Dirk Steinhauser

List of Publications by Year
in descending order

36 papers	6,016 citations	159358 30 h-index	377514 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. Plant Journal, 2018, 93, 355-376.	2.8	54
2	Dynamics of lipids and metabolites during the cell cycle of <i>Chlamydomonas reinhardtii</i>. Plant Journal, 2017, 92, 331-343.	2.8	38
3	Organization and Evolution of Brain Lipidome Revealed by Large-Scale Analysis of Human, Chimpanzee, Macaque, and Mouse Tissues. Neuron, 2015, 85, 695-702.	3.8	123
4	Metabolomic analysis indicates a pivotal role of the hepatotoxin microcystin in high light adaptation of <scp><i>M</i></scp><i>icrocystis</i>. Environmental Microbiology, 2015, 17, 1497-1509.	1.8	94
5	Exceptional Evolutionary Divergence of Human Muscle and Brain Metabolomes Parallels Human Cognitive and Physical Uniqueness. PLoS Biology, 2014, 12, e1001871.	2.6	80
6	Analysis of Subcellular Metabolite Distributions Within Arabidopsis thaliana Leaf Tissue: A Primer for Subcellular Metabolomics. Methods in Molecular Biology, 2014, 1062, 575-596.	0.4	28
7	On the role of the mitochondrial 2-oxoglutarate dehydrogenase complex in amino acid metabolism. Amino Acids, 2013, 44, 683-700.	1.2	55
8	Unraveling retrograde signaling pathways: finding candidate signaling molecules via metabolomics and systems biology driven approaches. Frontiers in Plant Science, 2012, 3, 267.	1.7	18
9	Unusual cyanobacterial TCA cycles: not broken just different. Trends in Plant Science, 2012, 17, 503-509.	4.3	97
10	High‐resolution plant metabolomics: from mass spectral features to metabolites and from whole‐cell analysis to subcellular metabolite distributions. Plant Journal, 2012, 70, 39-50.	2.8	151
11	Analysis of the compartmentalized metabolome – a validation of the non-aqueous fractionation technique. Frontiers in Plant Science, 2011, 2, 55.	1.7	49
12	High‐density kinetic analysis of the metabolomic and transcriptomic response of Arabidopsis to eight environmental conditions. Plant Journal, 2011, 67, 869-884.	2.8	251
13	Sample amount alternatives for data adjustment in comparative cyanobacterial metabolomics. Analytical and Bioanalytical Chemistry, 2011, 399, 3503-3517.	1.9	32
14	Identification of Enzyme Activity Quantitative Trait Loci in a Solanum lycopersicum Ã— Solanum pennellii Introgression Line Population Â Â. Plant Physiology, 2011, 157, 998-1014.	2.3	36
15	Toward the Storage Metabolome: Profiling the Barley Vacuole Â Â. Plant Physiology, 2011, 157, 1469-1482.	2.3	92
16	A Topological Map of the Compartmentalized Arabidopsis thaliana Leaf Metabolome. PLoS ONE, 2011, 6, e17806.	1.1	101
17	Metabolomic and transcriptomic stress response of <i>Escherichia coli</i>. Molecular Systems Biology, 2010, 6, 364.	3.2	451
18	Combined Transcript and Metabolite Profiling of Arabidopsis Grown under Widely Variant Growth Conditions Facilitates the Identification of Novel Metabolite-Mediated Regulation of Gene Expression Â. Plant Physiology, 2010, 152, 2120-2129.	2.3	70

#	Article	IF	Citations
19	Enzyme Activity Profiles during Fruit Development in Tomato Cultivars and<i>Solanum pennellii</i>Â Â Â. Plant Physiology, 2010, 153, 80-98.	2.3	92
20	Assessment of sampling strategies for gas chromatographyâ€"mass spectrometry (GCâ€"MS) based metabolomics of cyanobacteria. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 2952-2960.	1.2	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>. Plant, Cell and Environment, 2009, 32, 349-367.	2.8	139
22	Coâ€expression tools for plant biology: opportunities for hypothesis generation and caveats. Plant, Cell and Environment, 2009, 32, 1633-1651.	2.8	480
23	Transcription factors relevant to auxin signalling coordinate broad-spectrum metabolic shifts including sulphur metabolism. Journal of Experimental Botany, 2008, 59, 2831-2846.	2.4	54
24	Analysis of Cytosolic and Plastidic Serine Acetyltransferase Mutants and Subcellular Metabolite Distributions Suggests Interplay of the Cellular Compartments for Cysteine Biosynthesis in Arabidopsis. Plant, Cell and Environment, 2008, 32, 349-67.	2.8	69
25	ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. BMC Bioinformatics, 2007, 8, 216.	1.2	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. BMC Bioinformatics, 2006, 7, 535.	1.2	309
28	Enhancing Vacuolar Sucrose Cleavage Within the Developing Potato Tuber has only Minor Effects on Metabolism. Plant and Cell Physiology, 2006, 47, 277-289.	1.5	16
29	Inferring Hypotheses on Functional Relationships of Genes: Analysis of the Arabidopsis thaliana Subtilase Gene Family. PLoS Computational Biology, 2005, 1, e40.	1.5	157
30	Extension of the Visualization Tool MapMan to Allow Statistical Analysis of Arrays, Display of Coresponding Genes, and Comparison with Known Responses. Plant Physiology, 2005, 138, 1195-1204.	2.3	576
31	Identification of brassinosteroid-related genes by means of transcript co-response analyses. Nucleic Acids Research, 2005, 33, 2685-2696.	6.5	64
32	GMD@CSB.DB: the Golm Metabolome Database. Bioinformatics, 2005, 21, 1635-1638.	1.8	1,247
33	GC-MS libraries for the rapid identification of metabolites in complex biological samples. FEBS Letters, 2005, 579, 1332-1337.	1.3	596
34	CSB.DB: a comprehensive systems-biology database. Bioinformatics, 2004, 20, 3647-3651.	1.8	152
35	Hypothesis-driven approach to predict transcriptional units from gene expression data. Bioinformatics, 2004, 20, 1928-1939.	1.8	33
36	Bioinformatics Tools to Discover Co-Expressed Genes in Plants. , 0, , 307-335.		1