

# Todd C Mockler

## List of Publications by Year in descending order

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Version: 2024-02-01

103  
papers

14,364  
citations

20797

60  
h-index

30058

103  
g-index

123  
all docs

123  
docs citations

123  
times ranked

16641  
citing authors

#	ARTICLE	IF	CITATIONS
1	Data-Driven Artificial Intelligence for Calibration of Hyperspectral Big Data. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2022, 60, 1-20.	2.7	16
2	The recent evolutionary rescue of a staple crop depended on over half a century of global germplasm exchange. <i>Science Advances</i> , 2022, 8, eabj4633.	4.7	9
3	Escalation in the host-pathogen arms race: A host resistance response corresponds to a heightened bacterial virulence response. <i>PLoS Pathogens</i> , 2021, 17, e1009175.	2.1	5
4	<i>DCT4</i> A New Member of the Dicarboxylate Transporter Family in C4 Grasses. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	1
5	Genomic patterns of structural variation among diverse genotypes of <i>Sorghum bicolor</i> and a potential role for deletions in local adaptation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	9
6	Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , 2021, 7, 17-24.	4.7	52
7	Genome and time-of-day transcriptome of <i>Wolffia australiana</i> link morphological minimization with gene loss and less growth control. <i>Genome Research</i> , 2021, 31, 225-238.	2.4	56
8	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. <i>Nature Communications</i> , 2020, 11, 884.	5.8	101
9	Expansion of the circadian transcriptome in <i>Brassica rapa</i> and genome-wide diversification of paralog expression patterns. <i>ELife</i> , 2020, 9, .	2.8	26
10	Time of day and network reprogramming during drought induced CAM photosynthesis in <i>Sedum album</i> . <i>PLoS Genetics</i> , 2019, 15, e1008209.	1.5	59
11	Target Capture Sequencing Unravels <i>Rubus</i> Evolution. <i>Frontiers in Plant Science</i> , 2019, 10, 1615.	1.7	73
12	Chromosome-scale scaffolding of the black raspberry ( <i>Rubus occidentalis</i> L.) genome based on chromatin interaction data. <i>Horticulture Research</i> , 2018, 5, 8.	2.9	50
13	Extreme haplotype variation in the desiccation-tolerant clubmoss <i>Selaginella lepidophylla</i> . <i>Nature Communications</i> , 2018, 9, 13.	5.8	89
14	Climate-smart crops with enhanced photosynthesis. <i>Journal of Experimental Botany</i> , 2018, 69, 3801-3809.	2.4	50
15	Characterization of aphid resistance loci in black raspberry ( <i>Rubus occidentalis</i> L.). <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	8
16	A near complete, chromosome-scale assembly of the black raspberry ( <i>Rubus occidentalis</i> ) genome. <i>GigaScience</i> , 2018, 7, .	3.3	86
17	Sequence and Analysis of the Black Raspberry ( <i>Rubus occidentalis</i> ) Genome. <i>Compendium of Plant Genomes</i> , 2018, , 185-197.	0.3	3
18	High density SNP mapping and QTL analysis for time of leaf budburst in <i>Corylus avellana</i> L.. <i>PLoS ONE</i> , 2018, 13, e0195408.	1.1	52

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19	Whole-Plant Manual and Image-Based Phenotyping in Controlled Environments. <i>Current Protocols in Plant Biology</i> , 2017, 2, 1-21.	2.8	6
20	Precise insertion and guided editing of higher plant genomes using Cpf1 CRISPR nucleases. <i>Scientific Reports</i> , 2017, 7, 11606.	1.6	164
21	Seed desiccation mechanisms co-opted for vegetative desiccation in the resurrection grass <i>Oropetium thomaeum</i> . <i>Plant, Cell and Environment</i> , 2017, 40, 2292-2306.	2.8	49
22	High throughput phenotyping to accelerate crop breeding and monitoring of diseases in the field. <i>Current Opinion in Plant Biology</i> , 2017, 38, 184-192.	3.5	242
23	Temporal and spatial transcriptomic and microRNA dynamics of CAM photosynthesis in pineapple. <i>Plant Journal</i> , 2017, 92, 19-30.	2.8	78
24	Cross-species complementation reveals conserved functions for EARLY FLOWERING 3 between monocots and dicots. <i>Plant Direct</i> , 2017, 1, e00018.	0.8	21
25	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017, 32, 380-393.	1.4	237
26	Comprehensive definition of genome features in <i>Spirodela polyrhiza</i> by high-depth physical mapping and short-read DNA sequencing strategies. <i>Plant Journal</i> , 2017, 89, 617-635.	2.8	115
27	Temporal network analysis identifies early physiological and transcriptomic indicators of mild drought in <i>Brassica rapa</i> . <i>ELife</i> , 2017, 6, .	2.8	95
28	Comparative Analysis of Vertebrate Diurnal/Circadian Transcriptomes. <i>PLoS ONE</i> , 2017, 12, e0169923.	1.1	29
29	The genome of black raspberry ( <i>Rubus occidentalis</i> ). <i>Plant Journal</i> , 2016, 87, 535-547.	2.8	111
30	Grasses suppress shoot-borne roots to conserve water during drought. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8861-8866.	3.3	111
31	Rapid Synthesis of a Long Double-Stranded Oligonucleotide from a Single-Stranded Nucleotide Using Magnetic Beads and an Oligo Library. <i>PLoS ONE</i> , 2016, 11, e0149774.	1.1	7
32	Highly sensitive image-derived indices of water-stressed plants using hyperspectral imaging in SWIR and histogram analysis. <i>Scientific Reports</i> , 2015, 5, 15919.	1.6	78
33	A genetic linkage map of black raspberry ( <i>Rubus occidentalis</i> ) and the mapping of Ag 4 conferring resistance to the aphid <i>Amphorophora agathonica</i> . <i>Theoretical and Applied Genetics</i> , 2015, 128, 1631-1646.	1.8	35
34	Extensive Transcriptome Changes During Natural Onset and Release of Vegetative Bud Dormancy in <i>Populus</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 989.	1.7	91
35	Single-molecule sequencing of the desiccation-tolerant grass <i>Oropetium thomaeum</i> . <i>Nature</i> , 2015, 527, 508-511.	13.7	291
36	Translatome analyses capture of opposing tissue-specific brassinosteroid signals orchestrating root meristem differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 923-928.	3.3	113

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37	Environmental Stresses Modulate Abundance and Timing of Alternatively Spliced Circadian Transcripts in Arabidopsis. <i>Molecular Plant</i> , 2015, 8, 207-227.	3.9	142
38	Transcriptional networks in crops, clocks, and abiotic stress. <i>Current Opinion in Plant Biology</i> , 2015, 24, 39-46.	3.5	70
39	A Versatile Phenotyping System and Analytics Platform Reveals Diverse Temporal Responses to Water Availability in Setaria. <i>Molecular Plant</i> , 2015, 8, 1520-1535.	3.9	202
40	Editorial overview: Genome studies and molecular genetics: data-driven approaches to genotype-to-phenotype studies in crops. <i>Current Opinion in Plant Biology</i> , 2015, 24, iv-vi.	3.5	1
41	Alternative splicing in plants: directing traffic at the crossroads of adaptation and environmental stress. <i>Current Opinion in Plant Biology</i> , 2015, 24, 125-135.	3.5	215
42	Highly specific gene silencing in a monocot species by artificial microRNAs derived from chimeric miRNA precursors. <i>Plant Journal</i> , 2015, 82, 1061-1075.	2.8	45
43	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
44	The Brachypodium distachyon Reference Genome. <i>Plant Genetics and Genomics: Crops and Models</i> , 2015, , 55-70.	0.3	2
45	Sequencing and characterization of the anadromous steelhead ( <i>Oncorhynchus mykiss</i> ) transcriptome. <i>Marine Genomics</i> , 2014, 15, 13-15.	0.4	18
46	Comparative analyses of C4 and C3 photosynthesis in developing leaves of maize and rice. <i>Nature Biotechnology</i> , 2014, 32, 1158-1165.	9.4	228
47	Environmental Stresses Modulate Abundance and Timing of Alternatively Spliced Circadian Transcripts in Arabidopsis. <i>Molecular Plant</i> , 2014, , .	3.9	9
48	A new alternative in plant retrograde signaling. <i>Genome Biology</i> , 2014, 15, 117.	13.9	8
49	Genome diversity in <i>Brachypodium distachyon</i> : deep sequencing of highly diverse inbred lines. <i>Plant Journal</i> , 2014, 79, 361-374.	2.8	80
50	Analysis of Global Gene Expression in <i>Brachypodium distachyon</i> Reveals Extensive Network Plasticity in Response to Abiotic Stress. <i>PLoS ONE</i> , 2014, 9, e87499.	1.1	80
51	Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	13.9	329
52	Methylome reorganization during in vitro dedifferentiation and regeneration of <i>Populus trichocarpa</i> . <i>BMC Plant Biology</i> , 2013, 13, 92.	1.6	51
53	Functional characterization of cinnamyl alcohol dehydrogenase and caffeic acid O-methyltransferase in <i>Brachypodium distachyon</i> . <i>BMC Biotechnology</i> , 2013, 13, 61.	1.7	84
54	Architecture and evolution of a minute plant genome. <i>Nature</i> , 2013, 498, 94-98.	13.7	293

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55	Subset of heat-shock transcription factors required for the early response of <i>Arabidopsis</i> to excess light. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14474-14479.	3.3	123
56	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of <i>Brachypodium distachyon</i> . <i>Genome Biology</i> , 2013, 14, R145.	13.9	67
57	Assembly and Characterization of the European Hazelnut "Jefferson"™ Transcriptome. <i>Crop Science</i> , 2012, 52, 2679-2686.	0.8	35
58	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	3.5	173
59	Detection and Quantification of Alternative Splicing Variants Using RNA-seq. <i>Methods in Molecular Biology</i> , 2012, 883, 97-110.	0.4	22
60	Dynamic DNA cytosine methylation in the <i>Populus trichocarpa</i> genome: tissue-level variation and relationship to gene expression. <i>BMC Genomics</i> , 2012, 13, 27.	1.2	136
61	Comparative analyses reveal potential uses of <i>Brachypodium distachyon</i> as a model for cold stress responses in temperate grasses. <i>BMC Plant Biology</i> , 2012, 12, 65.	1.6	46
62	Unproductive alternative splicing and nonsense mRNAs: A widespread phenomenon among plant circadian clock genes. <i>Biology Direct</i> , 2012, 7, 20.	1.9	125
63	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. <i>PLoS ONE</i> , 2012, 7, e31745.	1.1	249
64	Host-Selective Toxins of <i>Pyrenophora tritici-repentis</i> Induce Common Responses Associated with Host Susceptibility. <i>PLoS ONE</i> , 2012, 7, e40240.	1.1	34
65	De Novo Short-Read Assembly. , 2012, , 85-105.		0
66	Exploring the Switchgrass Transcriptome Using Second-Generation Sequencing Technology. <i>PLoS ONE</i> , 2012, 7, e34225.	1.1	60
67	Development and Evaluation of a 9K SNP Array for Peach by Internationally Coordinated SNP Detection and Validation in Breeding Germplasm. <i>PLoS ONE</i> , 2012, 7, e35668.	1.1	199
68	Development and Evaluation of a Genome-Wide 6K SNP Array for Diploid Sweet Cherry and Tetraploid Sour Cherry. <i>PLoS ONE</i> , 2012, 7, e48305.	1.1	109
69	Global Profiling of Rice and Poplar Transcriptomes Highlights Key Conserved Circadian-Controlled Pathways and cis-Regulatory Modules. <i>PLoS ONE</i> , 2011, 6, e16907.	1.1	188
70	GENE-Counter: A Computational Pipeline for the Analysis of RNA-Seq Data for Gene Expression Differences. <i>PLoS ONE</i> , 2011, 6, e25279.	1.1	66
71	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. <i>Genome Biology and Evolution</i> , 2011, 3, 641-653.	1.1	87
72	The genome of woodland strawberry ( <i>Fragaria vesca</i> ). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091

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73	A multi-organ transcriptome resource for the Burmese Python ( <i>Python molurus bivittatus</i> ). <i>BMC Research Notes</i> , 2011, 4, 310.	0.6	18
74	Expression, Splicing, and Evolution of the Myosin Gene Family in Plants. <i>Plant Physiology</i> , 2011, 155, 1191-1204.	2.3	78
75	Brachypodium as a Model for the Grasses: Today and the Future. <i>Plant Physiology</i> , 2011, 157, 3-13.	2.3	243
76	Cell-autonomous circadian clock of hepatocytes drives rhythms in transcription and polyamine synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18560-18565.	3.3	37
77	An SSR-based genetic linkage map of the model grass <i>Brachypodium distachyon</i> . <i>Genome</i> , 2010, 53, 1-13.	0.9	55
78	Supersplat: spliced RNA-seq alignment. <i>Bioinformatics</i> , 2010, 26, 1500-1505.	1.8	41
79	Genome-wide mapping of alternative splicing in <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2010, 20, 45-58.	2.4	825
80	Analysis of Transcriptome Changes Induced by Ptr ToxA in Wheat Provides Insights into the Mechanisms of Plant Susceptibility. <i>Molecular Plant</i> , 2009, 2, 1067-1083.	3.9	54
81	A Recommendation for Naming Transcription Factor Proteins in the Grasses. <i>Plant Physiology</i> , 2009, 149, 4-6.	2.3	45
82	cis-Regulatory elements in plant cell signaling. <i>Current Opinion in Plant Biology</i> , 2009, 12, 643-649.	3.5	105
83	QSORA: a quality-value guided de novo short read assembler. <i>BMC Bioinformatics</i> , 2009, 10, 69.	1.2	53
84	Genome scale transcriptome analysis of shoot organogenesis in <i>Populus</i> . <i>BMC Plant Biology</i> , 2009, 9, 132.	1.6	45
85	Strong population structure characterizes weediness gene evolution in the invasive grass species <i>Brachypodium distachyon</i> . <i>Molecular Ecology</i> , 2009, 18, 2588-2601.	2.0	37
86	IDN1 and IDN2 are required for de novo DNA methylation in <i>Arabidopsis thaliana</i> . <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1325-1327.	3.6	98
87	Applications of Ultra-high-Throughput Sequencing. <i>Methods in Molecular Biology</i> , 2009, 553, 79-108.	0.4	72
88	Conserved Daily Transcriptional Programs in <i>Carica papaya</i> . <i>Tropical Plant Biology</i> , 2008, 1, 236-245.	1.0	37
89	A zinc knuckle protein that negatively controls morning-specific growth in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17193-17198.	3.3	67
90	Development of Genetic and Genomic Research Resources for <i>Brachypodium distachyon</i> , a New Model System for Grass Crop Research. <i>Crop Science</i> , 2008, 48, S-69.	0.8	133

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91	Multiplex sequencing of plant chloroplast genomes using Solexa sequencing-by-synthesis technology. <i>Nucleic Acids Research</i> , 2008, 36, e122-e122.	6.5	356
92	Network Discovery Pipeline Elucidates Conserved Time-of-Day-Specific cis-Regulatory Modules. <i>PLoS Genetics</i> , 2008, 4, e14.	1.5	474
93	A Morning-Specific Phytohormone Gene Expression Program underlying Rhythmic Plant Growth. <i>PLoS Biology</i> , 2008, 6, e225.	2.6	197
94	Signals from chloroplasts converge to regulate nuclear gene expression. <i>Science</i> , 2007, 316, 715-9.	6.0	638
95	Signals from Chloroplasts Converge to Regulate Nuclear Gene Expression. <i>Science</i> , 2007, 316, 715-719.	6.0	196
96	Applications of DNA tiling arrays for whole-genome analysis. <i>Genomics</i> , 2005, 85, 1-15.	1.3	376
97	Interdependency of Brassinosteroid and Auxin Signaling in Arabidopsis. <i>PLoS Biology</i> , 2004, 2, e258.	2.6	499
98	Regulation of flowering time in Arabidopsis by K homology domain proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12759-12764.	3.3	150
99	Blue Light-Dependent in Vivo and in Vitro Phosphorylation of Arabidopsis Cryptochrome 1. <i>Plant Cell</i> , 2003, 15, 2421-2429.	3.1	175
100	Regulation of photoperiodic flowering by Arabidopsis photoreceptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2140-2145.	3.3	273
101	Regulation of Arabidopsis cryptochrome 2 by blue-light-dependent phosphorylation. <i>Nature</i> , 2002, 417, 763-767.	13.7	271
102	SUB1, an Arabidopsis Ca <sup>2+</sup> -Binding Protein Involved in Cryptochrome and Phytochrome Coaction. <i>Science</i> , 2001, 291, 487-490.	6.0	141
103	Regulation of Flowering Time by Arabidopsis Photoreceptors. <i>Science</i> , 1998, 279, 1360-1363.	6.0	713