Marek Mutwil

List of Publications by Year
in descending order

55 papers	3,483 citations	230014 27 h-index	182931 54 g-index
75 all docs	75 docs citations	75 times ranked	4934 citing authors

#	Article	IF	Citations
1	The *Arabidopsis* electron‑transfer flavoprotein:ubiquinone oxidoreductase is required during normal seed development and germination. Plant Journal, 2022, 109, 196-214.	2.8	6
2	Bacteria.guru: Comparative Transcriptomics and Co-Expression Database for Bacterial Pathogens. Journal of Molecular Biology, 2022, 434, 167380.	2.0	4
3	Protist.guru: A Comparative Transcriptomics Database for Protists. Journal of Molecular Biology, 2022, 434, 167502.	2.0	4
4	Exploiting plant transcriptomic databases: Resources, tools, and approaches. Plant Communications, 2022, 3, 100323.	3.6	20
5	Removing auto-activators from yeast-two-hybrid assays by conditional negative selection. Scientific Reports, 2021, 11, 5477.	1.6	6
6	LSTrAP-Kingdom: an automated pipeline to generate annotated gene expression atlases for kingdoms of life. Bioinformatics, 2021, 37, 3053-3055.	1.8	3
7	Structural landscape of the complete genomes of dengue virus serotypes and other viral hemorrhagic fevers. BMC Genomics, 2021, 22, 352.	1.2	6
8	Comparative transcriptomic analysis reveals conserved programmes underpinning organogenesis and reproduction in land plants. Nature Plants, 2021, 7, 1143-1159.	4.7	61
9	Diurnal.plant.tools: Comparative Transcriptomic and Co-expression Analyses of Diurnal Gene Expression of the Archaeplastida Kingdom. Plant and Cell Physiology, 2020, 61, 212-220.	1.5	11
10	Malaria.tools—comparative genomic and transcriptomic database for Plasmodium species. Nucleic Acids Research, 2020, 48, D768-D775.	6.5	15
11	Inferring biosynthetic and gene regulatory networks from Artemisia annua RNA sequencing data on a credit card-sized ARM computer. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2020, 1863, 194429.	0.9	12
12	Gene expression analysis of *Cyanophora paradoxa* reveals conserved abiotic stress responses between basal algae and flowering plants. New Phytologist, 2020, 225, 1562-1577.	3.5	10
13	Transcriptomic and Proteomic Insights into *Amborella trichopoda* Male Gametophyte Functions. Plant Physiology, 2020, 184, 1640-1657.	2.3	7
14	LSTrAP-Crowd: prediction of novel components of bacterial ribosomes with crowd-sourced analysis of RNA sequencing data. BMC Biology, 2020, 18, 114.	1.7	8
15	Fungi.guru: Comparative genomic and transcriptomic resource for the fungi kingdom. Computational and Structural Biotechnology Journal, 2020, 18, 3788-3795.	1.9	8
16	Computational approaches to unravel the pathways and evolution of specialized metabolism. Current Opinion in Plant Biology, 2020, 55, 38-46.	3.5	22
17	Expression Atlas of *Selaginella moellendorffii* Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. Plant Cell, 2020, 32, 853-870.	3.1	39
18	LSTrAP-Cloud: A User-Friendly Cloud Computing Pipeline to Infer Coexpression Networks. Genes, 2020, 11, 428.	1.0	12

#	ARTICLE	IF	CITATIONS
19	Using Gene Expression to Study Specialized Metabolismâ€"A Practical Guide. Frontiers in Plant Science, 2020, 11, 625035.	1.7	24
20	Transcriptomics of manually isolated Amborella trichopoda egg apparatus cells. Plant Reproduction, 2019, 32, 15-27.	1.3	16
21	Analysis of an improved Cyanophora paradoxa genome assembly. DNA Research, 2019, 26, 287-299.	1.5	35
22	Cellulose Synthesis â€" Central Components and Their Evolutionary Relationships. Trends in Plant Science, 2019, 24, 402-412.	4.3	62
23	Appropriate Thiamin Pyrophosphate Levels Are Required for Acclimation to Changes in Photoperiod. Plant Physiology, 2019, 180, 185-197.	2.3	24
24	Kingdom-wide comparison reveals the evolution of diurnal gene expression in Archaeplastida. Nature Communications, 2019, 10, 737.	5.8	52
25	The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17081-17089.	3.3	134
26	PhytoNet: comparative co-expression network analyses across phytoplankton and land plants. Nucleic Acids Research, 2018, 46, W76-W83.	6.5	16
27	CoNekT: an open-source framework for comparative genomic and transcriptomic network analyses. Nucleic Acids Research, 2018, 46, W133-W140.	6.5	81
28	Ensemble gene function prediction database reveals genes important for complex I formation in <i>Arabidopsis thaliana</i>. New Phytologist, 2018, 217, 1521-1534.	3.5	27
29	<i>AtRsgA</i> from <i>Arabidopsis thaliana</i> is important for maturation of the small subunit of the chloroplast ribosome. Plant Journal, 2018, 96, 404-420.	2.8	9
30	Beyond Genomics: Studying Evolution with Gene Coexpression Networks. Trends in Plant Science, 2017, 22, 298-307.	4.3	96
31	Phylogenomic analysis of gene coâ€expression networks reveals the evolution of functional modules. Plant Journal, 2017, 90, 447-465.	2.8	97
32	Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in <i>Brachypodium distachyon</i>. New Phytologist, 2017, 215, 1009-1025.	3.5	108
33	PlaNet: Comparative Co-Expression Network Analyses for Plants. Methods in Molecular Biology, 2017, 1533, 213-227.	0.4	42
34	Revisiting ancestral polyploidy in plants. Science Advances, 2017, 3, e1603195.	4.7	73
35	LSTrAP: efficiently combining RNA sequencing data into co-expression networks. BMC Bioinformatics, 2017, 18, 444.	1.2	35
36	Combined Use of Genome-Wide Association Data and Correlation Networks Unravels Key Regulators of Primary Metabolism in Arabidopsis thaliana. PLoS Genetics, 2016, 12, e1006363.	1.5	67

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37	FamNet: A Framework to Identify Multiplied Modules Driving Pathway Expansion in Plants. Plant Physiology, 2016, 170, 1878-1894.	2.3	63
38	Tools of the trade: studying molecular networks in plants. Current Opinion in Plant Biology, 2016, 30, 143-150.	3.5	31
39	Salt-Related MYB1 Coordinates Abscisic Acid Biosynthesis and Signaling during Salt Stress in Arabidopsis. Plant Physiology, 2015, 169, 1027-1041.	2.3	66
40	Elucidating gene function and function evolution through comparison of co-expression networks of plants. Frontiers in Plant Science, 2014, 5, 394.	1.7	77
41	Towards revealing the functions of all genes in plants. Trends in Plant Science, 2014, 19, 212-221.	4.3	221
42	Molecular Biology of Lignification in Grasses. Advances in Botanical Research, 2012, , 77-112.	0.5	9
43	Inferring gene functions through dissection of relevance networks: interleaving the intra- and inter-species views. Molecular BioSystems, 2012, 8, 2233.	2.9	9
44	Large-Scale Co-Expression Approach to Dissect Secondary Cell Wall Formation Across Plant Species. Frontiers in Plant Science, 2011, 2, 23.	1.7	127
45	Diverging functions among calreticulin isoforms in higher plants. Plant Signaling and Behavior, 2011, 6, 905-910.	1.2	19
46	Toward the Storage Metabolome: Profiling the Barley Vacuole Â Â. Plant Physiology, 2011, 157, 1469-1482.	2.3	92
47	PlaNet: Combined Sequence and Expression Comparisons across Plant Networks Derived from Seven Species Â. Plant Cell, 2011, 23, 895-910.	3.1	297
48	ANALYZING GENE COEXPRESSION DATA BY AN EVOLUTIONARY MODEL. , 2010, , .		0
49	Assembly of an Interactive Correlation Network for the Arabidopsis Genome Using a Novel Heuristic Clustering Algorithm Â. Plant Physiology, 2009, 152, 29-43.	2.3	174
50	Transcriptional Wiring of Cell Wall-Related Genes in Arabidopsis. Molecular Plant, 2009, 2, 1015-1024.	3.9	60
51	Coâ€expression tools for plant biology: opportunities for hypothesis generation and caveats. Plant, Cell and Environment, 2009, 32, 1633-1651.	2.8	480
52	Cellulose synthesis: a complex complex. Current Opinion in Plant Biology, 2008, 11, 252-257.	3.5	152
53	Laying down the bricks: logistic aspects of cell wall biosynthesis. Current Opinion in Plant Biology, 2008, 11, 647-652.	3.5	45
54	Functional Analysis of the Cellulose Synthase-Like Genes <i>CSLD1</i>, <i>CSLD2</i>, and <i>CSLD4</i> in Tip-Growing Arabidopsis Cells. Plant Physiology, 2008, 148, 1238-1253.	2.3	142

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55	GeneCATâ€"novel webtools that combine BLAST and co-expression analyses. Nucleic Acids Research, 2008, 36, W320-W326.	6.5	139