

# Lothar Willmitzer

## List of Publications by Year in descending order

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Version: 2024-02-01

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	PROMISed: A novel web-based tool to facilitate analysis and visualization of the molecular interaction networks from co-fractionation mass spectrometry (CF-MS) experiments. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5117-5125.	4.1	9
2	Global mapping of protein-metabolite interactions in <i>Saccharomyces cerevisiae</i> reveals that Ser-Leu dipeptide regulates phosphoglycerate kinase activity. <i>Communications Biology</i> , 2021, 4, 181.	4.4	32
3	The NAC transcription factor FaRIF controls fruit ripening in strawberry. <i>Plant Cell</i> , 2021, 33, 1574-1593.	6.6	95
4	Lipidome alterations in human prefrontal cortex during development, aging, and cognitive disorders. <i>Molecular Psychiatry</i> , 2020, 25, 2952-2969.	7.9	66
5	Characterizing the involvement of <i>FaMADS9</i> in the regulation of strawberry fruit receptacle development. <i>Plant Biotechnology Journal</i> , 2020, 18, 929-943.	8.3	25
6	Characterization of three different classes of non-fermented teas using untargeted metabolomics. <i>Food Research International</i> , 2019, 121, 697-704.	6.2	24
7	An integrated multi-layered analysis of the metabolic networks of different tissues uncovers key genetic components of primary metabolism in maize. <i>Plant Journal</i> , 2018, 93, 1116-1128.	5.7	38
8	Mapping the Arabidopsis Metabolic Landscape by Untargeted Metabolomics at Different Environmental Conditions. <i>Molecular Plant</i> , 2018, 11, 118-134.	8.3	116
9	Genetic diversity of strawberry germplasm using metabolomic biomarkers. <i>Scientific Reports</i> , 2018, 8, 14386.	3.3	46
10	Classification-driven framework to predict maize hybrid field performance from metabolic profiles of young parental roots. <i>PLoS ONE</i> , 2018, 13, e0196038.	2.5	2
11	PROMIS, global analysis of protein-metabolite interactions using size separation in <i>Arabidopsis thaliana</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 12440-12453.	3.4	55
12	Integrated genomics-based mapping reveals the genetics underlying maize flavonoid biosynthesis. <i>BMC Plant Biology</i> , 2017, 17, 17.	3.6	34
13	Metabolic robustness in young roots underpins a predictive model of maize hybrid performance in the field. <i>Plant Journal</i> , 2017, 90, 319-329.	5.7	30
14	System-wide detection of protein-small molecule complexes suggests extensive metabolite regulation in plants. <i>Scientific Reports</i> , 2017, 7, 42387.	3.3	37
15	Lipidome determinants of maximal lifespan in mammals. <i>Scientific Reports</i> , 2017, 7, 5.	3.3	60
16	Affinity purification with metabolomic and proteomic analysis unravels diverse roles of nucleoside diphosphate kinases. <i>Journal of Experimental Botany</i> , 2017, 68, 3487-3499.	4.8	30
17	Omics-based hybrid prediction in maize. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1927-1939.	3.6	90
18	Changes in Lipidome Composition during Brain Development in Humans, Chimpanzees, and Macaque Monkeys. <i>Molecular Biology and Evolution</i> , 2017, 34, 1155-1166.	8.9	28

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19	Combined Use of Genome-Wide Association Data and Correlation Networks Unravels Key Regulators of Primary Metabolism in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2016, 12, e1006363.	3.5	67
20	Medicinal Bioprospecting of the Amazon Rainforest: A Modern Eldorado?. <i>Trends in Biotechnology</i> , 2016, 34, 781-790.	9.3	39
21	A naturally occurring promoter polymorphism of the <i>Arabidopsis thaliana</i> <i>FUM2</i> gene causes expression variation, and is associated with metabolic and growth traits. <i>Plant Journal</i> , 2016, 88, 826-838.	5.7	35
22	Metabolomic Profiling of 13 Diatom Cultures and Their Adaptation to Nitrate-Limited Growth Conditions. <i>PLoS ONE</i> , 2015, 10, e0138965.	2.5	41
23	Organization and Evolution of Brain Lipidome Revealed by Large-Scale Analysis of Human, Chimpanzee, Macaque, and Mouse Tissues. <i>Neuron</i> , 2015, 85, 695-702.	8.1	123
24	The transcription factor PHR1 regulates lipid remodeling and triacylglycerol accumulation in <i>Arabidopsis thaliana</i> during phosphorus starvation. <i>Journal of Experimental Botany</i> , 2015, 66, 1907-1918.	4.8	146
25	Exceptional Evolutionary Divergence of Human Muscle and Brain Metabolomes Parallels Human Cognitive and Physical Uniqueness. <i>PLoS Biology</i> , 2014, 12, e1001871.	5.6	80
26	Systems Analysis of the Response of Photosynthesis, Metabolism, and Growth to an Increase in Irradiance in the Photosynthetic Model Organism <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2014, 26, 2310-2350.	6.6	123
27	From systems biology to systems chemistry: metabolomic procedures enable insight into complex chemical reaction networks in water. <i>RSC Advances</i> , 2014, 4, 16777.	3.6	3
28	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. <i>Nature Genetics</i> , 2012, 44, 217-220.	21.4	532
29	Transcript and metabolite analysis of the <i>Trichoderma</i> -induced systemic resistance response to <i>Pseudomonas syringae</i> in <i>Arabidopsis thaliana</i> . <i>Microbiology (United Kingdom)</i> , 2012, 158, 139-146.	1.8	172
30	A tyrosine aminotransferase involved in tocopherol synthesis in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2012, 71, 850-859.	5.7	82
31	High-density kinetic analysis of the metabolomic and transcriptomic response of <i>Arabidopsis</i> to eight environmental conditions. <i>Plant Journal</i> , 2011, 67, 869-884.	5.7	251
32	Elemental formula annotation of polar and lipophilic metabolites using <sup>13</sup> C, <sup>15</sup> N and <sup>34</sup> S isotope labelling, in combination with high-resolution mass spectrometry. <i>Plant Journal</i> , 2011, 68, 364-376.	5.7	319
33	Corn hybrids display lower metabolite variability and complex metabolite inheritance patterns. <i>Plant Journal</i> , 2011, 68, 326-336.	5.7	75
34	TargetSearch - a Bioconductor package for the efficient preprocessing of GC-MS metabolite profiling data. <i>BMC Bioinformatics</i> , 2009, 10, 428.	2.6	211
35	Identification of metabolic and biomass QTL in <i>Arabidopsis thaliana</i> in a parallel analysis of RIL and IL populations. <i>Plant Journal</i> , 2008, 53, 960-972.	5.7	211
36	Gas chromatography mass spectrometry-based metabolite profiling in plants. <i>Nature Protocols</i> , 2006, 1, 387-396.	12.0	1,808

#	ARTICLE	IF	CITATIONS
37	GMD@CSB.DB: the Golm Metabolome Database. <i>Bioinformatics</i> , 2005, 21, 1635-1638.	4.1	1,247
38	Metabolite profiling for plant functional genomics. <i>Nature Biotechnology</i> , 2000, 18, 1157-1161.	17.5	1,936