Todd C Mockler

List of Publications by Year
in descending order

103 papers	14,364 citations	20817 60 h-index	30087 103 g-index
123 all docs	123 docs citations	123 times ranked	16641 citing authors

#	Article	IF	Citations
1	The genome of woodland strawberry (Fragaria vesca). Nature Genetics, 2011, 43, 109-116.	21.4	1,091
2	Genome-wide mapping of alternative splicing in <i>Arabidopsis thaliana</i>. Genome Research, 2010, 20, 45-58.	5.5	825
3	Regulation of Flowering Time by Arabidopsis Photoreceptors. Science, 1998, 279, 1360-1363.	12.6	713
4	Signals from chloroplasts converge to regulate nuclear gene expression. Science, 2007, 316, 715-9.	12.6	638
5	Interdependency of Brassinosteroid and Auxin Signaling in Arabidopsis. PLoS Biology, 2004, 2, e258.	5.6	499
6	Network Discovery Pipeline Elucidates Conserved Time-of-Dayâ€"Specific cis-Regulatory Modules. PLoS Genetics, 2008, 4, e14.	3.5	474
7	The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442.	21.4	472
8	Applications of DNA tiling arrays for whole-genome analysis. Genomics, 2005, 85, 1-15.	2.9	376
9	Multiplex sequencing of plant chloroplast genomes using Solexa sequencing-by-synthesis technology. Nucleic Acids Research, 2008, 36, e122-e122.	14.5	356
10	Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). Genome Biology, 2013, 14, R41.	9.6	329
11	Architecture and evolution of a minute plant genome. Nature, 2013, 498, 94-98.	27.8	293
12	Single-molecule sequencing of the desiccation-tolerant grass Oropetium thomaeum. Nature, 2015, 527, 508-511.	27.8	291
13	Regulation of photoperiodic flowering by Arabidopsis photoreceptors. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2140-2145.	7.1	273
14	Regulation of Arabidopsis cryptochrome 2 by blue-light-dependent phosphorylation. Nature, 2002, 417, 763-767.	27.8	271
15	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. PLoS ONE, 2012, 7, e31745.	2.5	249
16	Brachypodium as a Model for the Grasses: Today and the Future Â. Plant Physiology, 2011, 157, 3-13.	4.8	243
17	High throughput phenotyping to accelerate crop breeding and monitoring of diseases in the field. Current Opinion in Plant Biology, 2017, 38, 184-192.	7.1	242
18	Guidelines for Genome-Scale Analysis of Biological Rhythms. Journal of Biological Rhythms, 2017, 32, 380-393.	2.6	237

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19	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. Nature Biotechnology, 2014, 32, 1158-1165.	17.5	228
20	Alternative splicing in plants: directing traffic at the crossroads of adaptation and environmental stress. Current Opinion in Plant Biology, 2015, 24, 125-135.	7.1	215
21	A Versatile Phenotyping System and Analytics Platform Reveals Diverse Temporal Responses to Water Availability in Setaria. Molecular Plant, 2015, 8, 1520-1535.	8.3	202
22	Development and Evaluation of a 9K SNP Array for Peach by Internationally Coordinated SNP Detection and Validation in Breeding Germplasm. PLoS ONE, 2012, 7, e35668.	2.5	199
23	A Morning-Specific Phytohormone Gene Expression Program underlying Rhythmic Plant Growth. PLoS Biology, 2008, 6, e225.	5.6	197
24	Signals from Chloroplasts Converge to Regulate Nuclear Gene Expression. Science, 2007, 316, 715-719.	12.6	196
25	Global Profiling of Rice and Poplar Transcriptomes Highlights Key Conserved Circadian-Controlled Pathways and cis-Regulatory Modules. PLoS ONE, 2011, 6, e16907.	2.5	188
26	Blue Light-Dependent in Vivo and in Vitro Phosphorylation of Arabidopsis Cryptochrome 1. Plant Cell, 2003, 15, 2421-2429.	6.6	175
27	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i>. New Phytologist, 2012, 196, 713-725.	7.3	173
28	Precise insertion and guided editing of higher plant genomes using Cpf1 CRISPR nucleases. Scientific Reports, 2017, 7, 11606.	3.3	164
29	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.	7.1	150
30	Environmental Stresses Modulate Abundance andÂTiming of Alternatively Spliced Circadian Transcripts in Arabidopsis. Molecular Plant, 2015, 8, 207-227.	8.3	142
31	SUB1, an Arabidopsis Ca2+-Binding Protein Involved in Cryptochrome and Phytochrome Coaction. Science, 2001, 291, 487-490.	12.6	141
32	Dynamic DNA cytosine methylation in the Populus trichocarpa genome: tissue-level variation and relationship to gene expression. BMC Genomics, 2012, 13, 27.	2.8	136
33	Development of Genetic and Genomic Research Resources for <i>Brachypodium distachyon</i>, a New Model System for Grass Crop Research. Crop Science, 2008, 48, S-69.	1.8	133
34	Unproductive alternative splicing and nonsense mRNAs: A widespread phenomenon among plant circadian clock genes. Biology Direct, 2012, 7, 20.	4.6	125
35	Subset of heat-shock transcription factors required for the early response of <i>Arabidopsis</i> to excess light. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14474-14479.	7.1	123
36	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.	5.7	115

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37	Translatome analyses capture of opposing tissue-specific brassinosteroid signals orchestrating root meristem differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 923-928.	7.1	113
38	The genome of black raspberry (<i>Rubus occidentalis</i>). Plant Journal, 2016, 87, 535-547.	5.7	111
39	Grasses suppress shoot-borne roots to conserve water during drought. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8861-8866.	7.1	111
40	Development and Evaluation of a Genome-Wide 6K SNP Array for Diploid Sweet Cherry and Tetraploid Sour Cherry. PLoS ONE, 2012, 7, e48305.	2.5	109
41	cis-Regulatory elements in plant cell signaling. Current Opinion in Plant Biology, 2009, 12, 643-649.	7.1	105
42	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. Nature Communications, 2020, 11, 884.	12.8	101
43	IDN1 and IDN2 are required for de novo DNA methylation in Arabidopsis thaliana. Nature Structural and Molecular Biology, 2009, 16, 1325-1327.	8.2	98
44	Temporal network analysis identifies early physiological and transcriptomic indicators of mild drought in Brassica rapa. ELife, 2017, 6, .	6.0	95
45	Extensive Transcriptome Changes During Natural Onset and Release of Vegetative Bud Dormancy in Populus. Frontiers in Plant Science, 2015, 6, 989.	3.6	91
46	Extreme haplotype variation in the desiccation-tolerant clubmoss Selaginella lepidophylla. Nature Communications, 2018, 9, 13.	12.8	89
47	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. Genome Biology and Evolution, 2011, 3, 641-653.	2.5	87
48	A near complete, chromosome-scale assembly of the black raspberry (Rubus occidentalis) genome. GigaScience, 2018, 7, .	6.4	86
49	Functional characterization of cinnamyl alcohol dehydrogenase and caffeic acid O-methyltransferase in Brachypodium distachyon. BMC Biotechnology, 2013, 13, 61.	3.3	84
50	Genome diversity in <i>Brachypodium distachyon:</i> deep sequencing of highly diverse inbred lines. Plant Journal, 2014, 79, 361-374.	5.7	80
51	Analysis of Global Gene Expression in Brachypodium distachyon Reveals Extensive Network Plasticity in Response to Abiotic Stress. PLoS ONE, 2014, 9, e87499.	2.5	80
52	Expression, Splicing, and Evolution of the Myosin Gene Family in Plants Â Â. Plant Physiology, 2011, 155, 1191-1204.	4.8	78
53	Highly sensitive image-derived indices of water-stressed plants using hyperspectral imaging in SWIR and histogram analysis. Scientific Reports, 2015, 5, 15919.	3.3	78
54	Temporal and spatial transcriptomic and micro<scp>RNA</scp> dynamics of <scp>CAM</scp> photosynthesis in pineapple. Plant Journal, 2017, 92, 19-30.	5.7	78

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55	Target Capture Sequencing Unravels Rubus Evolution. Frontiers in Plant Science, 2019, 10, 1615.	3.6	73
56	Applications of Ultra-high-Throughput Sequencing. Methods in Molecular Biology, 2009, 553, 79-108.	0.9	72
57	Transcriptional networks â€” crops, clocks, and abiotic stress. Current Opinion in Plant Biology, 2015, 24, 39-46.	7.1	70
58	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.	7.1	67
59	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of Brachypodium distachyon. Genome Biology, 2013, 14, R145.	9.6	67
60	GENE-Counter: A Computational Pipeline for the Analysis of RNA-Seq Data for Gene Expression Differences. PLoS ONE, 2011, 6, e25279.	2.5	66
61	Exploring the Switchgrass Transcriptome Using Second-Generation Sequencing Technology. PLoS ONE, 2012, 7, e34225.	2.5	60
62	Time of day and network reprogramming during drought induced CAM photosynthesis in Sedum album. PLoS Genetics, 2019, 15, e1008209.	3.5	59
63	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.	5.5	56
64	An SSR-based genetic linkage map of the model grass Brachypodium distachyon. Genome, 2010, 53, 1-13.	2.0	55
65	Analysis of Transcriptome Changes Induced by Ptr ToxA in Wheat Provides Insights into the Mechanisms of Plant Susceptibility. Molecular Plant, 2009, 2, 1067-1083.	8.3	54
66	QSRA â€“ a quality-value guided de novo short read assembler. BMC Bioinformatics, 2009, 10, 69.	2.6	53
67	High density SNP mapping and QTL analysis for time of leaf budburst in Corylus avellana L.. PLoS ONE, 2018, 13, e0195408.	2.5	52
68	Comparative evolutionary genetics of deleterious load in sorghum and maize. Nature Plants, 2021, 7, 17-24.	9.3	52
69	Methylome reorganization during in vitro dedifferentiation and regeneration of Populus trichocarpa. BMC Plant Biology, 2013, 13, 92.	3.6	51
70	Chromosome-scale scaffolding of the black raspberry (Rubus occidentalis L.) genome based on chromatin interaction data. Horticulture Research, 2018, 5, 8.	6.3	50
71	Climate-smart crops with enhanced photosynthesis. Journal of Experimental Botany, 2018, 69, 3801-3809.	4.8	50
72	Seed desiccation mechanisms coâ€opted for vegetative desiccation in the resurrection grass <i>Oropetium thomaeum</i>. Plant, Cell and Environment, 2017, 40, 2292-2306.	5.7	49

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73	Comparative analyses reveal potential uses of Brachypodium distachyonas a model for cold stress responses in temperate grasses. BMC Plant Biology, 2012, 12, 65.	3.6	46
74	A Recommendation for Naming Transcription Factor Proteins in the Grasses. Plant Physiology, 2009, 149, 4-6.	4.8	45
75	Genome scale transcriptome analysis of shoot organogenesis in Populus. BMC Plant Biology, 2009, 9, 132.	3.6	45
76	Highly specific gene silencing in a monocot species by artificial micro<scp>RNA</scp>s derived from chimeric <i>mi<scp>RNA</scp></i> precursors. Plant Journal, 2015, 82, 1061-1075.	5.7	45
77	Supersplatâ€”spliced RNA-seq alignment. Bioinformatics, 2010, 26, 1500-1505.	4.1	41
78	Conserved Daily Transcriptional Programs in Carica papaya. Tropical Plant Biology, 2008, 1, 236-245.	1.9	37
79	Strong population structure characterizes weediness gene evolution in the invasive grass species <i>Brachypodium distachyon</i>. Molecular Ecology, 2009, 18, 2588-2601.	3.9	37
80	Cell-autonomous circadian clock of hepatocytes drives rhythms in transcription and polyamine synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18560-18565.	7.1	37
81	Assembly and Characterization of the European Hazelnut â€˜Jeffersonâ€™ Transcriptome. Crop Science, 2012, 52, 2679-2686.	1.8	35
82	A genetic linkage map of black raspberry (Rubus occidentalis) and the mapping of Ag 4 conferring resistance to the aphid Amphorophora agathonica. Theoretical and Applied Genetics, 2015, 128, 1631-1646.	3.6	35
83	Host-Selective Toxins of Pyrenophora tritici-repentis Induce Common Responses Associated with Host Susceptibility. PLoS ONE, 2012, 7, e40240.	2.5	34
84	Comparative Analysis of Vertebrate Diurnal/Circadian Transcriptomes. PLoS ONE, 2017, 12, e0169923.	2.5	29
85	Expansion of the circadian transcriptome in Brassica rapa and genome-wide diversification of paralog expression patterns. ELife, 2020, 9, .	6.0	26
86	Detection and Quantification of Alternative Splicing Variants Using RNA-seq. Methods in Molecular Biology, 2012, 883, 97-110.	0.9	22
87	Crossâ€species complementation reveals conserved functions for EARLY FLOWERING 3 between monocots and dicots. Plant Direct, 2017, 1, e00018.	1.9	21
88	A multi-organ transcriptome resource for the Burmese Python (Python molurus bivittatus). BMC Research Notes, 2011, 4, 310.	1.4	18
89	Sequencing and characterization of the anadromous steelhead (Oncorhynchus mykiss) transcriptome. Marine Genomics, 2014, 15, 13-15.	1.1	18
90	Data-Driven Artificial Intelligence for Calibration of Hyperspectral Big Data. IEEE Transactions on Geoscience and Remote Sensing, 2022, 60, 1-20.	6.3	16

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91	Environmental Stresses Modulate Abundance and Timing of Alternatively Spliced Circadian Transcripts in Arabidopsis. Molecular Plant, 2014, , .	8.3	9
92	Genomic patterns of structural variation among diverse genotypes of <i>Sorghum bicolor</i> and a potential role for deletions in local adaptation. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	9
93	The recent evolutionary rescue of a staple crop depended on over half a century of global germplasm exchange. Science Advances, 2022, 8, eabj4633.	10.3	9
94	A new alternative in plant retrograde signaling. Genome Biology, 2014, 15, 117.	9.6	8
95	Characterization of aphid resistance loci in black raspberry (Rubus occidentalis L.). Molecular Breeding, 2018, 38, 1.	2.1	8
96	Rapid Synthesis of a Long Double-Stranded Oligonucleotide from a Single-Stranded Nucleotide Using Magnetic Beads and an Oligo Library. PLoS ONE, 2016, 11, e0149774.	2.5	7
97	Wholeâ€Plant Manual and Imageâ€Based Phenotyping in Controlled Environments. Current Protocols in Plant Biology, 2017, 2, 1-21.	2.8	6
98	Escalation in the host-pathogen arms race: A host resistance response corresponds to a heightened bacterial virulence response. PLoS Pathogens, 2021, 17, e1009175.	4.7	5
99	Sequence and Analysis of the Black Raspberry (Rubus occidentalis) Genome. Compendium of Plant Genomes, 2018, , 185-197.	0.5	3
100	The Brachypodium distachyon Reference Genome. Plant Genetics and Genomics: Crops and Models, 2015, , 55-70.	0.3	2
101	Editorial overview: Genome studies and molecular genetics: data-driven approaches to genotype-to-phenotype studies in crops. Current Opinion in Plant Biology, 2015, 24, iv-vi.	7.1	1
102	<i>DCT4</i>â€"A New Member of the Dicarboxylate Transporter Family in C4 Grasses. Genome Biology and Evolution, 2021, 13, .	2.5	1
103	De Novo Short-Read Assembly. , 2012, , 85-105.		0