Alexander Erban

List of Publications by Year
in descending order

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91	5,698	87723	82410
papers	citations	38 h-index	72 g-index

97	97	97	8088
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	TagFinder for the quantitative analysis of gas chromatographyâ€"mass spectrometry (GC-MS)-based metabolite profiling experiments. Bioinformatics, 2008, 24, 732-737.	1.8	522
2	Mass appeal: metabolite identification in mass spectrometry-focused untargeted metabolomics. Metabolomics, 2013, 9, 44-66.	1.4	452
3	Phosphorus Stress in Common Bean: Root Transcript and Metabolic Responses. Plant Physiology, 2007, 144, 752-767.	2.3	300
4	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
5	Identification of primary and secondary metabolites with phosphorus statusâ€dependent abundance in <scp>A</scp>rabidopsis, 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.	2.8	196
6	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
7	Retention index thresholds for compound matching in GCâ€"MS metabolite profiling. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2008, 871, 182-190.	1.2	157
8	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
9	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
10	Comparative metabolomics of drought acclimation in model and forage legumes. Plant, Cell and Environment, 2012, 35, 136-149.	2.8	128
11	Systems Analysis of the Response of Photosynthesis, Metabolism, and Growth to an Increase in Irradiance in the Photosynthetic Model Organism Chlamydomonas reinhardtii Â Â Â. Plant Cell, 2014, 26, 2310-2350.	3.1	123
12	Comparative ionomics and metabolomics in extremophile and glycophytic Lotus species under salt stress challenge the metabolic preâ€adaptation hypothesis. Plant, Cell and Environment, 2011, 34, 605-617.	2.8	122
13	Inter-laboratory reproducibility of fast gas chromatographyâ€"electron impactâ€"time of flight mass spectrometry (GCâ€"Elâ€"TOF/MS) based plant metabolomics. Metabolomics, 2009, 5, 479-496.	1.4	120
14	Dissecting Rice Polyamine Metabolism under Controlled Long-Term Drought Stress. PLoS ONE, 2013, 8, e60325.	1.1	120
15	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
16	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
17	Extensive metabolic crossâ€talk in melon fruit revealed by spatial and developmental combinatorial metabolomics. New Phytologist, 2011, 190, 683-696.	3.5	111
18	Metabolic contribution to salt stress in two maize hybrids with contrasting resistance. Plant Science, 2015, 233, 107-115.	1.7	102

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19	Molecular signatures associated with increased freezing tolerance due to low temperature memory in Arabidopsis. Plant, Cell and Environment, 2019, 42, 854-873.	2.8	89
20	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
21	Plant Metabolomics and Its Potential for Systems Biology Research. Methods in Enzymology, 2011, 500, 299-336.	0.4	78
22	TagFinder: Preprocessing Software for the Fingerprinting and the Profiling of Gas Chromatographyâ€“Mass Spectrometry Based Metabolome Analyses. Methods in Molecular Biology, 2011, 860, 255-286.	0.4	75
23	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
24	Rapid transcriptional and metabolic regulation of the deacclimation process in cold acclimated Arabidopsis thaliana. BMC Genomics, 2017, 18, 731.	1.2	68
25	Metabolite and transcript markers for the prediction of potato drought tolerance. Plant Biotechnology Journal, 2018, 16, 939-950.	4.1	68
26	The drought response of potato reference cultivars with contrasting tolerance. Plant, Cell and Environment, 2016, 39, 2370-2389.	2.8	66
27	Primed primary metabolism in systemic leaves: a functional systems analysis. Scientific Reports, 2018, 8, 216.	1.6	64
28	Discovery of food identity markers by metabolomics and machine learning technology. Scientific Reports, 2019, 9, 9697.	1.6	56
29	Integrated analysis of rice transcriptomic and metabolomic responses to elevated night temperatures identifies sensitivityâ€•and toleranceâ€•related profiles. Plant, Cell and Environment, 2017, 40, 121-137.	2.8	54
30	Metabolic responses of rice cultivars with different tolerance to combined drought and heat stress under field conditions. GigaScience, 2019, 8, .	3.3	52
31	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
32	Highly Resolved Systems Biology to Dissect the Etioplast-to-Chloroplast Transition in Tobacco Leaves. Plant Physiology, 2019, 180, 654-681.	2.3	51
33	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
34	Cytoskeletal Components Define Protein Location to Membrane Microdomains*. Molecular and Cellular Proteomics, 2015, 14, 2493-2509.	2.5	45
35	Isolation and characterization of three new PGPR and their effects on the growth of Arabidopsis and Datura plants. Journal of Plant Interactions, 2017, 12, 1-6.	1.0	45
36	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

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37	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
38	Overexpression of Sinapine Esterase BnSCE3 in Oilseed Rape Seeds Triggers Global Changes in Seed Metabolism Â Â. Plant Physiology, 2011, 155, 1127-1145.	2.3	42
39	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
40	Characterization of the Wheat Leaf Metabolome during Grain Filling and under Varied N-Supply. Frontiers in Plant Science, 2017, 8, 2048.	1.7	42
41	Transcriptome and metabolome analyses provide insights into root and root-released organic anion responses to phosphorus deficiency in oat. Journal of Experimental Botany, 2018, 69, 3759-3771.	2.4	42
42	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
43	Opposite fates of the purine metabolite allantoin under water and nitrogen limitations in bread wheat. Plant Molecular Biology, 2019, 99, 477-497.	2.0	41
44	Metabolite profiling reveals novel multi-level cold responses in the diploid model Fragaria vesca (woodland strawberry). Phytochemistry, 2012, 77, 99-109.	1.4	39
45	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
46	Plant Temperature Acclimation and Growth Rely on Cytosolic Ribosome Biogenesis Factor Homologs. Plant Physiology, 2018, 176, 2251-2276.	2.3	39
47	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
48	Comparative Metabolomics and Molecular Phylogenetics of Melon (Cucumis melo, Cucurbitaceae) Biodiversity. Metabolites, 2020, 10, 121.	1.3	35
49	Selective induction and subcellular distribution of ACONITASE 3 reveal the importance of cytosolic citrate metabolism during lipid mobilization in Arabidopsis. Biochemical Journal, 2014, 463, 309-317.	1.7	33
50	Multi-omics reveals mechanisms of total resistance to extreme illumination of a desert alga. Nature Plants, 2020, 6, 1031-1043.	4.7	33
51	Global mapping of proteinâ€“metabolite interactions in Saccharomyces cerevisiae reveals that Ser-Leu dipeptide regulates phosphoglycerate kinase activity. Communications Biology, 2021, 4, 181.	2.0	32
52	Functional associations between the metabolome and manganese tolerance in Vigna unguiculata. Journal of Experimental Botany, 2012, 63, 329-340.	2.4	28
53	Metabolomics Identifies a Biomarker Revealing In Vivo Loss of Functional Î²-Cell Mass Before Diabetes Onset. Diabetes, 2019, 68, 2272-2286.	0.3	28
54	Transcriptional, hormonal, and metabolic changes in susceptible grape berries under powdery mildew infection. Journal of Experimental Botany, 2021, 72, 6544-6569.	2.4	24

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55	Imbalanced Regulation of Fungal Nutrient Transports According to Phosphate Availability in a Symbiocosm Formed by Poplar, Sorghum, and Rhizophagus irregularis. Frontiers in Plant Science, 2019, 10, 1617.	1.7	23
56	Ionâ€dependent metabolic responses of Vicia faba L. to salt stress. Plant, Cell and Environment, 2019, 42, 295-309.	2.8	22
57	Impact of seasonal warming on overwintering and spring phenology of blackcurrant. Environmental and Experimental Botany, 2017, 140, 96-109.	2.0	21
58	NLR Mutations Suppressing Immune Hybrid Incompatibility and Their Effects on Disease Resistance. Plant Physiology, 2018, 177, 1152-1169.	2.3	21
59	Season Affects Yield and Metabolic Profiles of Rice (Oryza sativa) under High Night Temperature Stress in the Field. International Journal of Molecular Sciences, 2020, 21, 3187.	1.8	21
60	Acquisition of Volatile Compounds by Gas Chromatographyâ€“Mass Spectrometry (GC-MS). Methods in Molecular Biology, 2018, 1778, 225-239.	0.4	20
61	Riboswitch-mediated inducible expression of an astaxanthin biosynthetic operon in plastids. Plant Physiology, 2022, 188, 637-652.	2.3	20
62	Comprehensive Metabolomics Studies of Plant Developmental Senescence. Methods in Molecular Biology, 2018, 1744, 339-358.	0.4	19
63	Underground isoleucine biosynthesis pathways in E. coli. ELife, 2020, 9, .	2.8	19
64	Unravelling the Metabolic and Hormonal Machinery During Key Steps of Somatic Embryogenesis: A Case Study in Coffee. International Journal of Molecular Sciences, 2019, 20, 4665.	1.8	18
65	Establishment of a GCâ€MSâ€based ¹³Câ€positional isotopomer approach suitable for investigating metabolic fluxes in plant primary metabolism. Plant Journal, 2021, 108, 1213-1233.	2.8	18
66	Rationales and Approaches for Studying Metabolism in Eukaryotic Microalgae. Metabolites, 2014, 4, 184-217.	1.3	18
67	Consequences of induced brassinosteroid deficiency in Arabidopsis leaves. BMC Plant Biology, 2014, 14, 309.	1.6	17
68	Symbiosis dependent accumulation of primary metabolites in arbuscule-containing cells. BMC Plant Biology, 2015, 15, 234.	1.6	17
69	Integrative â€œomicâ€•analysis reveals distinctive cold responses in leaves and roots of strawberry, Fragaria Ã— ananassa â€˜Koronaâ€™. Frontiers in Plant Science, 2015, 6, 826.	1.7	17
70	Salt stress responses in a geographically diverse collection of Eutrema/Thellungiella spp. accessions. Functional Plant Biology, 2016, 43, 590.	1.1	17
71	Natural Variation in Freezing Tolerance and Cold Acclimation Response in Arabidopsis thaliana and Related Species. Advances in Experimental Medicine and Biology, 2018, 1081, 81-98.	0.8	16
72	Assessing Dynamic Changes of Taste-Related Primary Metabolism During Ripening of Durian Pulp Using Metabolomic and Transcriptomic Analyses. Frontiers in Plant Science, 2021, 12, 687799.	1.7	16

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73	Multiplexed Profiling and Data Processing Methods to Identify Temperature-Regulated Primary Metabolites Using Gas Chromatography Coupled to Mass Spectrometry. Methods in Molecular Biology, 2020, 2156, 203-239.	0.4	16
74	The ironâ€stress activated RNA 1 (IsaR1) coordinates osmotic acclimation and iron starvation responses in the cyanobacterium Synechocystis sp. PCC 6803. Environmental Microbiology, 2018, 20, 2757-2768.	1.8	15
75	Metabolic responses of rice source and sink organs during recovery from combined drought and heat stress in the field. GigaScience, 2019, 8, .	3.3	14
76	Aroma and quality of breads baked from old and modern wheat varieties and their prediction from genomic and flour-based metabolite profiles. Food Research International, 2020, 129, 108748.	2.9	13
77	Functional specialization of one copy of glutamine phosphoribosyl pyrophosphate amidotransferase in ureide production from symbiotically fixed nitrogen in Phaseolus vulgaris. Plant, Cell and Environment, 2016, 39, 1767-1779.	2.8	12
78	The fungal endophyte Fusarium solani provokes differential effects on the fitness of two Lotus species. Plant Physiology and Biochemistry, 2019, 144, 100-109.	2.8	12
79	Characterization of the Heat-Stable Proteome during Seed Germination in Arabidopsis with Special Focus on LEA Proteins. International Journal of Molecular Sciences, 2021, 22, 8172.	1.8	12
80	Acclimatisation of guard cell metabolism to longâ€term salinity. Plant, Cell and Environment, 2021, 44, 870-884.	2.8	11
81	Increasing abscisic acid levels by immunomodulation in barley grains induces precocious maturation without changing grain composition. Journal of Experimental Botany, 2016, 67, 2675-2687.	2.4	10
82	The Impact of Metabolic Sciona€"Rootstock Interactions in Different Grapevine Tissues and Phloem Exudates. Metabolites, 2021, 11, 349.	1.3	10
83	Metabolomic linkage reveals functional interaction between glucose-dependent insulinotropic polypeptide and ghrelin in humans. American Journal of Physiology - Endocrinology and Metabolism, 2011, 301, E608-E617.	1.8	8
84	Cysteine and Methionine Biosynthetic Enzymes Have Distinct Effects on Seed Nutritional Quality and on Molecular Phenotypes Associated With Accumulation of a Methionine-Rich Seed Storage Protein in Rice. Frontiers in Plant Science, 2020, 11, 1118.	1.7	8
85	Metabolic Profiling and Metabolite Correlation Network Analysis Reveal That Fusarium solani Induces Differential Metabolic Responses in Lotus japonicus and Lotus tenuis against Severe Phosphate Starvation. Journal of Fungi (Basel, Switzerland), 2021, 7, 765.	1.5	7
86	Effect of Senescence Phenotypes and Nitrate Availability on Wheat Leaf Metabolome during Grain Filling. Agronomy, 2019, 9, 305.	1.3	6
87	Untargeted metabolomics as a hypothesis-generation tool in plant protection product discovery: Highlighting the potential of trehalose and glycerol metabolism of fungal conidiospores as novel targets. Metabolomics, 2020, 16, 79.	1.4	5
88	Metabolite Profiling Reveals Sensitivity-Dependent Metabolic Shifts in Rice (Oryza Sativa L.) Cultivars under High Night Temperature Stress. Procedia Environmental Sciences, 2015, 29, 72.	1.3	4
89	Differentiation of the High Night Temperature Response in Leaf Segments of Rice Cultivars with Contrasting Tolerance. International Journal of Molecular Sciences, 2021, 22, 10451.	1.8	2
90	Sugar Starvation of Rice Anthers is a Factor in Reproductive Failure under Heat and Drought Stress, as shown by Metabolite and Transcript Profiling. Procedia Environmental Sciences, 2015, 29, 70-71.	1.3	0

#	Article	IF	Citations
91	Plasma metabolomic markers of insulin resistance in humans.. Endocrine Abstracts, 0, , .	0.0	0