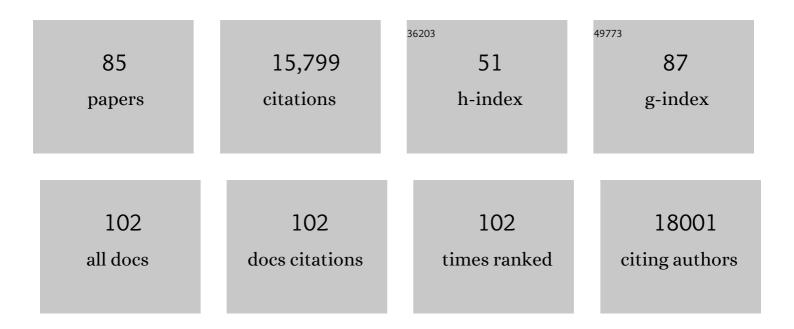
## Todd P Michael

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome sequencing and analysis of the model grass Brachypodium distachyon. Nature, 2010, 463, 763-768.	13.7	1,685
2	Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. Nature, 2010, 465, 627-631.	13.7	1,651
3	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. Cell, 2016, 166, 481-491.	13.5	1,107
4	The genome of woodland strawberry (Fragaria vesca). Nature Genetics, 2011, 43, 109-116.	9.4	1,091
5	The draft genome of the transgenic tropical fruit tree papaya (Carica papaya Linnaeus). Nature, 2008, 452, 991-996.	13.7	964
6	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	6.0	794
7	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. Cell, 2016, 166, 492-505.	13.5	594
8	Network Discovery Pipeline Elucidates Conserved Time-of-Day–Specific cis-Regulatory Modules. PLoS Genetics, 2008, 4, e14.	1.5	474
9	Feeding the future. Nature, 2013, 499, 23-24.	13.7	464
10	Enhanced Fitness Conferred by Naturally Occurring Variation in the Circadian Clock. Science, 2003, 302, 1049-1053.	6.0	411
11	Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). Genome Biology, 2013, 14, R41.	13.9	329
12	Architecture and evolution of a minute plant genome. Nature, 2013, 498, 94-98.	13.7	293
13	Single-molecule sequencing of the desiccation-tolerant grass Oropetium thomaeum. Nature, 2015, 527, 508-511.	13.7	291
14	High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell. Nature Communications, 2018, 9, 541.	5.8	243
15	The First 50 Plant Genomes. Plant Genome, 2013, 6, plantgenome2013.03.0001in.	1.6	228
16	A Morning-Specific Phytohormone Gene Expression Program underlying Rhythmic Plant Growth. PLoS Biology, 2008, 6, e225.	2.6	197
17	Progress, challenges and the future of crop genomes. Current Opinion in Plant Biology, 2015, 24, 71-81.	3.5	197
18	The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of Arabidopsis thaliana. Nature Genetics, 2006, 38, 711-715.	9.4	191

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19	Global Profiling of Rice and Poplar Transcriptomes Highlights Key Conserved Circadian-Controlled Pathways and cis-Regulatory Modules. PLoS ONE, 2011, 6, e16907.	1.1	188
20	The genetic and epigenetic landscape of the <i>Arabidopsis</i> centromeres. Science, 2021, 374, eabi7489.	6.0	188
21	Genome-wide patterns of single-feature polymorphism in <i>Arabidopsis thaliana</i> . Proceedings of the United States of America, 2007, 104, 12057-12062.	3.3	157
22	Enhancer Trapping Reveals Widespread Circadian Clock Transcriptional Control in Arabidopsis Â. Plant Physiology, 2003, 132, 629-639.	2.3	156
23	Regulation of flowering time in Arabidopsis by K homology domain proteins. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 12759-12764.	3.3	150
24	Integrative analysis of chromatin states in <scp>A</scp> rabidopsis identified potential regulatory mechanisms for natural antisense transcript production. Plant Journal, 2013, 73, 77-90.	2.8	147
25	Phase-Specific Circadian Clock Regulatory Elements in Arabidopsis. Plant Physiology, 2002, 130, 627-638.	2.3	146
26	Two Arabidopsis circadian oscillators can be distinguished by differential temperature sensitivity. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6878-6883.	3.3	143
27	Plant genome size variation: bloating and purging DNA. Briefings in Functional Genomics, 2014, 13, 308-317.	1.3	137
28	Building near-complete plant genomes. Current Opinion in Plant Biology, 2020, 54, 26-33.	3.5	135
29	SOPRA: Scaffolding algorithm for paired reads via statistical optimization. BMC Bioinformatics, 2010, 11, 345.	1.2	133
30	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by highâ€depth physical mapping and shortâ€read <scp>DNA</scp> sequencing strategies. Plant Journal, 2017, 89, 617-635.	2.8	115
31	Type II protein arginine methyltransferase 5 (PRMT5) is required for circadian period determination in <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21211-21216.	3.3	113
32	Tcf4 Regulates Synaptic Plasticity, DNA Methylation, and Memory Function. Cell Reports, 2016, 16, 2666-2685.	2.9	113
33	Evolution of genome size and chromosome number in the carnivorous plant genus Genlisea (Lentibulariaceae), with a new estimate of the minimum genome size in angiosperms. Annals of Botany, 2014, 114, 1651-1663.	1.4	111
34	The genome of black raspberry ( <i>Rubus occidentalis</i> ). Plant Journal, 2016, 87, 535-547.	2.8	111
35	Return of the Lemnaceae: duckweed as a model plant system in the genomics and postgenomics era. Plant Cell, 2021, 33, 3207-3234.	3.1	111
36	Isolation and analysis of high quality nuclear DNA with reduced organellar DNA for plant genome sequencing and resequencing. BMC Biotechnology, 2011, 11, 54.	1.7	110

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37	Cis-regulatory Changes at FLOWERING LOCUS T Mediate Natural Variation in Flowering Responses of Arabidopsis thaliana. Genetics, 2009, 183, 723-732.	1.2	109
38	The complex architecture and epigenomic impact of plant T-DNA insertions. PLoS Genetics, 2019, 15, e1007819.	1.5	109
39	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. Nature Communications, 2020, 11, 884.	5.8	101
40	The out of phase 1 Mutant Defines a Role for PHYB in Circadian Phase Control in Arabidopsis. Plant Physiology, 2002, 129, 1674-1685.	2.3	99
41	Elevated temperature drives kelp microbiome dysbiosis, while elevated carbon dioxide induces water microbiome disruption. PLoS ONE, 2018, 13, e0192772.	1.1	95
42	Extreme haplotype variation in the desiccation-tolerant clubmoss Selaginella lepidophylla. Nature Communications, 2018, 9, 13.	5.8	89
43	A new <i>Cannabis</i> genome assembly associates elevated cannabidiol (CBD) with hemp introgressed into marijuana. New Phytologist, 2021, 230, 1665-1679.	3.5	87
44	Analysis of Global Gene Expression in Brachypodium distachyon Reveals Extensive Network Plasticity in Response to Abiotic Stress. PLoS ONE, 2014, 9, e87499.	1.1	80
45	Evolution of Genome Size in Duckweeds ( <i>Lemnaceae</i> ). Journal of Botany, 2011, 2011, 1-9.	1.2	79
46	Cytochrome P450 Monooxygenases as Reporters for Circadian-Regulated Pathways   Â. Plant Physiology, 2009, 150, 858-878.	2.3	75
47	A zinc knuckle protein that negatively controls morning-specific growth in <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17193-17198.	3.3	67
48	Generating a highâ€confidence reference genome map of the Greater Duckweed by integration of cytogenomic, optical mapping, and Oxford Nanopore technologies. Plant Journal, 2018, 96, 670-684.	2.8	64
49	Simple Sequence Repeats Provide a Substrate for Phenotypic Variation in the Neurospora crassa Circadian Clock. PLoS ONE, 2007, 2, e795.	1.1	61
50	Time of day and network reprogramming during drought induced CAM photosynthesis in Sedum album. PLoS Genetics, 2019, 15, e1008209.	1.5	59
51	The Chloroplast Genome of Utricularia reniformis Sheds Light on the Evolution of the ndh Gene Complex of Terrestrial Carnivorous Plants from the Lentibulariaceae Family. PLoS ONE, 2016, 11, e0165176.	1.1	57
52	Genome and time-of-day transcriptome of <i>Wolffia australiana</i> link morphological minimization with gene loss and less growth control. Genome Research, 2021, 31, 225-238.	2.4	56
53	Underwater CAM photosynthesis elucidated by Isoetes genome. Nature Communications, 2021, 12, 6348.	5.8	56
54	An SSR-based genetic linkage map of the model grass Brachypodium distachyon. Genome, 2010, 53, 1-13.	0.9	55

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55	The carnivorous bladderwort (Utricularia, Lentibulariaceae): a system inflates. Journal of Experimental Botany, 2010, 61, 5-9.	2.4	51
56	Lycophyte plastid genomics: extreme variation in <scp>GC</scp> , gene and intron content and multiple inversions between a direct and inverted orientation of the <scp>rRNA</scp> repeat. New Phytologist, 2019, 222, 1061-1075.	3.5	51
57	Seed desiccation mechanisms coâ€opted for vegetative desiccation in the resurrection grass <i>Oropetium thomaeum</i> . Plant, Cell and Environment, 2017, 40, 2292-2306.	2.8	49
58	Scalable Biosynthesis of the Seaweed Neurochemical, Kainic Acid. Angewandte Chemie - International Edition, 2019, 58, 8454-8457.	7.2	49
59	Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, Scomber japonicus. MSphere, 2020, 5, .	1.3	49
60	Conserved Daily Transcriptional Programs in Carica papaya. Tropical Plant Biology, 2008, 1, 236-245.	1.0	37
61	The Terrestrial Carnivorous Plant Utricularia reniformis Sheds Light on Environmental and Life-Form Genome Plasticity. International Journal of Molecular Sciences, 2020, 21, 3.	1.8	30
62	Filtering error from SOLiD Output. Bioinformatics, 2010, 26, 849-850.	1.8	29
63	Improved <i>Spirodela polyrhiza</i> genome and proteomic analyses reveal a conserved chromosomal structure with high abundance of chloroplastic proteins favoring energy production. Journal of Experimental Botany, 2021, 72, 2491-2500.	2.4	25
64	The mitochondrial genome of the terrestrial carnivorous plant Utricularia reniformis (Lentibulariaceae): Structure, comparative analysis and evolutionary landmarks. PLoS ONE, 2017, 12, e0180484.	1.1	24
65	Intraspecific Variation within the Utricularia amethystina Species Morphotypes Based on Chloroplast Genomes. International Journal of Molecular Sciences, 2019, 20, 6130.	1.8	23
66	Large structural variations in the haplotypeâ€resolved African cassava genome. Plant Journal, 2021, 108, 1830-1848.	2.8	22
67	The Arabidopsis Circadian System. The Arabidopsis Book, 2002, 1, e0044.	0.5	21
68	An Antisense Oligonucleotide Leads to Suppressed Transcription of Hdac2 and Long-Term Memory Enhancement. Molecular Therapy - Nucleic Acids, 2020, 19, 1399-1412.	2.3	18
69	Comparative genomic analysis of Genlisea (corkscrew plants—Lentibulariaceae) chloroplast genomes reveals an increasing loss of the ndh genes. PLoS ONE, 2018, 13, e0190321.	1.1	17
70	Estimation of nuclear DNA content of cultivated <i>Ocimum</i> species by using flow cytometry. Israel Journal of Plant Sciences, 2010, 58, 183-189.	0.3	16
71	Changes in ambient temperature are the prevailing cue in determining <i>Brachypodium distachyon</i> diurnal gene regulation. New Phytologist, 2020, 227, 1709-1724.	3.5	16
72	Contrasting a reference cranberry genome to a crop wild relative provides insights into adaptation, domestication, and breeding. PLoS ONE, 2022, 17, e0264966.	1.1	13

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73	The genome and preliminary single-nuclei transcriptome of <i>Lemna minuta</i> reveals mechanisms of invasiveness. Plant Physiology, 2022, 188, 879-897.	2.3	13
74	Wolffia, a minimalist plant and synthetic biology chassis. Trends in Plant Science, 2022, 27, 430-439.	4.3	13
75	The tomato genome fleshed out. Nature Biotechnology, 2012, 30, 765-767.	9.4	12
76	Sequence-guided approach to genotyping plant clones and species using polymorphic NB-ARC-related genes. Plant Molecular Biology, 2018, 98, 219-231.	2.0	8
77	The complete chloroplast genome sequence of the leafy bladderwort, Utricularia foliosa L. (Lentibulariaceae). Conservation Genetics Resources, 2017, 9, 213-216.	0.4	5
78	A pan-genome method to determine core regions of the Bacillus subtilis and Escherichia coli genomes. F1000Research, 2021, 10, 286.	0.8	5
79	Core circadian clock and light signaling genes brought into genetic linkage across the green lineage. Plant Physiology, 2022, 190, 1037-1056.	2.3	5
80	Development of microsatellite markers for the carnivorous plant Genlisea aurea (Lentibulariaceae) using genomics data of NGS. Molecular Biology Reports, 2018, 45, 57-61.	1.0	4
81	Scalable Biosynthesis of the Seaweed Neurochemical, Kainic Acid. Angewandte Chemie, 2019, 131, 8542-8545.	1.6	4
82	HorizontalÂtransfer andÂevolution ofÂwallÂteichoicÂacidÂgeneÂcassettes inÂBacillus subtilis. F1000Research, 2021, 10, 354.	0.8	4
83	Sequence and Analysis of the Black Raspberry (Rubus occidentalis) Genome. Compendium of Plant Genomes, 2018, , 185-197.	0.3	3
84	A pan-genome method to determine core regions of the Bacillus subtilis and Escherichia coli genomes. F1000Research, 2021, 10, 286.	0.8	3
85	The complete mitochondrial genome of carnivorous Genlisea tuberosa (Lentibulariaceae): Structure and evolutionary aspects. Gene, 2022, 824, 146391.	1.0	3