics of labelling of organic and amino acids in potato tubers by gas chromatography-mass spectrometry following incubation in (13)C labelled isotopes. *Plant Journal*, **2004**, 39, 668-79	6.9	113
37	A proposed framework for the description of plant metabolomics experiments and their results. *Nature Biotechnology*, **2004**, 22, 1601-6	44.5	260
36	Potential of metabolomics as a functional genomics tool. *Trends in Plant Science*, **2004**, 9, 418-25	13.1	627
35	Enzymes of glycolysis are functionally associated with the mitochondrion in Arabidopsis cells. *Plant Cell*, **2003**, 15, 2140-51	11.6	305
34	De novo amino acid biosynthesis in potato tubers is regulated by sucrose levels. *Plant Physiology*, **2003**, 133, 683-92	6.6	64
33	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, 158-67	4.7	87
32	Parallel analysis of transcript and metabolic profiles: a new approach in systems biology. *EMBO Reports*, **2003**, 4, 989-93	6.5	267
31	The sucrose transporter StSUT1 localizes to sieve elements in potato tuber phloem and influences tuber physiology and development. *Plant Physiology*, **2003**, 131, 102-13	6.6	109

30	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, 1359-67	4.9	16
29	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	6.6	298
28	Metabolic profiling and biochemical phenotyping of plant systems. *Plant Cell Reports*, **2002**, 21, 189-196	5.1	59
27	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, 510-20	4.7	67
26	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	8.4	22
25	Analysis of the Compartmentation of Glycolytic Intermediates, Nucleotides, Sugars, Organic Acids, Amino Acids, and Sugar Alcohols in Potato Tubers Using a Nonaqueous Fractionation Method. *Plant Physiology*, **2001**, 127, 685-700	6.6	
24	The contribution of plastidial phosphoglucomutase to the control of starch synthesis within the potato tuber. *Planta*, **2001**, 213, 418-26	4.7	72
23	Simultaneous antagonistic modulation of enzyme activities in transgenic plants through the expression of a chimeric transcript. *Plant Physiology and Biochemistry*, **2001**, 39, 825-830	5.4	4
22	Metabolic Profiling Allows Comprehensive Phenotyping of Genetically or Environmentally Modified Plant Systems. *Plant Cell*, **2001**, 13, 11	11.6	15
21	Analysis of the compartmentation of glycolytic intermediates, nucleotides, sugars, organic acids, amino acids, and sugar alcohols in potato tubers using a nonaqueous fractionation method. *Plant Physiology*, **2001**, 127, 685-700	6.6	233
20	Antisense Inhibition of Threonine Synthase Leads to High Methionine Content in Transgenic Potato Plants. *Plant Physiology*, **2001**, 127, 792-802	6.6	106
19	The sucrose analog palatinose leads to a stimulation of sucrose degradation and starch synthesis when supplied to discs of growing potato tubers. *Plant Physiology*, **2001**, 125, 1967-77	6.6	75
18	High-Resolution Metabolic Phenotyping of Genetically and Environmentally Diverse Potato Tuber Systems. Identification of Phenocopies. *Plant Physiology*, **2001**, 127, 749-764	6.6	157
17	Metabolic profiling allows comprehensive phenotyping of genetically or environmentally modified plant systems. *Plant Cell*, **2001**, 13, 11-29	11.6	877
16	High-Resolution Metabolic Phenotyping of Genetically and Environmentally Diverse Potato Tuber Systems. Identification of Phenocopies. *Plant Physiology*, **2001**, 127, 749-764	6.6	23
15	Technical advance: simultaneous analysis of metabolites in potato tuber by gas chromatography-mass spectrometry. *Plant Journal*, **2000**, 23, 131-42	6.9	959
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