

Ute Roessner

List of Publications by Year in descending order

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195
papers

16,370
citations

25034

57
h-index

17592

121
g-index

214
all docs

214
docs citations

214
times ranked

18459
citing authors

#	ARTICLE	IF	CITATIONS
1	A Historical Overview of Natural Products in Drug Discovery. <i>Metabolites</i> , 2012, 2, 303-336.	2.9	1,254
2	Simultaneous analysis of metabolites in potato tuber by gas chromatography-mass spectrometry. <i>Plant Journal</i> , 2000, 23, 131-142.	5.7	1,058
3	Metabolic Profiling Allows Comprehensive Phenotyping of Genetically or Environmentally Modified Plant Systems. <i>Plant Cell</i> , 2001, 13, 11-29.	6.6	984
4	Comprehensive metabolic profiling and phenotyping of interspecific introgression lines for tomato improvement. <i>Nature Biotechnology</i> , 2006, 24, 447-454.	17.5	707
5	Potential of metabolomics as a functional genomics tool. <i>Trends in Plant Science</i> , 2004, 9, 418-425.	8.8	685
6	GC-MS libraries for the rapid identification of metabolites in complex biological samples. <i>FEBS Letters</i> , 2005, 579, 1332-1337.	2.8	596
7	The genome of <i>Chenopodium quinoa</i> . <i>Nature</i> , 2017, 542, 307-312.	27.8	569
8	Insights Into Oxidized Lipid Modification in Barley Roots as an Adaptation Mechanism to Salinity Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 1.	3.6	477
9	Metabolic responses to salt stress of barley (<i>Hordeum vulgare</i> L.) cultivars, Sahara and Clipper, which differ in salinity tolerance. <i>Journal of Experimental Botany</i> , 2009, 60, 4089-4103.	4.8	375
10	Drought Responses of Leaf Tissues from Wheat Cultivars of Differing Drought Tolerance at the Metabolite Level. <i>Molecular Plant</i> , 2012, 5, 418-429.	8.3	370
11	Enzymes of Glycolysis Are Functionally Associated with the Mitochondrion in <i>Arabidopsis</i> Cells. <i>Plant Cell</i> , 2003, 15, 2140-2151.	6.6	345
12	Metabolic Profiling of Transgenic Tomato Plants Overexpressing Hexokinase Reveals That the Influence of Hexose Phosphorylation Diminishes during Fruit Development. <i>Plant Physiology</i> , 2003, 133, 84-99.	4.8	331
13	Parallel analysis of transcript and metabolic profiles: a new approach in systems biology. <i>EMBO Reports</i> , 2003, 4, 989-993.	4.5	308
14	Plant metabolomics reveals conserved and divergent metabolic responses to salinity. <i>Physiologia Plantarum</i> , 2008, 132, 209-219.	5.2	290
15	A proposed framework for the description of plant metabolomics experiments and their results. <i>Nature Biotechnology</i> , 2004, 22, 1601-1606.	17.5	283
16	Facile synthesis, stabilization, and anti-bacterial performance of discrete Ag nanoparticles using <i>Medicago sativa</i> seed exudates. <i>Journal of Colloid and Interface Science</i> , 2011, 353, 433-444.	9.4	251
17	Analysis of the Compartmentation of Glycolytic Intermediates, Nucleotides, Sugars, Organic Acids, Amino Acids, and Sugar Alcohols in Potato Tubers Using a Nonaqueous Fractionation Method. <i>Plant Physiology</i> , 2001, 127, 685-700.	4.8	247
18	A combined reduction in activity of starch synthases II and III of potato has novel effects on the starch of tubers. <i>Plant Journal</i> , 1999, 17, 251-261.	5.7	213

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19	Mass spectrometry imaging for plant biology: a review. <i>Phytochemistry Reviews</i> , 2016, 15, 445-488.	6.5	210
20	Normalizing and Integrating Metabolomics Data. <i>Analytical Chemistry</i> , 2012, 84, 10768-10776.	6.5	183
21	Optimal nutrient exchange and immune responses operate in partner specificity in the cnidarian-dinoflagellate symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13194-13199.	7.1	181
22	An Investigation of Boron Toxicity in Barley Using Metabolomics. <i>Plant Physiology</i> , 2006, 142, 1087-1101.	4.8	174
23	High-Resolution Metabolic Phenotyping of Genetically and Environmentally Diverse Potato Tuber Systems. Identification of Phenocopies. <i>Plant Physiology</i> , 2001, 127, 749-764.	4.8	173
24	Metabolite Profiling Reveals Distinct Changes in Carbon and Nitrogen Metabolism in Phosphate-Deficient Barley Plants (<i>Hordeum vulgare</i> L.). <i>Plant and Cell Physiology</i> , 2008, 49, 691-703.	3.1	169
25	What is metabolomics all about?. <i>BioTechniques</i> , 2009, 46, 363-365.	1.8	160
26	Cell-Type-Specific H ⁺ -ATPase Activity in Root Tissues Enables K ⁺ Retention and Mediates Acclimation of Barley (<i>Hordeum vulgare</i> L.) to Salinity Stress. <i>Plant Physiology</i> , 2016, 172, 2445-2458.	4.8	158
27	Root spatial metabolite profiling of two genotypes of barley (<i>Hordeum vulgare</i> L.) reveals differences in response to short-term salt stress. <i>Journal of Experimental Botany</i> , 2016, 67, 3731-3745.	4.8	137
28	The Sucrose Transporter StSUT1 Localizes to Sieve Elements in Potato Tuber Phloem and Influences Tuber Physiology and Development. <i>Plant Physiology</i> , 2003, 131, 102-113.	4.8	134
29	Antisense Inhibition of Threonine Synthase Leads to High Methionine Content in Transgenic Potato Plants. <i>Plant Physiology</i> , 2001, 127, 792-802.	4.8	122
30	Kinetics of labelling of organic and amino acids in potato tubers by gas chromatography-mass spectrometry following incubation in ¹³ C labelled isotopes. <i>Plant Journal</i> , 2004, 39, 668-679.	5.7	118
31	Minimum reporting standards for plant biology context information in metabolomic studies. <i>Metabolomics</i> , 2007, 3, 195-201.	3.0	116
32	Whole-Genome Mapping of Agronomic and Metabolic Traits to Identify Novel Quantitative Trait Loci in Bread Wheat Grown in a Water-Limited Environment. <i>Plant Physiology</i> , 2013, 162, 1266-1281.	4.8	115
33	Alleviation of salinity stress in plants by endophytic plant-fungal symbiosis: Current knowledge, perspectives and future directions. <i>Plant and Soil</i> , 2021, 461, 219-244.	3.7	109
34	The response of the maize nitrate transport system to nitrogen demand and supply across the lifecycle. <i>New Phytologist</i> , 2013, 198, 82-94.	7.3	108
35	Comprehensive Profiling and Quantitation of Amine Group Containing Metabolites. <i>Analytical Chemistry</i> , 2011, 83, 7523-7530.	6.5	107
36	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. <i>Planta</i> , 2003, 217, 158-167.	3.2	101

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37	Epidermal bladder cells confer salinity stress tolerance in the halophyte quinoa and <i>Atriplex</i> species. <i>Plant, Cell and Environment</i> , 2017, 40, 1900-1915.	5.7	98
38	Quantitative profiling of polar primary metabolites of two chickpea cultivars with contrasting responses to salinity. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 1000, 1-13.	2.3	96
39	The contribution of plastidial phosphoglucomutase to the control of starch synthesis within the potato tuber. <i>Planta</i> , 2001, 213, 418-426.	3.2	91
40	Proposed quantitative and alphanumeric metabolite identification metrics. <i>Metabolomics</i> , 2014, 10, 1047-1049.	3.0	91
41	Antisense Repression of Hexokinase 1 Leads to an Overaccumulation of Starch in Leaves of Transgenic Potato Plants But Not to Significant Changes in Tuber Carbohydrate Metabolism. <i>Plant Physiology</i> , 1999, 121, 123-134.	4.8	87
42	Changes in the Sugarcane Metabolome with Stem Development. Are They Related to Sucrose Accumulation?. <i>Plant and Cell Physiology</i> , 2007, 48, 573-584.	3.1	87
43	Metabolite profiling of symbiont and host during thermal stress and bleaching in the coral <i>Acropora aspera</i> . <i>Coral Reefs</i> , 2017, 36, 105-118.	2.2	87
44	Low doses of the neonicotinoid insecticide imidacloprid induce ROS triggering neurological and metabolic impairments in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25840-25850.	7.1	85
45	The Sucrose Analog Palatinose Leads to a Stimulation of Sucrose Degradation and Starch Synthesis When Supplied to Discs of Growing Potato Tubers. <i>Plant Physiology</i> , 2001, 125, 1967-1977.	4.8	82
46	Pyruvate Decarboxylase Provides Growing Pollen Tubes with a Competitive Advantage in <i>Petunia</i> . <i>Plant Cell</i> , 2005, 17, 2355-2368.	6.6	82
47	Antisense repression of cytosolic phosphoglucomutase in potato (<i>Solanum tuberosum</i>) results in severe growth retardation, reduction in tuber number and altered carbon metabolism. <i>Planta</i> , 2002, 214, 510-520.	3.2	76
48	Metabolite analysis for the comparison of irrigated and non-irrigated field grown tomato of varying genotype. <i>Metabolomics</i> , 2007, 3, 289-295.	3.0	72
49	Detection of QTL for metabolic and agronomic traits in wheat with adjustments for variation at genetic loci that affect plant phenology. <i>Plant Science</i> , 2015, 233, 143-154.	3.6	72
50	Partner switching and metabolic flux in a model cnidarian-dinoflagellate symbiosis. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, .	2.6	72
51	De Novo Amino Acid Biosynthesis in Potato Tubers Is Regulated by Sucrose Levels. <i>Plant Physiology</i> , 2003, 133, 683-692.	4.8	71
52	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. <i>Metabolomics</i> , 2018, 14, 63.	3.0	69
53	Metabolic profiling and biochemical phenotyping of plant systems. <i>Plant Cell Reports</i> , 2002, 21, 189-196.	5.6	66
54	Profiling of polar metabolites in biological extracts using diamond hydride-based aqueous normal phase chromatography. <i>Journal of Separation Science</i> , 2009, 32, 2273-2280.	2.5	63

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55	PyMS: a Python toolkit for processing of gas chromatography-mass spectrometry (GC-MS) data. Application and comparative study of selected tools. <i>BMC Bioinformatics</i> , 2012, 13, 115.	2.6	63
56	A Quantitative Profiling Method of Phytohormones and Other Metabolites Applied to Barley Roots Subjected to Salinity Stress. <i>Frontiers in Plant Science</i> , 2016, 7, 2070.	3.6	63
57	Advances in functional genomics for investigating salinity stress tolerance mechanisms in cereals. <i>Frontiers in Plant Science</i> , 2013, 4, 123.	3.6	62
58	Characterization of Ion Contents and Metabolic Responses to Salt Stress of Different Arabidopsis AtHKT1;1 Genotypes and Their Parental Strains. <i>Molecular Plant</i> , 2013, 6, 350-368.	8.3	61
59	¹³ C metabolomics reveals widespread change in carbon fate during coral bleaching. <i>Metabolomics</i> , 2018, 14, 12.	3.0	60
60	Morphological and metabolic responses to salt stress of rice (<i>Oryza sativa</i> L.) cultivars which differ in salinity tolerance. <i>Plant Physiology and Biochemistry</i> , 2019, 144, 427-435.	5.8	59
61	The impact of constitutive heterologous expression of a moss Na ⁺ transporter on the metabolomes of rice and barley. <i>Metabolomics</i> , 2007, 3, 307-317.	3.0	57
62	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. <i>Proteomics</i> , 2013, 13, 2046-2062.	2.2	55
63	Genetic variation in the root growth response of barley genotypes to salinity stress. <i>Functional Plant Biology</i> , 2013, 40, 516.	2.1	53
64	Mechanisms associated with Fe deficiency tolerance and signaling in shoots of <i>Pisum sativum</i> . <i>Physiologia Plantarum</i> , 2013, 147, 381-395.	5.2	53
65	Mapping carbon fate during bleaching in a model cnidarian symbiosis: the application of ¹³ C metabolomics. <i>New Phytologist</i> , 2017, 214, 1551-1562.	7.3	53
66	Feeding the Walls: How Does Nutrient Availability Regulate Cell Wall Composition?. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2691.	4.1	52
67	Salt-stress induced alterations in the root lipidome of two barley genotypes with contrasting responses to salinity. <i>Functional Plant Biology</i> , 2016, 43, 207.	2.1	48
68	A high-resolution HPLC-QqTOF platform using parallel reaction monitoring for in-depth lipid discovery and rapid profiling. <i>Analytica Chimica Acta</i> , 2018, 1026, 87-100.	5.4	47
69	Spatio-Temporal Metabolite and Elemental Profiling of Salt Stressed Barley Seeds During Initial Stages of Germination by MALDI-MSI and μ -XRF Spectrometry. <i>Frontiers in Plant Science</i> , 2019, 10, 1139.	3.6	46
70	LC-MS and GC-MS metabolite profiling of nickel(II) complexes in the latex of the nickel-hyperaccumulating tree <i>Sebertia acuminata</i> and identification of methylated aldaric acid as a new nickel(II) ligand. <i>Phytochemistry</i> , 2008, 69, 240-251.	2.9	45
71	Modulators or facilitators? Roles of lipids in plant root-microbe interactions. <i>Trends in Plant Science</i> , 2022, 27, 180-190.	8.8	45
72	Elemental imaging of leaves from the metal hyperaccumulating plant <i>Noccaea caerulea</i> shows different spatial distribution of Ni, Zn and Cd. <i>RSC Advances</i> , 2016, 6, 2337-2344.	3.6	42

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73	Functional Traits 2.0: The power of the metabolome for ecology. <i>Journal of Ecology</i> , 2022, 110, 4-20.	4.0	42
74	Opposite fates of the purine metabolite allantoin under water and nitrogen limitations in bread wheat. <i>Plant Molecular Biology</i> , 2019, 99, 477-497.	3.9	41
75	Metabolomics of capsicum ripening reveals modification of the ethylene related-pathway and carbon metabolism. <i>Postharvest Biology and Technology</i> , 2014, 89, 19-31.	6.0	40
76	Phenotypic and metabolic plasticity shapes life-history strategies under combinations of abiotic stresses. <i>Plant Direct</i> , 2019, 3, e00113.	1.9	39
77	Elemental and metabolite profiling of nickel hyperaccumulators from New Caledonia. <i>Phytochemistry</i> , 2012, 81, 80-89.	2.9	38
78	Metabolic profiling of transgenic wheat over-expressing the high-molecular-weight Dx5 glutenin subunit. <i>Metabolomics</i> , 2009, 5, 239-252.	3.0	36
79	Characterisation of HvALMT1 function in transgenic barley plants. <i>Functional Plant Biology</i> , 2011, 38, 163.	2.1	35
80	Metabolic profiling of a transgenic <i>Caenorhabditis elegans</i> Alzheimer model. <i>Metabolomics</i> , 2015, 11, 477-486.	3.0	33
81	De novo transcriptome assembly and analysis of differentially expressed genes of two barley genotypes reveal root-zone-specific responses to salt exposure. <i>Scientific Reports</i> , 2016, 6, 31558.	3.3	33
82	Genotypic Variation in the Root and Shoot Metabolite Profiles of Wheat (<i>Triticum aestivum</i> L.) Indicate Sustained, Preferential Carbon Allocation as a Potential Mechanism in Phosphorus Efficiency. <i>Frontiers in Plant Science</i> , 2019, 10, 995.	3.6	32
83	Characterization of Starch-Debranching Enzymes in Pea Embryos. <i>Plant Physiology</i> , 1998, 118, 581-590.	4.8	31
84	Transcriptional and metabolic profiles of stress-induced, embryogenic tobacco microspores. <i>Plant Molecular Biology</i> , 2006, 63, 137-149.	3.9	31
85	Metabolite profiling of wheat (<i>Triticum aestivum</i> L.) phloem exudate. <i>Plant Methods</i> , 2014, 10, 27.	4.3	31
86	EXIMS: an improved data analysis pipeline based on a new peak picking method for EXploring Imaging Mass Spectrometry data. <i>Bioinformatics</i> , 2015, 31, 3198-3206.	4.1	31
87	From common to rare Zingiberaceae plants - A metabolomics study using GC-MS. <i>Phytochemistry</i> , 2017, 140, 141-150.	2.9	31
88	Phenotyping reproductive stage chilling and frost tolerance in wheat using targeted metabolome and lipidome profiling. <i>Metabolomics</i> , 2019, 15, 144.	3.0	31
89	Hyperaccumulation of zinc by <i>Noccaea caerulea</i> results in a cascade of stress responses and changes in the elemental profile. <i>Metallomics</i> , 2014, 6, 1671-1682.	2.4	30
90	Insights into Lipidomic Perturbations in Zebrafish Tissues upon Exposure to Microcystin-LR and Microcystin-RR. <i>Environmental Science & Technology</i> , 2013, 47, 14376-14384.	10.0	29

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91	RNA Catabolites Contribute to the Nitrogen Pool and Support Growth Recovery of Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 1539.	3.6	29
92	Inactivation of Mitochondrial Complex I Induces the Expression of a Twin Cysteine Protein that Targets and Affects Cytosolic, Chloroplastidic and Mitochondrial Function. <i>Molecular Plant</i> , 2016, 9, 696-710.	8.3	28
93	Metabolomics as an emerging tool to study plant-microbe interactions. <i>Emerging Topics in Life Sciences</i> , 2022, 6, 175-183.	2.6	28
94	A Golgi UDP-GlcNAc transporter delivers substrates for N-linked glycans and sphingolipids. <i>Nature Plants</i> , 2018, 4, 792-801.	9.3	27
95	Comparative metabolic and ionic profiling of two cultivars of <i>Stevia rebaudiana</i> Bert. (Bertoni) grown under salinity stress. <i>Plant Physiology and Biochemistry</i> , 2018, 129, 56-70.	5.8	26
96	Integrative Multi-omics Analyses of Barley Rootzones under Salinity Stress Reveal Two Distinctive Salt Tolerance Mechanisms. <i>Plant Communications</i> , 2020, 1, 100031.	7.7	26
97	The use of metabolomics in the study of metals in biological systems. <i>Metallomics</i> , 2015, 7, 29-38.	2.4	25
98	Diurnal Changes in Transcript and Metabolite Levels during the Iron Deficiency Response of Rice. <i>Rice</i> , 2017, 10, 14.	4.0	25
99	Salt stress alters membrane lipid content and lipid biosynthesis pathways in the plasma membrane and tonoplast. <i>Plant Physiology</i> , 2022, 189, 805-826.	4.8	25
100	High-Resolution Metabolic Phenotyping of Genetically and Environmentally Diverse Potato Tuber Systems. Identification of Phenocopies. <i>Plant Physiology</i> , 2001, 127, 749-764.	4.8	24
101	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. <i>Plant, Cell and Environment</i> , 2002, 25, 1133-1143.	5.7	24
102	Shooting control by brassinosteroids: metabolomic analysis and effect of brassinazole on <i>Malus prunifolia</i> , the Marubakaido apple rootstock. <i>Tree Physiology</i> , 2009, 29, 607-620.	3.1	24
103	Water availability moderates N ₂ fixation benefit from elevated [CO ₂]: A 2-year free-air CO ₂ enrichment study on lentil (<i>Lens culinaris</i> MEDIK.) in a water limited agroecosystem. <i>Plant, Cell and Environment</i> , 2018, 41, 2418-2434.	5.7	24
104	Antioxidant system status of cucumber plants under pesticides treatment. <i>Acta Physiologiae Plantarum</i> , 2020, 42, 1.	2.1	24
105	Plant metabolomics. , 2012, , 67-81.		23
106	Identification of physiological changes and key metabolites coincident with postharvest internal browning of pineapple (<i>Ananas comosus</i> L.) fruit. <i>Postharvest Biology and Technology</i> , 2018, 137, 56-65.	6.0	23
107	Comparative spatial lipidomics analysis reveals cellular lipid remodelling in different developmental zones of barley roots in response to salinity. <i>Plant, Cell and Environment</i> , 2020, 43, 327-343.	5.7	23
108	Metabolite Measurements. , 2009, , 39-69.		23

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109	Single cell-type analysis of cellular lipid remodelling in response to salinity in the epidermal bladder cells of the model halophyte <i>Mesembryanthemum crystallinum</i> . <i>Plant, Cell and Environment</i> , 2018, 41, 2390-2403.	5.7	22
110	A SIEVE-RAFT HYPOTHESIS FOR THE REGULATION OF ENDOTHELIAL FENESTRATIONS. <i>Computational and Structural Biotechnology Journal</i> , 2013, 8, e201308003.	4.1	21
111	Dietary intervention rescues myopathy associated with neurofibromatosis type 1. <i>Human Molecular Genetics</i> , 2018, 27, 577-588.	2.9	21
112	Comparative metabolomics implicates threitol as a fungal signal supporting colonization of <i>Armillaria luteobubalina</i> on eucalypt roots. <i>Plant, Cell and Environment</i> , 2020, 43, 374-386.	5.7	19
113	Metabolite pools of the reef building coral <i>Montipora capitata</i> are unaffected by Symbiodiniaceae community composition. <i>Coral Reefs</i> , 2020, 39, 1727-1737.	2.2	19
114	Arabidopsis REI-LIKE proteins activate ribosome biogenesis during cold acclimation. <i>Scientific Reports</i> , 2021, 11, 2410.	3.3	19
115	Expression of a Bacterial Xylose Isomerase in Potato Tubers Results in an Altered Hexose Composition and a Consequent Induction of Metabolism. <i>Plant and Cell Physiology</i> , 2003, 44, 1359-1367.	3.1	18
116	Metabolomics – The Combination of Analytical Biochemistry, Biology, and Informatics. , 2011, , 447-459.		18
117	Prospection and identification of nematotoxic compounds from <i>Canavalia ensiformis</i> seeds effective in the control of the root knot nematode <i>Meloidogyne incognita</i> . <i>Biotechnology Research and Innovation</i> , 2017, 1, 87-100.	0.9	18
118	An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. <i>Plant Journal</i> , 2021, 107, 287-302.	5.7	18
119	Proteomic and Metabolic Profiling of Rice Suspension Culture Cells as a Model to Study Abscisic Acid Signaling Response Pathways in Plants. <i>Journal of Proteome Research</i> , 2010, 9, 6623-6634.	3.7	17
120	Determination of amino acids in urine of patients with prostate cancer and benign prostate growth. <i>European Journal of Cancer Prevention</i> , 2017, 26, 131-134.	1.3	17
121	The Influence of Contrasting Microbial Lifestyles on the Pre-symbiotic Metabolite Responses of <i>Eucalyptus grandis</i> Roots. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	17
122	Metabolic Profiling Allows Comprehensive Phenotyping of Genetically or Environmentally Modified Plant Systems. <i>Plant Cell</i> , 2001, 13, 11.	6.6	16
123	Nitrogen assimilation system in maize is regulated by developmental and tissue-specific mechanisms. <i>Plant Molecular Biology</i> , 2016, 92, 293-312.	3.9	16
124	MASTR-MS: a web-based collaborative laboratory information management system (LIMS) for metabolomics. <i>Metabolomics</i> , 2017, 13, 14.	3.0	16
125	Systems-based approaches enable identification of gene targets which improve the flavour profile of low-ethanol wine yeast strains. <i>Metabolic Engineering</i> , 2018, 49, 178-191.	7.0	16
126	The state of the art in plant lipidomics. <i>Molecular Omics</i> , 2021, 17, 894-910.	2.8	16

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127	Reproductive Stage Drought Tolerance in Wheat: Importance of Stomatal Conductance and Plant Growth Regulators. <i>Genes</i> , 2021, 12, 1742.	2.4	16
128	Low doses of the organic insecticide spinosad trigger lysosomal defects, elevated ROS, lipid dysregulation, and neurodegeneration in flies. <i>ELife</i> , 2022, 11, .	6.0	16
129	Metabolomics, Standards, and Metabolic Modeling for Synthetic Biology in Plants. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 167.	4.1	15
130	Beta-glucan-depleted, glycopeptide-rich extracts from Brewerâ€™s and Bakerâ€™s yeast (<i>Saccharomyces</i>) Tj ETQq0.0.0 rgBT /Overlock Chemistry, 2016, 197, 761-768.	8.2	15
131	A comprehensive comparison of four methods for extracting lipids from Arabidopsis tissues. <i>Plant Methods</i> , 2020, 16, 155.	4.3	15
132	Membrane-Enriched Proteomics Link Ribosome Accumulation and Proteome Reprogramming With Cold Acclimation in Barley Root Meristems. <i>Frontiers in Plant Science</i> , 2021, 12, 656683.	3.6	15
133	Sampling and Sample Preparation. , 0, , 39-82.		14
134	Phenotyping the Chilling and Freezing Responses of Young Microspore Stage Wheat Spikes Using Targeted Metabolome and Lipidome Profiling. <i>Cells</i> , 2020, 9, 1309.	4.1	14
135	Plant Tissue Extraction for Metabolomics. <i>Methods in Molecular Biology</i> , 2013, 1055, 21-28.	0.9	14
136	Phylogenetic analysis and functional characterisation of strictosidine synthase-like genes in <i>Arabidopsis thaliana</i> . <i>Functional Plant Biology</i> , 2009, 36, 1098.	2.1	13
137	Inoculation of barley with <i>Trichoderma harzianum</i> T-22 modifies lipids and metabolites to improve salt tolerance. <i>Journal of Experimental Botany</i> , 2021, 72, 7229-7246.	4.8	13
138	Characterization of epidermal bladder cells in <i>Chenopodium quinoa</i> . <i>Plant, Cell and Environment</i> , 2021, 44, 3836-3852.	5.7	13
139	Metabolomic study reveals a selective accumulation of l-arginine in the d-ornithine treated tobacco cell suspension culture. <i>Process Biochemistry</i> , 2014, 49, 140-147.	3.7	12
140	A tandem liquid chromatographyâ€“mass spectrometry (LCâ€“MS) method for profiling small molecules in complex samples. <i>Metabolomics</i> , 2015, 11, 1552-1562.	3.0	12
141	Structural and functional measures of marine microbial communities: An experiment to assess implications for oil spill management. <i>Marine Pollution Bulletin</i> , 2018, 131, 525-529.	5.0	12
142	Exploratory analysis of high-throughput metabolomic data. <i>Metabolomics</i> , 2013, 9, 1311-1320.	3.0	11
143	Transition from a maternal to external nitrogen source in maize seedlings. <i>Journal of Integrative Plant Biology</i> , 2017, 59, 261-274.	8.5	11
144	Antisense Inhibition of Threonine Synthase Leads to High Methionine Content in Transgenic Potato Plants. <i>Plant Physiology</i> , 2001, 127, 792-802.	4.8	11

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145	Non-protein amino acids in Australian acacia seed: Implications for food security and recommended processing methods to reduce djenkolic acid. <i>Food Chemistry</i> , 2015, 179, 109-115.	8.2	10
146	Edaphic niche characterization of four Proteaceae reveals unique calcicole physiology linked to hyperendemism of <i>Grevillea thelemanniana</i> . <i>New Phytologist</i> , 2020, 228, 869-883.	7.3	10
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