

Julin N Maloof

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

88
papers

6,299
citations

43
h-index

79
g-index

188
ext. papers

7,775
ext. citations

8.8
avg, IF

5.51
L-index

#	Paper	IF	Citations
88	Flower orientation influences floral temperature, pollinator visits and plant fitness. <i>New Phytologist</i> , 2021 , 232, 868-879	9.8	4
87	Retrograde Induction of phyB Orchestrates Ethylene-Auxin Hierarchy to Regulate Growth. <i>Plant Physiology</i> , 2020 , 183, 1268-1280	6.6	13
86	The foxtail millet (<i>Setaria italica</i>) terpene synthase gene family. <i>Plant Journal</i> , 2020 , 103, 781-800	6.9	11
85	Leaf shape is a predictor of fruit quality and cultivar performance in tomato. <i>New Phytologist</i> , 2020 , 226, 851-865	9.8	13
84	Multiple Loci Control Variation in Plasticity to Foliar Shade Throughout Development in. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 4103-4114	3.2	0
83	MYCs and PIFs Act Independently in Arabidopsis Growth Regulation. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 1797-1807	3.2	2
82	Integrating transcriptomic network reconstruction and eQTL analyses reveals mechanistic connections between genomic architecture and Brassica rapa development. <i>PLoS Genetics</i> , 2019 , 15, e1008367	6	11
81	Tissue-Specific Transcriptome Analysis Reveals Candidate Genes for Terpenoid and Phenylpropanoid Metabolism in the Medicinal Plant. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 807-816	3.2	13
80	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	10.2	34
79	The role of a class III gibberellin 2-oxidase in tomato internode elongation. <i>Plant Journal</i> , 2019 , 97, 603-615	6.5	16
78	Integrated QTL and eQTL Mapping Provides Insights and Candidate Genes for Fatty Acid Composition, Flowering Time, and Growth Traits in a F Population of a Novel Synthetic Allopolyploid. <i>Frontiers in Plant Science</i> , 2018 , 9, 1632	6.2	13
77	Network Analysis Reveals a Role for Salicylic Acid Pathway Components in Shade Avoidance. <i>Plant Physiology</i> , 2018 , 178, 1720-1732	6.6	17
76	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	6.5	25
75	The Generation of Doubled Haploid Lines for QTL Mapping. <i>Methods in Molecular Biology</i> , 2017 , 1610, 39-57	1.4	3
74	Using RNA-Seq for Genomic Scaffold Placement, Correcting Assemblies, and Genetic Map Creation in a Common Mapping Population. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2259-2270	3.2	10
73	Circadian rhythms vary over the growing season and correlate with fitness components. <i>Molecular Ecology</i> , 2017 , 26, 5528-5540	5.7	25
72	The Divergence of Flowering Time Modulated by Is Independent to Their Interaction and Binding Activities. <i>Frontiers in Plant Science</i> , 2017 , 8, 697	6.2	17

71	Morphological Plant Modeling: Unleashing Geometric and Topological Potential within the Plant Sciences. <i>Frontiers in Plant Science</i> , 2017 , 8, 900	6.2	41
70	Genetic architecture, biochemical underpinnings and ecological impact of floral UV patterning. <i>Molecular Ecology</i> , 2016 , 25, 1122-40	5.7	14
69	Domestication selected for deceleration of the circadian clock in cultivated tomato. <i>Nature Genetics</i> , 2016 , 48, 89-93	36.3	112
68	Molecular control of crop shade avoidance. <i>Current Opinion in Plant Biology</i> , 2016 , 30, 151-8	9.9	55
67	auxin biosynthetic genes are required for Arabidopsis shade avoidance. <i>PeerJ</i> , 2016 , 4, e2574	3.1	41
66	The Quantitative Basis of the Arabidopsis Innate Immune System to Endemic Pathogens Depends on Pathogen Genetics. <i>PLoS Genetics</i> , 2016 , 12, e1005789	6	44
65	Tomato phyE Is Required for Shade Avoidance in the Absence of phyB1 and phyB2. <i>Frontiers in Plant Science</i> , 2016 , 7, 1275	6.2	14
64	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	6.5	48
63	Neighbor Detection Induces Organ-Specific Transcriptomes, Revealing Patterns Underlying Hypocotyl-Specific Growth. <i>Plant Cell</i> , 2016 , 28, 2889-2904	11.6	76
62	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	3.2	19
61	Plant phenotyping using multi-view stereo vision with structured lights 2016 ,		4
60	eQTL Regulating Transcript Levels Associated with Diverse Biological Processes in Tomato. <i>Plant Physiology</i> , 2016 , 172, 328-40	6.6	38
59	Reassess the t Test: Interact with All Your Data via ANOVA. <i>Plant Cell</i> , 2015 , 27, 2088-94	11.6	40
58	Shade avoidance components and pathways in adult plants revealed by phenotypic profiling. <i>PLoS Genetics</i> , 2015 , 11, e1004953	6	57
57	Modeling development and quantitative trait mapping reveal independent genetic modules for leaf size and shape. <i>New Phytologist</i> , 2015 , 208, 257-68	9.8	21
56	Structured Light-Based 3D Reconstruction System for Plants. <i>Sensors</i> , 2015 , 15, 18587-612	3.8	88
55	GLO-Roots: an imaging platform enabling multidimensional characterization of soil-grown root systems. <i>ELife</i> , 2015 , 4,	8.9	143
54	Light-Induced Indeterminacy Alters Shade-Avoiding Tomato Leaf Morphology. <i>Plant Physiology</i> , 2015 , 169, 2030-47	6.6	33

53	Author response: GLO-Roots: an imaging platform enabling multidimensional characterization of soil-grown root systems 2015 ,		3
52	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	11.5	107
51	The genome of the stress-tolerant wild tomato species <i>Solanum pennellii</i> . <i>Nature Genetics</i> , 2014 , 46, 1034-8	36.3	269
50	Resolving distinct genetic regulators of tomato leaf shape within a heteroblastic and ontogenetic context. <i>Plant Cell</i> , 2014 , 26, 3616-29	11.6	45
49	A modern ampelography: a genetic basis for leaf shape and venation patterning in grape. <i>Plant Physiology</i> , 2014 , 164, 259-72	6.6	110
48	New <i>Arabidopsis</i> advanced intercross recombinant inbred lines reveal female control of nonrandom mating. <i>Plant Physiology</i> , 2014 , 165, 175-85	6.6	13
47	Polymorphism identification and improved genome annotation of <i>Brassica rapa</i> through Deep RNA sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 2065-78	3.2	25
46	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	11.5	260
45	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, 601-9	6	37
44	LeafJ: an ImageJ plugin for semi-automated leaf shape measurement. <i>Journal of Visualized Experiments</i> , 2013 ,	1.6	38
43	Dynamic transcriptomic profiles between tomato and a wild relative reflect distinct developmental architectures. <i>Plant Physiology</i> , 2013 , 162, 537-52	6.6	25
42	A quantitative genetic basis for leaf morphology in a set of precisely defined tomato introgression lines. <i>Plant Cell</i> , 2013 , 25, 2465-81	11.6	115
41	Identification of novel loci regulating interspecific variation in root morphology and cellular development in tomato. <i>Plant Physiology</i> , 2013 , 162, 755-68	6.6	50
40	Rapid creation of <i>Arabidopsis</i> 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, 4227-32	11.5	55
39	Native environment modulates leaf size and response to simulated foliar shade across wild tomato species. <i>PLoS ONE</i> , 2012 , 7, e29570	3.7	44
38	The developmental trajectory of leaflet morphology in wild tomato species. <i>Plant Physiology</i> , 2012 , 158, 1230-40	6.6	53
37	A genome-wide association study identifies variants underlying the <i>Arabidopsis thaliana</i> shade avoidance response. <i>PLoS Genetics</i> , 2012 , 8, e1002589	6	74
36	A High-Throughput Method for Illumina RNA-Seq Library Preparation. <i>Frontiers in Plant Science</i> , 2012 , 3, 202	6.2	102

35	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, 2109-23	6.6	84
34	PIF genes mediate the effect of sucrose on seedling growth dynamics. <i>PLoS ONE</i> , 2011 , 6, e19894	3.7	74
33	COP1-mediated degradation of BBX22/LZF1 optimizes seedling development in Arabidopsis. <i>Plant Physiology</i> , 2011 , 156, 228-39	6.6	84
32	Genomic analysis of circadian clock-, light-, and growth-correlated genes reveals PHYTOCHROME-INTERACTING FACTOR5 as a modulator of auxin signaling in Arabidopsis. <i>Plant Physiology</i> , 2011 , 156, 357-72	6.6	112
31	Network quantitative trait loci mapping of circadian clock outputs identifies metabolic pathway-to-clock linkages in Arabidopsis. <i>Plant Cell</i> , 2011 , 23, 471-85	11.6	112
30	Circadian oscillation of gibberellin signaling in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 9292-7	11.5	107
29	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, 1729-34	11.5	65
28	Genomic analysis of QTLs and genes altering natural variation in stochastic noise. <i>PLoS Genetics</i> , 2011 , 7, e1002295	6	77
27	Genes underlying quantitative variation in ecologically important traits: PIF4 (phytochrome interacting factor 4) is associated with variation in internode length, flowering time, and fruit set in Arabidopsis thaliana. <i>Molecular Ecology</i> , 2010 , 19, 1187-99	5.7	39
26	Network analysis identifies ELF3 as a QTL for the shade avoidance response in Arabidopsis. <i>PLoS Genetics</i> , 2010 , 6, e1001100	6	88
25	Floral genetic architecture: an examination of QTL architecture underlying floral (co)variation across environments. <i>Genetics</i> , 2010 , 186, 1451-65	4	22
24	Recent advances in regulation of flowering. <i>F1000 Biology Reports</i> , 2010 , 2,		1
23	Cis-regulatory changes at FLOWERING LOCUS T mediate natural variation in flowering responses of Arabidopsis thaliana. <i>Genetics</i> , 2009 , 183, 723-32, 1S1-7S1	4	95
22	Sequence diversity in three tomato species: SNPs, markers, and molecular evolution. <i>BMC Plant Biology</i> , 2009 , 9, 85	5.3	36
21	QTL mapping in new Arabidopsis thaliana advanced intercross-recombinant inbred lines. <i>PLoS ONE</i> , 2009 , 4, e4318	3.7	77
20	Global transcriptome analysis reveals circadian regulation of key pathways in plant growth and development. <i>Genome Biology</i> , 2008 , 9, R130	18.3	517
19	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, 3157-62	11.5	85
18	Rhythmic growth explained by coincidence between internal and external cues. <i>Nature</i> , 2007 , 448, 358-63	10.4	515

17	Antagonistic multilevel selection on size and architecture in variable density settings. <i>Evolution; International Journal of Organic Evolution</i> , 2007 , 61, 58-67	3.8	38
16	Diurnal regulation of plant growth. <i>Plant, Cell and Environment</i> , 2006 , 29, 396-408	8.4	86
15	The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2006 , 38, 711-5	36.3	171
14	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, 811-23	3.5	131
13	Light-response quantitative trait loci identified with composite interval and eXtreme array mapping in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2004 , 167, 907-17	4	74
12	Plant development: slowing root growth naturally. <i>Current Biology</i> , 2004 , 14, R395-6	6.3	5
11	QTL for plant growth and morphology. <i>Current Opinion in Plant Biology</i> , 2003 , 6, 85-90	9.9	51
10	Genomic approaches to analyzing natural variation in <i>Arabidopsis thaliana</i> . <i>Current Opinion in Genetics and Development</i> , 2003 , 13, 576-82	4.9	32
9	Building integrated models of plant growth and development. <i>Plant Physiology</i> , 2003 , 132, 436-9	6.6	21
8	The extent of linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 2002 , 30, 190-3	36.3	393
7	Quantitative trait loci controlling light and hormone response in two accessions of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2002 , 160, 683-96	4	101
6	Three redundant brassinosteroid early response genes encode putative bHLH transcription factors required for normal growth. <i>Genetics</i> , 2002 , 162, 1445-56	4	202
5	Natural variation in light sensitivity of <i>Arabidopsis</i> . <i>Nature Genetics</i> , 2001 , 29, 441-6	36.3	229
4	Natural variation in phytochrome signaling. <i>Seminars in Cell and Developmental Biology</i> , 2000 , 11, 523-30	7.5	27
3	Auxin signaling is a common factor underlying natural variation in tomato shade avoidance		2
2	eQTL regulating Transcript Levels Associated with Diverse Biological Processes in Tomato		2
1	A new advanced backcross tomato population enables high resolution leaf QTL mapping and gene identification		