Lothar Willmitzer

List of Publications by Year
in descending order

38 papers	8,333 citations	186265 28 h-index	302126 39 g-index
42 all docs	42 docs citations	42 times ranked	10225 citing authors

#	Article	IF	Citations
1	Metabolite profiling for plant functional genomics. Nature Biotechnology, 2000, 18, 1157-1161.	17.5	1,936
2	Gas chromatography mass spectrometry–based metabolite profiling in plants. Nature Protocols, 2006, 1, 387-396.	12.0	1,808
3	GMD@CSB.DB: the Golm Metabolome Database. Bioinformatics, 2005, 21, 1635-1638.	4.1	1,247
4	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. Nature Genetics, 2012, 44, 217-220.	21.4	532
5	Elemental formula annotation of polar and lipophilic metabolites using ^{13}C, ^{15}N and ^{34}S isotope labelling, in combination with high-resolution mass spectrometry. Plant Journal, 2011, 68, 364-376.	5.7	319
6	High-density kinetic analysis of the metabolomic and transcriptomic response of Arabidopsis to eight environmental conditions. Plant Journal, 2011, 67, 869-884.	5.7	251
7	Identification of metabolic and biomass QTL in *Arabidopsis thaliana* in a parallel analysis of RIL and IL populations. Plant Journal, 2008, 53, 960-972.	5.7	211
8	TargetSearch - a Bioconductor package for the efficient preprocessing of GC-MS metabolite profiling data. BMC Bioinformatics, 2009, 10, 428.	2.6	211
9	Transcript and metabolite analysis of the Trichoderma-induced systemic resistance response to Pseudomonas syringae in Arabidopsis thaliana. Microbiology (United Kingdom), 2012, 158, 139-146.	1.8	172
10	The transcription factor PHR1 regulates lipid remodeling and triacylglycerol accumulation in Arabidopsis thaliana during phosphorus starvation. Journal of Experimental Botany, 2015, 66, 1907-1918.	4.8	146
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.	6.6	123
12	Organization and Evolution of Brain Lipidome Revealed by Large-Scale Analysis of Human, Chimpanzee, Macaque, and Mouse Tissues. Neuron, 2015, 85, 695-702.	8.1	123
13	Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. Molecular Plant, 2018, 11, 118-134.	8.3	116
14	The NAC transcription factor FaRIF controls fruit ripening in strawberry. Plant Cell, 2021, 33, 1574-1593.	6.6	95
15	Omics-based hybrid prediction in maize. Theoretical and Applied Genetics, 2017, 130, 1927-1939.	3.6	90
16	A tyrosine aminotransferase involved in tocopherol synthesis in Arabidopsis. Plant Journal, 2012, 71, 850-859.	5.7	82
17	Exceptional Evolutionary Divergence of Human Muscle and Brain Metabolomes Parallels Human Cognitive and Physical Uniqueness. PLoS Biology, 2014, 12, e1001871.	5.6	80
18	Corn hybrids display lower metabolite variability and complex metabolite inheritance patterns. Plant Journal, 2011, 68, 326-336.	5.7	75

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19	Combined Use of Genome-Wide Association Data and Correlation Networks Unravels Key Regulators of Primary Metabolism in Arabidopsis thaliana. PLoS Genetics, 2016, 12, e1006363.	3.5	67
20	Lipidome alterations in human prefrontal cortex during development, aging, and cognitive disorders. Molecular Psychiatry, 2020, 25, 2952-2969.	7.9	66
21	Lipidome determinants of maximal lifespan in mammals. Scientific Reports, 2017, 7, 5.	3.3	60
22	PROMIS, global analysis of PROtein–metabolite interactions using size separation in Arabidopsis thaliana. Journal of Biological Chemistry, 2018, 293, 12440-12453.	3.4	55
23	Genetic diversity of strawberry germplasm using metabolomic biomarkers. Scientific Reports, 2018, 8, 14386.	3.3	46
24	Metabolomic Profiling of 13 Diatom Cultures and Their Adaptation to Nitrate-Limited Growth Conditions. PLoS ONE, 2015, 10, e0138965.	2.5	41
25	Medicinal Bioprospecting of the Amazon Rainforest: A Modern Eldorado?. Trends in Biotechnology, 2016, 34, 781-790.	9.3	39
26	An integrated multi–layered analysis of the metabolic networks of different tissues uncovers key genetic components of primary metabolism in maize. Plant Journal, 2018, 93, 1116-1128.	5.7	38
27	System-wide detection of protein-small molecule complexes suggests extensive metabolite regulation in plants. Scientific Reports, 2017, 7, 42387.	3.3	37
28	A naturally occurring promoter polymorphism of the Arabidopsis *FUM2* gene causes expression variation, and is associated with metabolic and growth traits. Plant Journal, 2016, 88, 826-838.	5.7	35
29	Integrated genomics-based mapping reveals the genetics underlying maize flavonoid biosynthesis. BMC Plant Biology, 2017, 17, 17.	3.6	34
30	Global mapping of protein–metabolite interactions in Saccharomyces cerevisiae reveals that Ser-Leu dipeptide regulates phosphoglycerate kinase activity. Communications Biology, 2021, 4, 181.	4.4	32
31	Metabolic robustness in young roots underpins a predictive model of maize hybrid performance in the field. Plant Journal, 2017, 90, 319-329.	5.7	30
32	Affinity purification with metabolomic and proteomic analysis unravels diverse roles of nucleoside diphosphate kinases. Journal of Experimental Botany, 2017, 68, 3487-3499.	4.8	30
33	Changes in Lipidome Composition during Brain Development in Humans, Chimpanzees, and Macaque Monkeys. Molecular Biology and Evolution, 2017, 34, 1155-1166.	8.9	28
34	Characterizing the involvement of *FaMADS9* in the regulation of strawberry fruit receptacle development. Plant Biotechnology Journal, 2020, 18, 929-943.	8.3	25
35	Characterization of three different classes of non-fermented teas using untargeted metabolomics. Food Research International, 2019, 121, 697-704.	6.2	24
36	PROMISed: A novel web-based tool to facilitate analysis and visualization of the molecular interaction networks from co-fractionation mass spectrometry (CF-MS) experiments. Computational and Structural Biotechnology Journal, 2021, 19, 5117-5125.	4.1	9

#	Article	IF	Citations
37	From systems biology to systems chemistry: metabolomic procedures enable insight into complex chemical reaction networks in water. RSC Advances, 2014, 4, 16777.	3.6	3
38	Classification-driven framework to predict maize hybrid field performance from metabolic profiles of young parental roots. PLoS ONE, 2018, 13, e0196038.	2.5	2