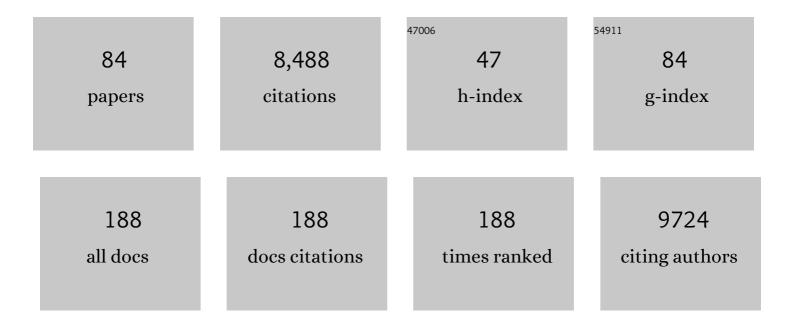
## Julin N Maloof

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7000136/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Flower orientation influences floral temperature, pollinator visits and plant fitness. New Phytologist, 2021, 232, 868-879.	7.3	22
2	Leaf shape is a predictor of fruit quality and cultivar performance in tomato. New Phytologist, 2020, 226, 851-865.	7.3	38
3	Multiple Loci Control Variation in Plasticity to Foliar Shade Throughout Development in <i>Arabidopsis thaliana</i> . G3: Genes, Genomes, Genetics, 2020, 10, 4103-4114.	1.8	1
4	Retrograde Induction of phyB Orchestrates Ethylene-Auxin Hierarchy to Regulate Growth. Plant Physiology, 2020, 183, 1268-1280.	4.8	27
5	The foxtail millet ( <i>Setaria italica</i> ) terpene synthase gene family. Plant Journal, 2020, 103, 781-800.	5.7	25
6	MYCs and PIFs Act Independently in Arabidopsis Growth Regulation. G3: Genes, Genomes, Genetics, 2020, 10, 1797-1807.	1.8	6
7	Integrating transcriptomic network reconstruction and eQTL analyses reveals mechanistic connections between genomic architecture and Brassica rapa development. PLoS Genetics, 2019, 15, e1008367.	3.5	15
8	Tissue-Specific Transcriptome Analysis Reveals Candidate Genes for Terpenoid and Phenylpropanoid Metabolism in the Medicinal Plant <i>Ferula assafoetida</i> . G3: Genes, Genomes, Genetics, 2019, 9, 807-816.	1.8	25
9	Multi-level Modulation of Light Signaling by GIGANTEA Regulates Both the Output and Pace of the Circadian Clock. Developmental Cell, 2019, 49, 840-851.e8.	7.0	53
10	The role of a class <scp>III</scp> gibberellin 2â€oxidase in tomato internode elongation. Plant Journal, 2019, 97, 603-615.	5.7	28
11	Integrated QTL and eQTL Mapping Provides Insights and Candidate Genes for Fatty Acid Composition, Flowering Time, and Growth Traits in a F2 Population of a Novel Synthetic Allopolyploid Brassica napus. Frontiers in Plant Science, 2018, 9, 1632.	3.6	25
12	Network Analysis Reveals a Role for Salicylic Acid Pathway Components in Shade Avoidance. Plant Physiology, 2018, 178, 1720-1732.	4.8	24
13	Quantifying time-series of leaf morphology using 2D and 3D photogrammetry methods for high-throughput plant phenotyping. Computers and Electronics in Agriculture, 2017, 135, 222-232.	7.7	51
14	The Generation of Doubled Haploid Lines for QTL Mapping. Methods in Molecular Biology, 2017, 1610, 39-57.	0.9	6
15	Using RNA-Seq for Genomic Scaffold Placement, Correcting Assemblies, and Genetic Map Creation in a Common <i>Brassica rapa</i> Mapping Population. G3: Genes, Genomes, Genetics, 2017, 7, 2259-2270.	1.8	15
16	Circadian rhythms vary over the growing season and correlate with fitness components. Molecular Ecology, 2017, 26, 5528-5540.	3.9	35
17	The Divergence of Flowering Time Modulated by FT/TFL1 Is Independent to Their Interaction and Binding Activities. Frontiers in Plant Science, 2017, 8, 697.	3.6	24
18	Morphological Plant Modeling: Unleashing Geometric and Topological Potential within the Plant Sciences. Frontiers in Plant Science, 2017, 8, 900.	3.6	61

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19	The Quantitative Basis of the Arabidopsis Innate Immune System to Endemic Pathogens Depends on Pathogen Genetics. PLoS Genetics, 2016, 12, e1005789.	3.5	83
20	Tomato phyE Is Required for Shade Avoidance in the Absence of phyB1 and phyB2. Frontiers in Plant Science, 2016, 7, 1275.	3.6	22
21	Plant high-throughput phenotyping using photogrammetry and imaging techniques to measure leaf length and rosette area. Computers and Electronics in Agriculture, 2016, 127, 376-394.	7.7	63
22	Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. Plant Cell, 2016, 28, 2889-2904.	6.6	128
23	A New Advanced Backcross Tomato Population Enables High Resolution Leaf QTL Mapping and Gene Identification. G3: Genes, Genomes, Genetics, 2016, 6, 3169-3184.	1.8	36
24	Plant phenotyping using multi-view stereo vision with structured lights. Proceedings of SPIE, 2016, , .	0.8	6
25	eQTL Regulating Transcript Levels Associated with Diverse Biological Processes in Tomato. Plant Physiology, 2016, 172, 328-340.	4.8	87
26	Genetic architecture, biochemical underpinnings and ecological impact of floral <scp>UV</scp> patterning. Molecular Ecology, 2016, 25, 1122-1140.	3.9	24
27	Domestication selected for deceleration of the circadian clock in cultivated tomato. Nature Genetics, 2016, 48, 89-93.	21.4	165
28	Molecular control of crop shade avoidance. Current Opinion in Plant Biology, 2016, 30, 151-158.	7.1	96
29	<i>YUCCA</i> auxin biosynthetic genes are required for Arabidopsis shade avoidance. PeerJ, 2016, 4, e2574.	2.0	68
30	Modeling development and quantitative trait mapping reveal independent genetic modules for leaf size and shape. New Phytologist, 2015, 208, 257-268.	7.3	41
31	Structured Light-Based 3D Reconstruction System for Plants. Sensors, 2015, 15, 18587-18612.	3.8	129
32	GLO-Roots: an imaging platform enabling multidimensional characterization of soil-grown root systems. ELife, 2015, 4, .	6.0	212
33	Light-induced indeterminacy alters shade avoiding tomato leaf morphology. Plant Physiology, 2015, 169, pp.01229.2015.	4.8	49
34	Reassess the <i>t</i> Test: Interact with All Your Data via ANOVA. Plant Cell, 2015, 27, 2088-2094.	6.6	48
35	Shade Avoidance Components and Pathways in Adult Plants Revealed by Phenotypic Profiling. PLoS Genetics, 2015, 11, e1004953.	3.5	76
36	Resolving Distinct Genetic Regulators of Tomato Leaf Shape within a Heteroblastic and Ontogenetic Context. Plant Cell, 2014, 26, 3616-3629.	6.6	75

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37	A Modern Ampelography: A Genetic Basis for Leaf Shape and Venation Patterning in Grape. Plant Physiology, 2014, 164, 259-272.	4.8	233
38	New Arabidopsis Advanced Intercross Recombinant Inbred Lines Reveal Female Control of Nonrandom Mating. Plant Physiology, 2014, 165, 175-185.	4.8	21
39	Polymorphism Identification and Improved Genome Annotation of <i>Brassica rapa</i> Through Deep RNA Sequencing. G3: Genes, Genomes, Genetics, 2014, 4, 2065-2078.	1.8	29
40	Evolutionary developmental transcriptomics reveals a gene network module regulating interspecific diversity in plant leaf shape. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2616-21.	7.1	178
41	The genome of the stress-tolerant wild tomato species Solanum pennellii. Nature Genetics, 2014, 46, 1034-1038.	21.4	391
42	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.	7.1	325
43	Fine genetic mapping of RXopI4, a bacterial spot disease resistance locus from Solanum pennellii LA716. Theoretical and Applied Genetics, 2013, 126, 601-609.	3.6	51
44	Leaf]: An ImageJ Plugin for Semi-automated Leaf Shape Measurement. Journal of Visualized Experiments, 2013, , .	0.3	52
45	Dynamic Transcriptomic Profiles between Tomato and a Wild Relative Reflect Distinct Developmental Architectures   Â. Plant Physiology, 2013, 162, 537-552.	4.8	41
46	A Quantitative Genetic Basis for Leaf Morphology in a Set of Precisely Defined Tomato Introgression Lines. Plant Cell, 2013, 25, 2465-2481.	6.6	209
47	Identification of Novel Loci Regulating Interspecific Variation in Root Morphology and Cellular Development in Tomato  Â. Plant Physiology, 2013, 162, 755-768.	4.8	68
48	The Developmental Trajectory of Leaflet Morphology in Wild Tomato Species  Â. Plant Physiology, 2012, 158, 1230-1240.	4.8	85
49	A Genome-Wide Association Study Identifies Variants Underlying the Arabidopsis thaliana Shade Avoidance Response. PLoS Genetics, 2012, 8, e1002589.	3.5	95
50	A High-Throughput Method for Illumina RNA-Seq Library Preparation. Frontiers in Plant Science, 2012, 3, 202.	3.6	145
51	Rapid creation of <i>Arabidopsis</i> doubled haploid lines for quantitative trait locus mapping. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4227-4232.	7.1	68
52	Native Environment Modulates Leaf Size and Response to Simulated Foliar Shade across Wild Tomato Species. PLoS ONE, 2012, 7, e29570.	2.5	54
53	BBX32, an Arabidopsis B-Box Protein, Functions in Light Signaling by Suppressing HY5-Regulated Gene Expression and Interacting with STH2/BBX21 Â. Plant Physiology, 2011, 156, 2109-2123.	4.8	140
54	PIF Genes Mediate the Effect of Sucrose on Seedling Growth Dynamics. PLoS ONE, 2011, 6, e19894.	2.5	92

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55	COP1-Mediated Degradation of BBX22/LZF1 Optimizes Seedling Development in Arabidopsis  Â. Plant Physiology, 2011, 156, 228-239.	4.8	102
56	Genomic Analysis of Circadian Clock-, Light-, and Growth-Correlated Genes Reveals PHYTOCHROME-INTERACTING FACTOR5 as a Modulator of Auxin Signaling in Arabidopsis   Â. Plant Physiology, 2011, 156, 357-372.	4.8	136
57	Network Quantitative Trait Loci Mapping of Circadian Clock Outputs Identifies Metabolic Pathway-to-Clock Linkages in <i>Arabidopsis</i> Â Â. Plant Cell, 2011, 23, 471-485.	6.6	139
58	Circadian oscillation of gibberellin signaling in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9292-9297.	7.1	131
59	Phytochromes inhibit hypocotyl negative gravitropism by regulating the development of endodermal amyloplasts through phytochrome-interacting factors. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1729-1734.	7.1	88
60	Genomic Analysis of QTLs and Genes Altering Natural Variation in Stochastic Noise. PLoS Genetics, 2011, 7, e1002295.	3.5	107
61	Genes underlying quantitative variation in ecologically important traits: <i>PIF4</i> ( <i>PHYTOCHROME) Tj ETQq1 set in<i>Arabidopsis thaliana</i>. Molecular Ecology, 2010, 19, 1187-1199.</i>	1 0.78431 3.9	l4 rgBT /Ove 43
62	Network Analysis Identifies ELF3 as a QTL for the Shade Avoidance Response in Arabidopsis. PLoS Genetics, 2010, 6, e1001100.	3.5	120
63	Floral Genetic Architecture: An Examination of QTL Architecture Underlying Floral (Co)Variation Across Environments. Genetics, 2010, 186, 1451-1465.	2.9	27
64	Recent advances in regulation of flowering. F1000 Biology Reports, 2010, 2, .	4.0	2
65	Cis-regulatory Changes at FLOWERING LOCUS T Mediate Natural Variation in Flowering Responses of Arabidopsis thaliana. Genetics, 2009, 183, 723-732.	2.9	109
66	Sequence diversity in three tomato species: SNPs, markers, and molecular evolution. BMC Plant Biology, 2009, 9, 85.	3.6	44
67	QTL Mapping in New Arabidopsis thaliana Advanced Intercross-Recombinant Inbred Lines. PLoS ONE, 2009, 4, e4318.	2.5	92
68	Global transcriptome analysis reveals circadian regulation of key pathways in plant growth and development. Genome Biology, 2008, 9, R130.	9.6	677
69	Amino acid polymorphisms in <i>Arabidopsis</i> phytochrome B cause differential responses to light. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3157-3162.	7.1	97
70	Rhythmic growth explained by coincidence between internal and external cues. Nature, 2007, 448, 358-361.	27.8	599
71	ANTAGONISTIC MULTILEVEL SELECTION ON SIZE AND ARCHITECTURE IN VARIABLE DENSITY SETTINGS. Evolution; International Journal of Organic Evolution, 2007, 61, 58-67.	2.3	41
72	Diurnal regulation of plant growth*. Plant, Cell and Environment, 2006, 29, 396-408.	5.7	107

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73	The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of Arabidopsis thaliana. Nature Genetics, 2006, 38, 711-715.	21.4	191
74	An Internal Motor Kinesin Is Associated with the Golgi Apparatus and Plays a Role in Trichome Morphogenesis in Arabidopsis. Molecular Biology of the Cell, 2005, 16, 811-823.	2.1	147
75	Light-Response Quantitative Trait Loci Identified with Composite Interval and eXtreme Array Mapping in Arabidopsis thalianaSequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY394847 and AY466496 Genetics, 2004, 167, 907-917.	2.9	83
76	Plant Development: Slowing Root Growth Naturally. Current Biology, 2004, 14, R395-R396.	3.9	6
77	QTL for plant growth and morphology. Current Opinion in Plant Biology, 2003, 6, 85-90.	7.1	53
78	Genomic approaches to analyzing natural variation in Arabidopsis thaliana. Current Opinion in Genetics and Development, 2003, 13, 576-582.	3.3	37
79	Building Integrated Models of Plant Growth and Development. Plant Physiology, 2003, 132, 436-439.	4.8	22
80	The extent of linkage disequilibrium in Arabidopsis thaliana. Nature Genetics, 2002, 30, 190-193.	21.4	425
81	Quantitative Trait Loci Controlling Light and Hormone Response in Two Accessions of <i>Arabidopsis thaliana</i> . Genetics, 2002, 160, 683-696.	2.9	127
82	Three Redundant Brassinosteroid Early Response Genes Encode Putative bHLH Transcription Factors Required for Normal Growth. Genetics, 2002, 162, 1445-1456.	2.9	259
83	Natural variation in light sensitivity of Arabidopsis. Nature Genetics, 2001, 29, 441-446.	21.4	261
84	Natural variation in phytochrome signaling. Seminars in Cell and Developmental Biology, 2000, 11, 523-530.	5.0	32