## Dirk Steinhauser

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1337313/publications.pdf

Version: 2024-02-01

36 papers 6,016 citations

30 h-index 377514 34 g-index

37 all docs

37 docs citations

37 times ranked

8655 citing authors

| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | GMD@CSB.DB: the Golm Metabolome Database. Bioinformatics, 2005, 21, 1635-1638.   | 1.8 | 1,247     |
| 2  | GC-MS libraries for the rapid identification of metabolites in complex biological samples. FEBS Letters, 2005, 579, 1332-1337.   | 1.3 | 596       |
| 3  | 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       |
| 4  | Coâ€expression tools for plant biology: opportunities for hypothesis generation and caveats. Plant, Cell and Environment, 2009, 32, 1633-1651.   | 2.8 | 480       |
| 5  | Metabolomic and transcriptomic stress response of <i>Escherichia coli</i> . Molecular Systems Biology, 2010, 6, 364.   | 3.2 | 451       |
| 6  | PageMan: An interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. BMC Bioinformatics, 2006, 7, 535.  | 1.2 | 309       |
| 7  | Highâ€density kinetic analysis of the metabolomic and transcriptomic response of Arabidopsis to eight environmental conditions. Plant Journal, 2011, 67, 869-884.  | 2.8 | 251       |
| 8  | Inferring Hypotheses on Functional Relationships of Genes: Analysis of the Arabidopsis thaliana Subtilase Gene Family. PLoS Computational Biology, 2005, 1, e40.   | 1.5 | 157       |
| 9  | CSB.DB: a comprehensive systems-biology database. Bioinformatics, 2004, 20, 3647-3651.   | 1.8 | 152       |
| 10 | Highâ€resolution plant metabolomics: from mass spectral features to metabolites and from wholeâ€eell analysis to subcellular metabolite distributions. Plant Journal, 2012, 70, 39-50.   | 2.8 | 151       |
| 11 | Analysis of cytosolic and plastidic serine acetyltransferase mutants and subcellular metabolite distributions suggests interplay of the cellular compartments for cysteine biosynthesis in $\langle i \rangle$ Arabidopsis $\langle i \rangle$ . Plant, Cell and Environment, 2009, 32, 349-367. | 2.8 | 139       |
| 12 | 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       |
| 13 | A Topological Map of the Compartmentalized Arabidopsis thaliana Leaf Metabolome. PLoS ONE, 2011, 6, e17806.  | 1.1 | 101       |
| 14 | Unusual cyanobacterial TCA cycles: not broken just different. Trends in Plant Science, 2012, 17, 503-509.  | 4.3 | 97        |
| 15 | ProMEX: a mass spectral reference database for proteins and protein phosphorylation sites. BMC Bioinformatics, 2007, 8, 216.   | 1.2 | 96        |
| 16 | Metabolomic analysis indicates a pivotal role of the hepatotoxin microcystin in high light adaptation of <scp><i>M</i></scp> <i>icrocystis</i>   | 1.8 | 94        |
| 17 | Enzyme Activity Profiles during Fruit Development in Tomato Cultivars and <i>Solanum pennellii </i> ÂÂÂ.<br>Plant Physiology, 2010, 153, 80-98.  | 2.3 | 92        |
| 18 | Toward the Storage Metabolome: Profiling the Barley Vacuole  Â. Plant Physiology, 2011, 157, 1469-1482.  | 2.3 | 92        |

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|----|--|-----|-----------|
| 19 | Exceptional Evolutionary Divergence of Human Muscle and Brain Metabolomes Parallels Human Cognitive and Physical Uniqueness. PLoS Biology, 2014, 12, e1001871.   | 2.6 | 80        |
| 20 | 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        |
| 21 | Analysis of Cytosolic and Plastidic Serine Acetyltransferase Mutants and Subcellular Metabolite<br>Distributions Suggests Interplay of the Cellular Compartments for Cysteine Biosynthesis in<br>Arabidopsis. Plant, Cell and Environment, 2008, 32, 349-67. | 2.8 | 69        |
| 22 | Identification of brassinosteroid-related genes by means of transcript co-response analyses. Nucleic Acids Research, 2005, 33, 2685-2696.  | 6.5 | 64        |
| 23 | Assessment of sampling strategies for gas chromatography–mass spectrometry (GC–MS) based metabolomics of cyanobacteria. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 2952-2960.                      | 1.2 | 64        |
| 24 | On the role of the mitochondrial 2-oxoglutarate dehydrogenase complex in amino acid metabolism. Amino Acids, 2013, 44, 683-700.  | 1.2 | 55        |
| 25 | 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        |
| 26 | 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        |
| 27 | Analysis of the compartmentalized metabolome – a validation of the non-aqueous fractionation technique. Frontiers in Plant Science, 2011, 2, 55.   | 1.7 | 49        |
| 28 | Dynamics of lipids and metabolites during the cell cycle of <i>Chlamydomonas reinhardtii</i> Journal, 2017, 92, 331-343.   | 2.8 | 38        |
| 29 | Identification of Enzyme Activity Quantitative Trait Loci in a Solanum lycopersicum × Solanum pennellii Introgression Line Population  Â. Plant Physiology, 2011, 157, 998-1014.   | 2.3 | 36        |
| 30 | Hypothesis-driven approach to predict transcriptional units from gene expression data.<br>Bioinformatics, 2004, 20, 1928-1939.   | 1.8 | 33        |
| 31 | Sample amount alternatives for data adjustment in comparative cyanobacterial metabolomics.<br>Analytical and Bioanalytical Chemistry, 2011, 399, 3503-3517.  | 1.9 | 32        |
| 32 | 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        |
| 33 | Methods, applications and concepts of metabolite profiling: Primary metabolism., 2007, 97, 171-194.  |     | 25        |
| 34 | 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        |
| 35 | 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        |
| 36 | Bioinformatics Tools to Discover Co-Expressed Genes in Plants. , 0, , 307-335.   |     | 1         |