# Bjrn Usadel

## List of Publications by Citations

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|---|---|
| 152 papers | 39,705 citations |
| 64 h-index | 159 g-index |
| 159 ext. papers | 57,012 ext. citations |
| 7.5 avg, IF | 8.07 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 152 | Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*, **2014**, 30, 2114-20 | 7.2 | 24714 |
| 151 | GMD@CSB.DB: the Golm Metabolome Database. *Bioinformatics*, **2005**, 21, 1635-8 | 7.2 | 1064 |
| 150 | RobiNA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. *Nucleic Acids Research*, **2012**, 40, W622-7 | 20.1 | 614 |
| 149 | Sugars and circadian regulation make major contributions to the global regulation of diurnal gene expression in Arabidopsis. *Plant Cell*, **2005**, 17, 3257-81 | 11.6 | 521 |
| 148 | Extension of the visualization tool MapMan to allow statistical analysis of arrays, display of corresponding genes, and comparison with known responses. *Plant Physiology*, **2005**, 138, 1195-204 | 6.6 | 514 |
| 147 | Genome-wide reprogramming of metabolism and regulatory networks of Arabidopsis in response to phosphorus. *Plant, Cell and Environment*, **2007**, 30, 85-112 | 8.4 | 447 |
| 146 | A guide to using MapMan to visualize and compare Omics data in plants: a case study in the crop species, Maize. *Plant, Cell and Environment*, **2009**, 32, 1211-29 | 8.4 | 398 |
| 145 | Starch as a major integrator in the regulation of plant growth. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 10348-53 | 11.5 | 381 |
| 144 | Mercator: a fast and simple web server for genome scale functional annotation of plant sequence data. *Plant, Cell and Environment*, **2014**, 37, 1250-8 | 8.4 | 373 |
| 143 | Co-expression tools for plant biology: opportunities for hypothesis generation and caveats. *Plant, Cell and Environment*, **2009**, 32, 1633-51 | 8.4 | 373 |
| 142 | Integrated analysis of metabolite and transcript levels reveals the metabolic shifts that underlie tomato fruit development and highlight regulatory aspects of metabolic network behavior. *Plant Physiology*, **2006**, 142, 1380-96 | 6.6 | 361 |
| 141 | PageMan: an interactive ontology tool to generate, display, and annotate overview graphs for profiling experiments. *BMC Bioinformatics*, **2006**, 7, 535 | 3.6 | 276 |
| 140 | The genome of the stress-tolerant wild tomato species Solanum pennellii. *Nature Genetics*, **2014**, 46, 1034-8 | 36.3 | 269 |
| 139 | Integration of metabolite with transcript and enzyme activity profiling during diurnal cycles in Arabidopsis rosettes. *Genome Biology*, **2006**, 7, R76 | 18.3 | 269 |
| 138 | Global transcript levels respond to small changes of the carbon status during progressive exhaustion of carbohydrates in Arabidopsis rosettes. *Plant Physiology*, **2008**, 146, 1834-61 | 6.6 | 262 |
| 137 | Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, E2655-62 | 11.5 | 260 |
| 136 | Quantitation in mass-spectrometry-based proteomics. *Annual Review of Plant Biology*, **2010**, 61, 491-516 | 30.7 | 257 |

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| 135 | Systems biology of tomato fruit development: combined transcript, protein, and metabolite analysis of tomato transcription factor (nor, rin) and ethylene receptor (Nr) mutants reveals novel regulatory interactions. *Plant Physiology*, **2011**, 157, 405-25 | 6.6 | 245 |
| 134 | PlaNet: combined sequence and expression comparisons across plant networks derived from seven species. *Plant Cell*, **2011**, 23, 895-910 | 11.6 | 245 |
| 133 | Arabidopsis and primary photosynthetic metabolism - more than the icing on the cake. *Plant Journal*, **2010**, 61, 1067-91 | 6.9 | 240 |
| 132 | Reprogramming a maize plant: transcriptional and metabolic changes induced by the fungal biotroph Ustilago maydis. *Plant Journal*, **2008**, 56, 181-195 | 6.9 | 235 |
| 131 | Temporal responses of transcripts, enzyme activities and metabolites after adding sucrose to carbon-deprived Arabidopsis seedlings. *Plant Journal*, **2007**, 49, 463-91 | 6.9 | 234 |
| 130 | Ribosome and transcript copy numbers, polysome occupancy and enzyme dynamics in Arabidopsis. *Molecular Systems Biology*, **2009**, 5, 314 | 12.2 | 229 |
| 129 | Barley grain maturation and germination: metabolic pathway and regulatory network commonalities and differences highlighted by new MapMan/PageMan profiling tools. *Plant Physiology*, **2008**, 146, 1738-58 | 6.6 | 222 |
| 128 | Regulatory features underlying pollination-dependent and -independent tomato fruit set revealed by transcript and primary metabolite profiling. *Plant Cell*, **2009**, 21, 1428-52 | 11.6 | 200 |
| 127 | RNA interference of LIN5 in tomato confirms its role in controlling Brix content, uncovers the influence of sugars on the levels of fruit hormones, and demonstrates the importance of sucrose cleavage for normal fruit development and fertility. *Plant Physiology*, **2009**, 150, 1204-18 | 6.6 | 185 |
| 126 | Antisense inhibition of the iron-sulphur subunit of succinate dehydrogenase enhances photosynthesis and growth in tomato via an organic acid-mediated effect on stomatal aperture. *Plant Cell*, **2011**, 23, 600-27 | 11.6 | 179 |
| 125 | Mapping metabolic and transcript temporal switches during germination in rice highlights specific transcription factors and the role of RNA instability in the germination process. *Plant Physiology*, **2009**, 149, 961-80 | 6.6 | 171 |
| 124 | Rapid structural phenotyping of plant cell wall mutants by enzymatic oligosaccharide fingerprinting. *Plant Physiology*, **2002**, 130, 1754-63 | 6.6 | 171 |
| 123 | Multilevel genomic analysis of the response of transcripts, enzyme activities and metabolites in Arabidopsis rosettes to a progressive decrease of temperature in the non-freezing range. *Plant, Cell and Environment*, **2008**, 31, 518-47 | 8.4 | 162 |
| 122 | Analysis of expressed sequence tags from Actinidia: applications of a cross species EST database for gene discovery in the areas of flavor, health, color and ripening. *BMC Genomics*, **2008**, 9, 351 | 4.5 | 154 |
| 121 | MapMan4: A Refined Protein Classification and Annotation Framework Applicable to Multi-Omics Data Analysis. *Molecular Plant*, **2019**, 12, 879-892 | 14.4 | 148 |
| 120 | Tomato facultative parthenocarpy results from SlAGAMOUS-LIKE 6 loss of function. *Plant Biotechnology Journal*, **2017**, 15, 634-647 | 11.6 | 147 |
| 119 | CSB.DB: a comprehensive systems-biology database. *Bioinformatics*, **2004**, 20, 3647-51 | 7.2 | 145 |
| 118 | The art of growing plants for experimental purposes: a practical guide for the plant biologist. *Functional Plant Biology*, **2012**, 39, 821-838 | 2.7 | 144 |

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| 99 | The lipopolysaccharide of Sinorhizobium meliloti suppresses defense-associated gene expression in cell cultures of the host plant Medicago truncatula. *Plant Physiology*, **2007**, 143, 825-37 | 6.6 | 86 |
| 98 | A topological map of the compartmentalized Arabidopsis thaliana leaf metabolome. *PLoS ONE*, **2011**, 6, e17806 | 3.7 | 84 |
| 97 | Measures for interoperability of phenotypic data: minimum information requirements and formatting. *Plant Methods*, **2016**, 12, 44 | 5.8 | 83 |
| 96 | Starting to gel: how Arabidopsis seed coat epidermal cells produce specialized secondary cell walls. *International Journal of Molecular Sciences*, **2015**, 16, 3452-73 | 6.3 | 79 |
| 95 | Footprints of parasitism in the genome of the parasitic flowering plant Cuscuta campestris. *Nature Communications*, **2018**, 9, 2515 | 17.4 | 79 |
| 94 | Interoperability with Moby 1.0--it@ better than sharing your toothbrush!. *Briefings in Bioinformatics*, **2008**, 9, 220-31 | 13.4 | 73 |
| 93 | Genome-Wide Analysis of Yield in Europe: Allelic Effects Vary with Drought and Heat Scenarios. *Plant Physiology*, **2016**, 172, 749-764 | 6.6 | 72 |
| 92 | Antisense inhibition of the 2-oxoglutarate dehydrogenase complex in tomato demonstrates its importance for plant respiration and during leaf senescence and fruit maturation. *Plant Cell*, **2012**, 24, 2328-51 | 11.6 | 71 |
| 91 | Description and applications of a rapid and sensitive non-radioactive microplate-based assay for maximum and initial activity of D-ribulose-1,5-bisphosphate carboxylase/oxygenase. *Plant, Cell and Environment*, **2007**, 30, 1163-75 | 8.4 | 70 |
| 90 | GoMapMan: integration, consolidation and visualization of plant gene annotations within the MapMan ontology. *Nucleic Acids Research*, **2014**, 42, D1167-75 | 20.1 | 69 |
| 89 | The Multifaceted Role of Pectin Methylesterase Inhibitors (PMEIs). *International Journal of Molecular Sciences*, **2018**, 19, | 6.3 | 69 |
| 88 | Monitoring Polysaccharide Dynamics in the Plant Cell Wall. *Plant Physiology*, **2018**, 176, 2590-2600 | 6.6 | 61 |
| 87 | Highly Branched Xylan Made by IRREGULAR XYLEM14 and MUCILAGE-RELATED21 Links Mucilage to Arabidopsis Seeds. *Plant Physiology*, **2015**, 169, 2481-95 | 6.6 | 55 |
| 86 | An orange ripening mutant links plastid NAD(P)H dehydrogenase complex activity to central and specialized metabolism during tomato fruit maturation. *Plant Cell*, **2010**, 22, 1977-97 | 11.6 | 53 |
| 85 | Adaptation of the MapMan ontology to biotic stress responses: application in solanaceous species. *Plant Methods*, **2007**, 3, 10 | 5.8 | 51 |
| 84 | Identification of RNA-binding Proteins in Macrophages by Interactome Capture. *Molecular and Cellular Proteomics*, **2016**, 15, 2699-714 | 7.6 | 49 |
| 83 | De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant seg8. *Plant Journal*, **2010**, 64, 589-603 | 6.9 | 48 |
| 82 | Gene expression profiling in susceptible interaction of grapevine with its fungal pathogen Eutypa lata: extending MapMan ontology for grapevine. *BMC Plant Biology*, **2009**, 9, 104 | 5.3 | 44 |

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| 81 | Quantitative RT-PCR Platform to Measure Transcript Levels of C and N Metabolism-Related Genes in Durum Wheat: Transcript Profiles in Elevated [CO2] and High Temperature at Different Levels of N Supply. *Plant and Cell Physiology*, **2015**, 56, 1556-73 | 4.9 | 43 |
| 80 | Demethylation of oligogalacturonides by FaPE1 in the fruits of the wild strawberry Fragaria vesca triggers metabolic and transcriptional changes associated with defence and development of the fruit. *Journal of Experimental Botany*, **2011**, 62, 2855-73 | 7 | 43 |
| 79 | Enabling reusability of plant phenomic datasets with MIAPPE 1.1. *New Phytologist*, **2020**, 227, 260-273 | 9.8 | 42 |
| 78 | Algorithm-driven artifacts in median polish summarization of microarray data. *BMC Bioinformatics*, **2010**, 11, 553 | 3.6 | 42 |
| 77 | Genome assembly of wild tea tree DASZ reveals pedigree and selection history of tea varieties. *Nature Communications*, **2020**, 11, 3719 | 17.4 | 41 |
| 76 | Plant genome and transcriptome annotations: from misconceptions to simple solutions. *Briefings in Bioinformatics*, **2018**, 19, 437-449 | 13.4 | 40 |
| 75 | The genetic architecture of photosynthesis and plant growth-related traits in tomato. *Plant, Cell and Environment*, **2018**, 41, 327-341 | 8.4 | 40 |
| 74 | Analysis of plant nucleotide sugars by hydrophilic interaction liquid chromatography and tandem mass spectrometry. *Analytical Biochemistry*, **2014**, 448, 14-22 | 3.1 | 40 |
| 73 | Identification and characterization of a UDP-D-glucuronate 4-epimerase in Arabidopsis. *FEBS Letters*, **2004**, 569, 327-31 | 3.8 | 39 |
| 72 | Xeml Lab: a tool that supports the design of experiments at a graphical interface and generates computer-readable metadata files, which capture information about genotypes, growth conditions, environmental perturbations and sampling strategy. *Plant, Cell and Environment*, **2009**, 32, 1185-200 | 8.4 | 37 |
| 71 | Fluctuating Light Interacts with Time of Day and Leaf Development Stage to Reprogram Gene Expression. *Plant Physiology*, **2019**, 179, 1632-1657 | 6.6 | 36 |
| 70 | Transcriptional wiring of cell wall-related genes in Arabidopsis. *Molecular Plant*, **2009**, 2, 1015-24 | 14.4 | 35 |
| 69 | The FRIABLE1 gene product affects cell adhesion in Arabidopsis. *PLoS ONE*, **2012**, 7, e42914 | 3.7 | 34 |
| 68 | Computational aspects underlying genome to phenome analysis in plants. *Plant Journal*, **2019**, 97, 182-198 | 6.9 | 33 |
| 67 | Monitoring of Plant Protein Post-translational Modifications Using Targeted Proteomics. *Frontiers in Plant Science*, **2018**, 9, 1168 | 6.2 | 32 |
| 66 | The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. *Nucleic Acids Research*, **2012**, 40, D1313-7 | 20.1 | 32 |
| 65 | Early metabolic and transcriptional variations in fruit of natural white-fruited Fragaria vesca genotypes. *Scientific Reports*, **2017**, 7, 45113 | 4.9 | 31 |
| 64 | How to make a tumour: cell type specific dissection of Ustilago maydis-induced tumour development in maize leaves. *New Phytologist*, **2018**, 217, 1681-1695 | 9.8 | 31 |

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| 63 | A Transcriptional and Metabolic Framework for Secondary Wall Formation in Arabidopsis. *Plant Physiology*, **2016**, 172, 1334-1351 | 6.6 | 31 |
| 62 | Identification of enzyme activity quantitative trait loci in a Solanum lycopersicum x Solanum pennellii introgression line population. *Plant Physiology*, **2011**, 157, 998-1014 | 6.6 | 31 |
| 61 | Identification of Key Enzymes for Pectin Synthesis in Seed Mucilage. *Plant Physiology*, **2018**, 178, 1045-1064 | 6.6 | 31 |
| 60 | Transcriptome sequencing and microarray design for functional genomics in the extremophile Arabidopsis relative Thellungiella salsuginea (Eutrema salsugineum). *BMC Genomics*, **2013**, 14, 793 | 4.5 | 30 |
| 59 | An integrative genomics approach for deciphering the complex interactions between ascorbate metabolism and fruit growth and composition in tomato. *Comptes Rendus - Biologies*, **2009**, 332, 1007-21 | 1.4 | 30 |
| 58 | Tomato@ Green Gold: Bioeconomy Potential of Residual Tomato Leaf Biomass as a Novel Source for the Secondary Metabolite Rutin. *ACS Omega*, **2019**, 4, 19071-19080 | 3.9 | 30 |
| 57 | Reverse engineering: a key component of systems biology to unravel global abiotic stress cross-talk. *Frontiers in Plant Science*, **2012**, 3, 294 | 6.2 | 29 |
| 56 | Ethanol inducible expression of a mesophilic cellulase avoids adverse effects on plant development. *Biotechnology for Biofuels*, **2013**, 6, 53 | 7.8 | 28 |
| 55 | Temporal kinetics of the transcriptional response to carbon depletion and sucrose readdition in Arabidopsis seedlings. *Plant, Cell and Environment*, **2016**, 39, 768-86 | 8.4 | 27 |
| 54 | Chloroplast DnaJ-like proteins 3 and 4 (CDJ3/4) from Chlamydomonas reinhardtii contain redox-active Fe-S clusters and interact with stromal HSP70B. *Biochemical Journal*, **2010**, 427, 205-15 | 3.8 | 26 |
| 53 | Cell wall modification in tobacco by differential targeting of recombinant endoglucanase from Trichoderma reesei. *BMC Plant Biology*, **2015**, 15, 54 | 5.3 | 25 |
| 52 | LASSO modeling of the Arabidopsis thaliana seed/seedling transcriptome: a model case for detection of novel mucilage and pectin metabolism genes. *Molecular BioSystems*, **2012**, 8, 2566-74 | | 24 |
| 51 | Overexpression of a pectin methylesterase inhibitor in Arabidopsis thaliana leads to altered growth morphology of the stem and defective organ separation. *Plant Signaling and Behavior*, **2013**, 8, e26464 | 2.5 | 24 |
| 50 | HRE-type genes are regulated by growth-related changes in internal oxygen concentrations during the normal development of potato (Solanum tuberosum) tubers. *Plant and Cell Physiology*, **2011**, 52, 1957-72 | 4.9 | 23 |
| 49 | The Metabolic Signature of Biomass Formation in Barley. *Plant and Cell Physiology*, **2016**, 57, 1943-60 | 4.9 | 23 |
| 48 | Exploiting Natural Variation in Tomato to Define Pathway Structure and Metabolic Regulation of Fruit Polyphenolics in the Lycopersicum Complex. *Molecular Plant*, **2020**, 13, 1027-1046 | 14.4 | 23 |
| 47 | From plant genomes to phenotypes. *Journal of Biotechnology*, **2017**, 261, 46-52 | 3.7 | 22 |
| 46 | Metabolic Adaptation, a Specialized Leaf Organ Structure and Vascular Responses to Diurnal N Fixation by Sustain the Astonishing Productivity of Ferns without Nitrogen Fertilizer. *Frontiers in Plant Science*, **2017**, 8, 442 | 6.2 | 22 |

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| 45 | SLocX: Predicting Subcellular Localization of Arabidopsis Proteins Leveraging Gene Expression Data. *Frontiers in Plant Science*, **2011**, 2, 43 | 6.2 | 22 |
| 44 | One-Step Lignocellulose Fractionation by using 2,5-Furandicarboxylic Acid as a Biogenic and Recyclable Catalyst. *ChemSusChem*, **2018**, 11, 2051-2056 | 8.3 | 22 |
| 43 | Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. *Plant Physiology*, **2019**, 179, 1893-1907 | 6.6 | 21 |
| 42 | GabiPD - The GABI Primary Database integrates plant proteomic data with gene-centric information. *Frontiers in Plant Science*, **2012**, 3, 154 | 6.2 | 21 |
| 41 | De novo sequencing and analysis of the lily pollen transcriptome: an open access data source for an orphan plant species. *Plant Molecular Biology*, **2015**, 87, 69-80 | 4.6 | 20 |
| 40 | Oxford Nanopore sequencing: new opportunities for plant genomics?. *Journal of Experimental Botany*, **2020**, 71, 5313-5322 | 7 | 20 |
| 39 | Streptomyces thermoautotrophicus does not fix nitrogen. *Scientific Reports*, **2016**, 6, 20086 | 4.9 | 20 |
| 38 | Extensive Natural Variation in Arabidopsis Seed Mucilage Structure. *Frontiers in Plant Science*, **2016**, 7, 803 | 6.2 | 20 |
| 37 | Detecting Inconsistencies in Large Biological Networks with Answer Set Programming. *Lecture Notes in Computer Science*, **2008**, 130-144 | 0.9 | 19 |
| 36 | The role of COBRA-LIKE 2 function, as part of the complex network of interacting pathways regulating Arabidopsis seed mucilage polysaccharide matrix organization. *Plant Journal*, **2018**, 94, 497-512 | 6.9 | 17 |
| 35 | Insights into cell wall structure of Sida hermaphrodita and its influence on recalcitrance. *Carbohydrate Polymers*, **2017**, 168, 94-102 | 10.3 | 16 |
| 34 | A comparative analysis of nonhost resistance across the two Triticeae crop species wheat and barley. *BMC Plant Biology*, **2017**, 17, 232 | 5.3 | 16 |
| 33 | On the current status of Phakopsora pachyrhizi genome sequencing. *Frontiers in Plant Science*, **2014**, 5, 377 | 6.2 | 16 |
| 32 | The plant growth promoting substance, lumichrome, mimics starch, and ethylene-associated symbiotic responses in lotus and tomato roots. *Frontiers in Plant Science*, **2012**, 3, 120 | 6.2 | 16 |
| 31 | Large-scale phenotyping of transgenic tobacco plants (Nicotiana tabacum) to identify essential leaf functions. *Plant Biotechnology Journal*, **2008**, 6, 246-63 | 11.6 | 16 |
| 30 | Transcriptome Analysis of Durum Wheat Flag Leaves Provides New Insights Into the Regulatory Response to Elevated CO and High Temperature. *Frontiers in Plant Science*, **2019**, 10, 1605 | 6.2 | 16 |
| 29 | High precision genome sequencing of engineered Gluconobacter oxydans 621H by combining long nanopore and short accurate Illumina reads. *Journal of Biotechnology*, **2017**, 258, 197-205 | 3.7 | 15 |
| 28 | Modeling Protein Destiny in Developing Fruit. *Plant Physiology*, **2019**, 180, 1709-1724 | 6.6 | 15 |

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| 27 | Improving the utilization of lignocellulosic biomass by polysaccharide modification. *Process Biochemistry*, **2016**, 51, 288-296 | 4.8 | 15 |
| 26 | TRM4 is essential for cellulose deposition in Arabidopsis seed mucilage by maintaining cortical microtubule organization and interacting with CESA3. *New Phytologist*, **2019**, 221, 881-895 | 9.8 | 14 |
| 25 | Structure and putative function of NFX1-like proteins in plants. *Plant Biology*, **2010**, 12, 381-94 | 3.7 | 13 |
| 24 | Towards positional isolation of three quantitative trait loci conferring resistance to powdery mildew in two Spanish barley landraces. *PLoS ONE*, **2013**, 8, e67336 | 3.7 | 13 |
| 23 | Isolation of Open Chromatin Identifies Regulators of Systemic Acquired Resistance. *Plant Physiology*, **2019**, 181, 817-833 | 6.6 | 13 |
| 22 | Genotype-phenotype modeling considering intermediate level of biological variation: a case study involving sensory traits, metabolites and QTLs in ripe tomatoes. *Molecular BioSystems*, **2015**, 11, 3101-10 | | 12 |
| 21 | Plant Pathway Databases. *Methods in Molecular Biology*, **2016**, 1374, 71-87 | 1.4 | 11 |
| 20 | Transcriptional co-response analysis as a tool to identify new components of the wall biosynthetic machinery. *Plant Biosystems*, **2005**, 139, 69-73 | 1.6 | 11 |
| 19 | Correlation-maximizing surrogate gene space for visual mining of gene expression patterns in developing barley endosperm tissue. *BMC Bioinformatics*, **2007**, 8, 165 | 3.6 | 10 |
| 18 | RNAseq analysis of Ƀproteobacterium Gluconobacter oxydans 621H. *BMC Genomics*, **2018**, 19, 24 | 4.5 | 9 |
| 17 | Foliose Ulva Species Show Considerable Inter-Specific Genetic Diversity, Low Intra-Specific Genetic Variation, and the Rare Occurrence of Inter-Specific Hybrids in the Wild. *Journal of Phycology*, **2021**, 57, 219-233 | 3 | 9 |
| 16 | Smut infection of perennial hosts: the genome and the transcriptome of the Brassicaceae smut fungus Thecaphora thlaspeos reveal functionally conserved and novel effectors. *New Phytologist*, **2019**, 222, 1474-1492 | 9.8 | 8 |
| 15 | Bioinformatics in the plant genomic and phenomic domain: The German contribution to resources, services and perspectives. *Journal of Biotechnology*, **2017**, 261, 37-45 | 3.7 | 8 |
| 14 | Genetic and molecular characterization of multicomponent resistance of against allicin. *Life Science Alliance*, **2020**, 3, | 5.8 | 8 |
| 13 | Cell type specific transcriptional reprogramming of maize leaves during Ustilago maydis induced tumor formation. *Scientific Reports*, **2019**, 9, 10227 | 4.9 | 7 |
| 12 | The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. *Briefings in Bioinformatics*, **2013**, 14, 548-55 | 13.4 | 7 |
| 11 | Crystal structure and functional characterization of a glucosamine-6-phosphate N-acetyltransferase from Arabidopsis thaliana. *Biochemical Journal*, **2012**, 443, 427-37 | 3.8 | 7 |
| 10 | Transcriptomic and proteomic data in developing tomato fruit. *Data in Brief*, **2020**, 28, 105015 | 1.2 | 7 |

| 9 | The plant transcriptome-from integrating observations to models. *Frontiers in Plant Science*, **2013**, 4, 48 | 6.2 | 6 |
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| 8 | Seed hemicelluloses tailor mucilage properties and salt tolerance. *New Phytologist*, **2021**, 229, 1946-1954 | 9.8 | 4 |
| 7 | Parallel Metabolomic and Transcriptomic Analysis Reveals Key Factors for Quality Improvement of Tea Plants. *Journal of Agricultural and Food Chemistry*, **2020**, 68, 5483-5495 | 5.7 | 2 |
| 6 | Growing Near Net Shape Components from Renewable Materials. *Procedia CIRP*, **2015**, 29, 609-614 | 1.8 | 1 |
| 5 | Tomato leaves under stress: a comparison of stress response to mild abiotic stress between a cultivated and a wild tomato species. *Plant Molecular Biology*, **2021**, 107, 177-206 | 4.6 | 1 |
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| 3 | Hochdurchsatz-Sequenzierung und dann?. *BioSpektrum*, **2013**, 19, 458-460 | 0.1 | |
| 2 | Klassifikation pflanzlicher Genome im Schnelldurchlauf. *BioSpektrum*, **2012**, 18, 277-279 | 0.1 | |
| 1 | Visualisation of Transcriptomics Data in Metabolic Pathways **2010**, 335-342 | | |