

# Dirk Steinhauser

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

6,016  
citations

159585

30  
h-index

377865

34  
g-index

37  
all docs

37  
docs citations

37  
times ranked

8655  
citing authors

#	ARTICLE	IF	CITATIONS
1	The target of rapamycin kinase affects biomass accumulation and cell cycle progression by altering carbon/nitrogen balance in synchronized <i>Chlamydomonas reinhardtii</i> cells. <i>Plant Journal</i> , 2018, 93, 355-376.	5.7	54
2	Dynamics of lipids and metabolites during the cell cycle of <i>Chlamydomonas reinhardtii</i> . <i>Plant Journal</i> , 2017, 92, 331-343.	5.7	38
3	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
4	Metabolomic analysis indicates a pivotal role of the hepatotoxin microcystin in high light adaptation of <i>Microcystis</i> . <i>Environmental Microbiology</i> , 2015, 17, 1497-1509.	3.8	94
5	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
6	Analysis of Subcellular Metabolite Distributions Within <i>Arabidopsis thaliana</i> Leaf Tissue: A Primer for Subcellular Metabolomics. <i>Methods in Molecular Biology</i> , 2014, 1062, 575-596.	0.9	28
7	On the role of the mitochondrial 2-oxoglutarate dehydrogenase complex in amino acid metabolism. <i>Amino Acids</i> , 2013, 44, 683-700.	2.7	55
8	Unraveling retrograde signaling pathways: finding candidate signaling molecules via metabolomics and systems biology driven approaches. <i>Frontiers in Plant Science</i> , 2012, 3, 267.	3.6	18
9	Unusual cyanobacterial TCA cycles: not broken just different. <i>Trends in Plant Science</i> , 2012, 17, 503-509.	8.8	97
10	High-resolution plant metabolomics: from mass spectral features to metabolites and from whole-cell analysis to subcellular metabolite distributions. <i>Plant Journal</i> , 2012, 70, 39-50.	5.7	151
11	Analysis of the compartmentalized metabolome – a validation of the non-aqueous fractionation technique. <i>Frontiers in Plant Science</i> , 2011, 2, 55.	3.6	49
12	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
13	Sample amount alternatives for data adjustment in comparative cyanobacterial metabolomics. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 399, 3503-3517.	3.7	32
14	Identification of Enzyme Activity Quantitative Trait Loci in a <i>Solanum lycopersicum</i> – <i>Solanum pennellii</i> Introgression Line Population. <i>Plant Physiology</i> , 2011, 157, 998-1014.	4.8	36
15	Toward the Storage Metabolome: Profiling the Barley Vacuole. <i>Plant Physiology</i> , 2011, 157, 1469-1482.	4.8	92
16	A Topological Map of the Compartmentalized <i>Arabidopsis thaliana</i> Leaf Metabolome. <i>PLoS ONE</i> , 2011, 6, e17806.	2.5	101
17	Metabolomic and transcriptomic stress response of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2010, 6, 364.	7.2	451
18	Combined Transcript and Metabolite Profiling of <i>Arabidopsis</i> Grown under Widely Variant Growth Conditions Facilitates the Identification of Novel Metabolite-Mediated Regulation of Gene Expression. <i>Plant Physiology</i> , 2010, 152, 2120-2129.	4.8	70

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19	Enzyme Activity Profiles during Fruit Development in Tomato Cultivars and <i>Solanum pennellii</i> . <i>Plant Physiology</i> , 2010, 153, 80-98.	4.8	92
20	Assessment of sampling strategies for gas chromatography–mass spectrometry (GC–MS) based metabolomics of cyanobacteria. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 2952-2960.	2.3	64
21	Analysis of cytosolic and plastidic serine acetyltransferase mutants and subcellular metabolite distributions suggests interplay of the cellular compartments for cysteine biosynthesis in <i>Arabidopsis</i> . <i>Plant, Cell and Environment</i> , 2009, 32, 349-367.	5.7	139
22	Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. <i>Plant, Cell and Environment</i> , 2009, 32, 1633-1651.	5.7	480
23	Transcription factors relevant to auxin signalling coordinate broad-spectrum metabolic shifts including sulphur metabolism. <i>Journal of Experimental Botany</i> , 2008, 59, 2831-2846.	4.8	54
24	Analysis of Cytosolic and Plastidic Serine Acetyltransferase Mutants and Subcellular Metabolite Distributions Suggests Interplay of the Cellular Compartments for Cysteine Biosynthesis in <i>Arabidopsis</i> . <i>Plant, Cell and Environment</i> , 2008, 32, 349-67.	5.7	69
25	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. <i>BMC Bioinformatics</i> , 2007, 8, 216.	2.6	96
26	Methods, applications and concepts of metabolite profiling: Primary metabolism. , 2007, 97, 171-194.		25
27	PageMan: An interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. <i>BMC Bioinformatics</i> , 2006, 7, 535.	2.6	309
28	Enhancing Vacuolar Sucrose Cleavage Within the Developing Potato Tuber has only Minor Effects on Metabolism. <i>Plant and Cell Physiology</i> , 2006, 47, 277-289.	3.1	16
29	Inferring Hypotheses on Functional Relationships of Genes: Analysis of the <i>Arabidopsis thaliana</i> Subtilase Gene Family. <i>PLoS Computational Biology</i> , 2005, 1, e40.	3.2	157
30	Extension of the Visualization Tool MapMan to Allow Statistical Analysis of Arrays, Display of Corresponding Genes, and Comparison with Known Responses. <i>Plant Physiology</i> , 2005, 138, 1195-1204.	4.8	576
31	Identification of brassinosteroid-related genes by means of transcript co-response analyses. <i>Nucleic Acids Research</i> , 2005, 33, 2685-2696.	14.5	64
32	GMD@CSB.DB: the Golm Metabolome Database. <i>Bioinformatics</i> , 2005, 21, 1635-1638.	4.1	1,247
33	GC–MS libraries for the rapid identification of metabolites in complex biological samples. <i>FEBS Letters</i> , 2005, 579, 1332-1337.	2.8	596
34	CSB.DB: a comprehensive systems-biology database. <i>Bioinformatics</i> , 2004, 20, 3647-3651.	4.1	152
35	Hypothesis-driven approach to predict transcriptional units from gene expression data. <i>Bioinformatics</i> , 2004, 20, 1928-1939.	4.1	33
36	Bioinformatics Tools to Discover Co-Expressed Genes in Plants. , 0, , 307-335.		1