

# Julin N Maloof

## List of Publications by Year in descending order

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84  
papers

8,488  
citations

53939

47  
h-index

62345

84  
g-index

188  
all docs

188  
docs citations

188  
times ranked

10802  
citing authors

#	ARTICLE	IF	CITATIONS
1	Flower orientation influences floral temperature, pollinator visits and plant fitness. <i>New Phytologist</i> , 2021, 232, 868-879.	3.5	22
2	Leaf shape is a predictor of fruit quality and cultivar performance in tomato. <i>New Phytologist</i> , 2020, 226, 851-865.	3.5	38
3	Multiple Loci Control Variation in Plasticity to Foliar Shade Throughout Development in <i>Arabidopsis thaliana</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4103-4114.	0.8	1
4	Retrograde Induction of phyB Orchestrates Ethylene-Auxin Hierarchy to Regulate Growth. <i>Plant Physiology</i> , 2020, 183, 1268-1280.	2.3	27
5	The foxtail millet ( <i>Setaria italica</i> ) terpene synthase gene family. <i>Plant Journal</i> , 2020, 103, 781-800.	2.8	25
6	MYCs and PIFs Act Independently in Arabidopsis Growth Regulation. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1797-1807.	0.8	6
7	Integrating transcriptomic network reconstruction and eQTL analyses reveals mechanistic connections between genomic architecture and Brassica rapa development. <i>PLoS Genetics</i> , 2019, 15, e1008367.	1.5	15
8	Tissue-Specific Transcriptome Analysis Reveals Candidate Genes for Terpenoid and Phenylpropanoid Metabolism in the Medicinal Plant <i>Ferula assafoetida</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 807-816.	0.8	25
9	Multi-level Modulation of Light Signaling by GIGANTEA Regulates Both the Output and Pace of the Circadian Clock. <i>Developmental Cell</i> , 2019, 49, 840-851.e8.	3.1	53
10	The role of a class III gibberellin oxidase in tomato internode elongation. <i>Plant Journal</i> , 2019, 97, 603-615.	2.8	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. <i>Frontiers in Plant Science</i> , 2018, 9, 1632.	1.7	25
12	Network Analysis Reveals a Role for Salicylic Acid Pathway Components in Shade Avoidance. <i>Plant Physiology</i> , 2018, 178, 1720-1732.	2.3	24
13	Quantifying time-series of leaf morphology using 2D and 3D photogrammetry methods for high-throughput plant phenotyping. <i>Computers and Electronics in Agriculture</i> , 2017, 135, 222-232.	3.7	51
14	The Generation of Doubled Haploid Lines for QTL Mapping. <i>Methods in Molecular Biology</i> , 2017, 1610, 39-57.	0.4	6
15	Using RNA-Seq for Genomic Scaffold Placement, Correcting Assemblies, and Genetic Map Creation in a Common Brassica rapa Mapping Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2259-2270.	0.8	15
16	Circadian rhythms vary over the growing season and correlate with fitness components. <i>Molecular Ecology</i> , 2017, 26, 5528-5540.	2.0	35
17	The Divergence of Flowering Time Modulated by FT/TFL1 Is Independent to Their Interaction and Binding Activities. <i>Frontiers in Plant Science</i> , 2017, 8, 697.	1.7	24
18	Morphological Plant Modeling: Unleashing Geometric and Topological Potential within the Plant Sciences. <i>Frontiers in Plant Science</i> , 2017, 8, 900.	1.7	61

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19	The Quantitative Basis of the Arabidopsis Innate Immune System to Endemic Pathogens Depends on Pathogen Genetics. <i>PLoS Genetics</i> , 2016, 12, e1005789.	1.5	83
20	Tomato phyE Is Required for Shade Avoidance in the Absence of phyB1 and phyB2. <i>Frontiers in Plant Science</i> , 2016, 7, 1275.	1.7	22
21	Plant high-throughput phenotyping using photogrammetry and imaging techniques to measure leaf length and rosette area. <i>Computers and Electronics in Agriculture</i> , 2016, 127, 376-394.	3.7	63
22	Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. <i>Plant Cell</i> , 2016, 28, 2889-2904.	3.1	128
23	A New Advanced Backcross Tomato Population Enables High Resolution Leaf QTL Mapping and Gene Identification. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3169-3184.	0.8	36
24	Plant phenotyping using multi-view stereo vision with structured lights. <i>Proceedings of SPIE</i> , 2016, , .	0.8	6
25	eQTL Regulating Transcript Levels Associated with Diverse Biological Processes in Tomato. <i>Plant Physiology</i> , 2016, 172, 328-340.	2.3	87
26	Genetic architecture, biochemical underpinnings and ecological impact of floral <sc>UV</sc> patterning. <i>Molecular Ecology</i> , 2016, 25, 1122-1140.	2.0	24
27	Domestication selected for deceleration of the circadian clock in cultivated tomato. <i>Nature Genetics</i> , 2016, 48, 89-93.	9.4	165
28	Molecular control of crop shade avoidance. <i>Current Opinion in Plant Biology</i> , 2016, 30, 151-158.	3.5	96
29	<i>YUCCA</i> auxin biosynthetic genes are required for Arabidopsis shade avoidance. <i>PeerJ</i> , 2016, 4, e2574.	0.9	68
30	Modeling development and quantitative trait mapping reveal independent genetic modules for leaf size and shape. <i>New Phytologist</i> , 2015, 208, 257-268.	3.5	41
31	Structured Light-Based 3D Reconstruction System for Plants. <i>Sensors</i> , 2015, 15, 18587-18612.	2.1	129
32	GLO-Roots: an imaging platform enabling multidimensional characterization of soil-grown root systems. <i>ELife</i> , 2015, 4, .	2.8	212
33	Light-induced indeterminacy alters shade avoiding tomato leaf morphology. <i>Plant Physiology</i> , 2015, 169, pp.01229.2015.	2.3	49
34	Reassess the <i>t</i> Test: Interact with All Your Data via ANOVA. <i>Plant Cell</i> , 2015, 27, 2088-2094.	3.1	48
35	Shade Avoidance Components and Pathways in Adult Plants Revealed by Phenotypic Profiling. <i>PLoS Genetics</i> , 2015, 11, e1004953.	1.5	76
36	Resolving Distinct Genetic Regulators of Tomato Leaf Shape within a Heteroblastic and Ontogenetic Context. <i>Plant Cell</i> , 2014, 26, 3616-3629.	3.1	75

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37	A Modern Ampelography: A Genetic Basis for Leaf Shape and Venation Patterning in Grape. <i>Plant Physiology</i> , 2014, 164, 259-272.	2.3	233
38	New Arabidopsis Advanced Intercross Recombinant Inbred Lines Reveal Female Control of Nonrandom Mating. <i>Plant Physiology</i> , 2014, 165, 175-185.	2.3	21
39	Polymorphism Identification and Improved Genome Annotation of <i>Brassica rapa</i> Through Deep RNA Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2065-2078.	0.8	29
40	Evolutionary developmental transcriptomics reveals a gene network module regulating interspecific diversity in plant leaf shape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2616-21.	3.3	178
41	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014, 46, 1034-1038.	9.4	391
42	Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2655-62.	3.3	325
43	Fine genetic mapping of RXopJ4, a bacterial spot disease resistance locus from <i>Solanum pennellii</i> LA716. <i>Theoretical and Applied Genetics</i> , 2013, 126, 601-609.	1.8	51
44	LeafJ: An ImageJ Plugin for Semi-automated Leaf Shape Measurement. <i>Journal of Visualized Experiments</i> , 2013, , .	0.2	52
45	Dynamic Transcriptomic Profiles between Tomato and a Wild Relative Reflect Distinct Developmental Architectures. <i>Plant Physiology</i> , 2013, 162, 537-552.	2.3	41
46	A Quantitative Genetic Basis for Leaf Morphology in a Set of Precisely Defined Tomato Introgression Lines. <i>Plant Cell</i> , 2013, 25, 2465-2481.	3.1	209
47	Identification of Novel Loci Regulating Interspecific Variation in Root Morphology and Cellular Development in Tomato. <i>Plant Physiology</i> , 2013, 162, 755-768.	2.3	68
48	The Developmental Trajectory of Leaflet Morphology in Wild Tomato Species. <i>Plant Physiology</i> , 2012, 158, 1230-1240.	2.3	85
49	A Genome-Wide Association Study Identifies Variants Underlying the Arabidopsis thaliana Shade Avoidance Response. <i>PLoS Genetics</i> , 2012, 8, e1002589.	1.5	95
50	A High-Throughput Method for Illumina RNA-Seq Library Preparation. <i>Frontiers in Plant Science</i> , 2012, 3, 202.	1.7	145
51	Rapid creation of Arabidopsis doubled haploid lines for quantitative trait locus mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4227-4232.	3.3	68
52	Native Environment Modulates Leaf Size and Response to Simulated Foliar Shade across Wild Tomato Species. <i>PLoS ONE</i> , 2012, 7, e29570.	1.1	54
53	BBX32, an Arabidopsis B-Box Protein, Functions in Light Signaling by Suppressing HY5-Regulated Gene Expression and Interacting with STH2/BBX21. <i>Plant Physiology</i> , 2011, 156, 2109-2123.	2.3	140
54	PIF Genes Mediate the Effect of Sucrose on Seedling Growth Dynamics. <i>PLoS ONE</i> , 2011, 6, e19894.	1.1	92

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55	COP1-Mediated Degradation of BBX22/LZF1 Optimizes Seedling Development in Arabidopsis. <i>Plant Physiology</i> , 2011, 156, 228-239.	2.3	102
56	Genomic Analysis of Circadian Clock-, Light-, and Growth-Related Genes Reveals PHYTOCHROME-INTERACTING FACTOR5 as a Modulator of Auxin Signaling in Arabidopsis. <i>Plant Physiology</i> , 2011, 156, 357-372.	2.3	136
57	Network Quantitative Trait Loci Mapping of Circadian Clock Outputs Identifies Metabolic Pathway-to-Clock Linkages in Arabidopsis. <i>Plant Cell</i> , 2011, 23, 471-485.	3.1	139
58	Circadian oscillation of gibberellin signaling in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9292-9297.	3.3	131
59	Phytochromes inhibit hypocotyl negative gravitropism by regulating the development of endodermal amyloplasts through phytochrome-interacting factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1729-1734.	3.3	88
60	Genomic Analysis of QTLs and Genes Altering Natural Variation in Stochastic Noise. <i>PLoS Genetics</i> , 2011, 7, e1002295.	1.5	107
61	Genes underlying quantitative variation in ecologically important traits: PIF4 (PHYTOCHROME) Tj ETQq1 set in Arabidopsis thaliana. <i>Molecular Ecology</i> , 2010, 19, 1187-1199.	1.0784314	43
62	Network Analysis Identifies ELF3 as a QTL for the Shade Avoidance Response in Arabidopsis. <i>PLoS Genetics</i> , 2010, 6, e1001100.	1.5	120
63	Floral Genetic Architecture: An Examination of QTL Architecture Underlying Floral (Co)Variation Across Environments. <i>Genetics</i> , 2010, 186, 1451-1465.	1.2	27
64	Recent advances in regulation of flowering. <i>F1000 Biology Reports</i> , 2010, 2, .	4.0	2
65	Cis-regulatory Changes at FLOWERING LOCUS T Mediate Natural Variation in Flowering Responses of Arabidopsis thaliana. <i>Genetics</i> , 2009, 183, 723-732.	1.2	109
66	Sequence diversity in three tomato species: SNPs, markers, and molecular evolution. <i>BMC Plant Biology</i> , 2009, 9, 85.	1.6	44
67	QTL Mapping in New Arabidopsis thaliana Advanced Intercross-Recombinant Inbred Lines. <i>PLoS ONE</i> , 2009, 4, e4318.	1.1	92
68	Global transcriptome analysis reveals circadian regulation of key pathways in plant growth and development. <i>Genome Biology</i> , 2008, 9, R130.	13.9	677
69	Amino acid polymorphisms in Arabidopsis phytochrome B cause differential responses to light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 3157-3162.	3.3	97
70	Rhythmic growth explained by coincidence between internal and external cues. <i>Nature</i> , 2007, 448, 358-361.	13.7	599
71	ANTAGONISTIC MULTILEVEL SELECTION ON SIZE AND ARCHITECTURE IN VARIABLE DENSITY SETTINGS. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 58-67.	1.1	41
72	Diurnal regulation of plant growth*. <i>Plant, Cell and Environment</i> , 2006, 29, 396-408.	2.8	107

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73	The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2006, 38, 711-715.	9.4	191
74	An Internal Motor Kinesin Is Associated with the Golgi Apparatus and Plays a Role in Trichome Morphogenesis in <i>Arabidopsis</i> . <i>Molecular Biology of the Cell</i> , 2005, 16, 811-823.	0.9	147
75	Light-Response Quantitative Trait Loci Identified with Composite Interval and eXtreme Array Mapping in <i>Arabidopsis thaliana</i> Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY394847 and AY466496.. <i>Genetics</i> , 2004, 167, 907-917.	1.2	83
76	Plant Development: Slowing Root Growth Naturally. <i>Current Biology</i> , 2004, 14, R395-R396.	1.8	6
77	QTL for plant growth and morphology. <i>Current Opinion in Plant Biology</i> , 2003, 6, 85-90.	3.5	53
78	Genomic approaches to analyzing natural variation in <i>Arabidopsis thaliana</i> . <i>Current Opinion in Genetics and Development</i> , 2003, 13, 576-582.	1.5	37
79	Building Integrated Models of Plant Growth and Development. <i>Plant Physiology</i> , 2003, 132, 436-439.	2.3	22
80	The extent of linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2002, 30, 190-193.	9.4	425
81	Quantitative Trait Loci Controlling Light and Hormone Response in Two Accessions of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2002, 160, 683-696.	1.2	127
82	Three Redundant Brassinosteroid Early Response Genes Encode Putative bHLH Transcription Factors Required for Normal Growth. <i>Genetics</i> , 2002, 162, 1445-1456.	1.2	259
83	Natural variation in light sensitivity of <i>Arabidopsis</i> . <i>Nature Genetics</i> , 2001, 29, 441-446.	9.4	261
84	Natural variation in phytochrome signaling. <i>Seminars in Cell and Developmental Biology</i> , 2000, 11, 523-530.	2.3	32