Todd P Michael

List of Publications by Citations

Source: https://exaly.com/author-pdf/608848/todd-p-michael-publications-by-citations.pdf

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

89 46 11,541 102 h-index g-index citations papers 6.5 14,328 102 13.1 L-index avg, IF ext. citations ext. papers

| # | Paper | IF | Citations |
|----|---|----------------|-----------|
| 89 | Genome sequencing and analysis of the model grass Brachypodium distachyon. <i>Nature</i> , 2010 , 463, 763- | 850.4 | 1399 |
| 88 | Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. <i>Nature</i> , 2010 , 465, 627-31 | 50.4 | 1257 |
| 87 | The genome of woodland strawberry (Fragaria vesca). <i>Nature Genetics</i> , 2011 , 43, 109-16 | 36.3 | 881 |
| 86 | The draft genome of the transgenic tropical fruit tree papaya (Carica papaya Linnaeus). <i>Nature</i> , 2008 , 452, 991-6 | 50.4 | 826 |
| 85 | The Selaginella genome identifies genetic changes associated with the evolution of vascular plants. <i>Science</i> , 2011 , 332, 960-3 | 33.3 | 622 |
| 84 | 1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. <i>Cell</i> , 2016 , 166, 481 | - 40 .2 | 620 |
| 83 | Network discovery pipeline elucidates conserved time-of-day-specific cis-regulatory modules. <i>PLoS Genetics</i> , 2008 , 4, e14 | 6 | 389 |
| 82 | Agriculture: Feeding the future. <i>Nature</i> , 2013 , 499, 23-4 | 50.4 | 363 |
| 81 | Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , 2016 , 166, 492-505 | 56.2 | 353 |
| 80 | Enhanced fitness conferred by naturally occurring variation in the circadian clock. <i>Science</i> , 2003 , 302, 1049-53 | 33.3 | 347 |
| 79 | Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.). <i>Genome Biology</i> , 2013 , 14, R41 | 18.3 | 241 |
| 78 | Architecture and evolution of a minute plant genome. <i>Nature</i> , 2013 , 498, 94-8 | 50.4 | 237 |
| 77 | Single-molecule sequencing of the desiccation-tolerant grass Oropetium thomaeum. <i>Nature</i> , 2015 , 527, 508-11 | 50.4 | 208 |
| 76 | The First 50 Plant Genomes. <i>Plant Genome</i> , 2013 , 6, plantgenome2013.03.0001in | 4.4 | 182 |
| 75 | A morning-specific phytohormone gene expression program underlying rhythmic plant growth. <i>PLoS Biology</i> , 2008 , 6, e225 | 9.7 | 174 |
| 74 | The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of Arabidopsis thaliana. <i>Nature Genetics</i> , 2006 , 38, 711-5 | 36.3 | 171 |
| 73 | High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , 2018 , 9, 541 | 17.4 | 164 |

(2020-2015)

| 72 | Progress, challenges and the future of crop genomes. Current Opinion in Plant Biology, 2015, 24, 71-81 | 9.9 | 149 |
|----|--|--------------|-----|
| 71 | Enhancer trapping reveals widespread circadian clock transcriptional control in Arabidopsis. <i>Plant Physiology</i> , 2003 , 132, 629-39 | 6.6 | 149 |
| 70 | Genome-wide patterns of single-feature polymorphism in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 12057-62 | 11.5 | 147 |
| 69 | Phase-specific circadian clock regulatory elements in Arabidopsis. <i>Plant Physiology</i> , 2002 , 130, 627-38 | 6.6 | 135 |
| 68 | Global profiling of rice and poplar transcriptomes highlights key conserved circadian-controlled pathways and cis-regulatory modules. <i>PLoS ONE</i> , 2011 , 6, e16907 | 3.7 | 132 |
| 67 | 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, 12759-64 | 11.5 | 128 |
| 66 | Two Arabidopsis circadian oscillators can be distinguished by differential temperature sensitivity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 6878-83 | 11.5 | 123 |
| 65 | Integrative analysis of chromatin states in Arabidopsis identified potential regulatory mechanisms for natural antisense transcript production. <i>Plant Journal</i> , 2013 , 73, 77-90 | 6.9 | 116 |
| 64 | SOPRA: Scaffolding algorithm for paired reads via statistical optimization. <i>BMC Bioinformatics</i> , 2010 , 11, 345 | 3.6 | 101 |
| 63 | Type II protein arginine methyltransferase 5 (PRMT5) is required for circadian period determination in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 21211-6 | 11.5 | 99 |
| 62 | Cis-regulatory changes at FLOWERING LOCUS T mediate natural variation in flowering responses of Arabidopsis thaliana. <i>Genetics</i> , 2009 , 183, 723-32, 1SI-7SI | 4 | 95 |
| 61 | Plant genome size variation: bloating and purging DNA. <i>Briefings in Functional Genomics</i> , 2014 , 13, 308- | 17 .9 | 91 |
| 60 | 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. <i>Annals of Botany</i> , 2014 , 114, 1651-63 | 4.1 | 85 |
| 59 | The out of phase 1 mutant defines a role for PHYB in circadian phase control in Arabidopsis. <i>Plant Physiology</i> , 2002 , 129, 1674-85 | 6.6 | 83 |
| 58 | The genome of black raspberry (Rubus occidentalis). Plant Journal, 2016, 87, 535-47 | 6.9 | 78 |
| 57 | Tcf4 Regulates Synaptic Plasticity, DNA Methylation, and Memory Function. <i>Cell Reports</i> , 2016 , 16, 2666 | 5-26.85 | 74 |
| 56 | Comprehensive definition of genome features in Spirodela polyrhiza by high-depth physical mapping and short-read DNA sequencing strategies. <i>Plant Journal</i> , 2017 , 89, 617-635 | 6.9 | 73 |
| 55 | Building near-complete plant genomes. Current Opinion in Plant Biology, 2020, 54, 26-33 | 9.9 | 71 |

| 54 | Isolation and analysis of high quality nuclear DNA with reduced organellar DNA for plant genome sequencing and resequencing. <i>BMC Biotechnology</i> , 2011 , 11, 54 | 3.5 | 62 |
|----|--|------|----|
| 53 | Analysis of global gene expression in Brachypodium distachyon reveals extensive network plasticity in response to abiotic stress. <i>PLoS ONE</i> , 2014 , 9, e87499 | 3.7 | 62 |
| 52 | The complex architecture and epigenomic impact of plant T-DNA insertions. <i>PLoS Genetics</i> , 2019 , 15, e1007819 | 6 | 61 |
| 51 | A zinc knuckle protein that negatively controls morning-specific growth in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 17193-8 | 11.5 | 58 |
| 50 | Evolution of Genome Size in Duckweeds (Lemnaceae). <i>Journal of Botany</i> , 2011 , 2011, 1-9 | О | 57 |
| 49 | Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. <i>Nature Communications</i> , 2020 , 11, 884 | 17.4 | 51 |
| 48 | Elevated temperature drives kelp microbiome dysbiosis, while elevated carbon dioxide induces water microbiome disruption. <i>PLoS ONE</i> , 2018 , 13, e0192772 | 3.7 | 51 |
| 47 | Cytochrome P450 monooxygenases as reporters for circadian-regulated pathways. <i>Plant Physiology</i> , 2009 , 150, 858-78 | 6.6 | 50 |
| 46 | Extreme haplotype variation in the desiccation-tolerant clubmoss Selaginella lepidophylla. <i>Nature Communications</i> , 2018 , 9, 13 | 17.4 | 48 |
| 45 | Simple sequence repeats provide a substrate for phenotypic variation in the Neurospora crassa circadian clock. <i>PLoS ONE</i> , 2007 , 2, e795 | 3.7 | 48 |
| 44 | The carnivorous bladderwort (Utricularia, Lentibulariaceae): a system inflates. <i>Journal of Experimental Botany</i> , 2010 , 61, 5-9 | 7 | 46 |
| 43 | An SSR-based genetic linkage map of the model grass Brachypodium distachyon. <i>Genome</i> , 2010 , 53, 1-1 | 32.4 | 45 |
| 42 | A complete Cannabis chromosome assembly and adaptive admixture for elevated cannabidiol (CBD) content | | 40 |
| 41 | Generating a high-confidence reference genome map of the Greater Duckweed by integration of cytogenomic, optical mapping, and Oxford Nanopore technologies. <i>Plant Journal</i> , 2018 , 96, 670-684 | 6.9 | 38 |
| 40 | Seed desiccation mechanisms co-opted for vegetative desiccation in the resurrection grass Oropetium thomaeum. <i>Plant, Cell and Environment</i> , 2017 , 40, 2292-2306 | 8.4 | 34 |
| 39 | Conserved Daily Transcriptional Programs in Carica papaya. <i>Tropical Plant Biology</i> , 2008 , 1, 236-245 | 1.6 | 33 |
| 38 | Scalable Biosynthesis of the Seaweed Neurochemical, Kainic Acid. <i>Angewandte Chemie - International Edition</i> , 2019 , 58, 8454-8457 | 16.4 | 31 |
| 37 | Time of day and network reprogramming during drought induced CAM photosynthesis in Sedum album. <i>PLoS Genetics</i> , 2019 , 15, e1008209 | 6 | 29 |

| 36 | Lycophyte plastid genomics: extreme variation in GC, gene and intron content and multiple inversions between a direct and inverted orientation of the rRNA repeat. <i>New Phytologist</i> , 2019 , 222, 1061-1075 | 9.8 | 29 |
|----|---|-------|----|
| 35 | The Chloroplast Genome of Utricularia reniformis Sheds Light on the Evolution of the ndh Gene Complex of Terrestrial Carnivorous Plants from the Lentibulariaceae Family. <i>PLoS ONE</i> , 2016 , 11, e016. | 51376 | 28 |
| 34 | A new Cannabis genome assembly associates elevated cannabidiol (CBD) with hemp introgressed into marijuana. <i>New Phytologist</i> , 2021 , 230, 1665-1679 | 9.8 | 28 |
| 33 | Filtering error from SOLiD Output. <i>Bioinformatics</i> , 2010 , 26, 849-50 | 7.2 | 25 |
| 32 | Return of the Lemnaceae: duckweed as a model plant system in the genomics and postgenomics era. <i>Plant Cell</i> , 2021 , 33, 3207-3234 | 11.6 | 22 |
| 31 | The mitochondrial genome of the terrestrial carnivorous plant Utricularia reniformis (Lentibulariaceae): Structure, comparative analysis and evolutionary landmarks. <i>PLoS ONE</i> , 2017 , 12, e0180484 | 3.7 | 19 |
| 30 | Genome and time-of-day transcriptome of link morphological minimization with gene loss and less growth control. <i>Genome Research</i> , 2020 , | 9.7 | 17 |
| 29 | The genetic and epigenetic landscape of the centromeres. <i>Science</i> , 2021 , 374, eabi7489 | 33.3 | 15 |
| 28 | Intraspecific Variation within the Species Morphotypes Based on Chloroplast Genomes. <i>International Journal of Molecular Sciences</i> , 2019 , 20, | 6.3 | 14 |
| 27 | An Antisense Oligonucleotide Leads to Suppressed Transcription of Hdac2 and Long-Term Memory Enhancement. <i>Molecular Therapy - Nucleic Acids</i> , 2020 , 19, 1399-1412 | 10.7 | 12 |
| 26 | Estimation of nuclear DNA content of cultivated Ocimum species by using flow cytometry. <i>Israel Journal of Plant Sciences</i> , 2010 , 58, 183-189 | 0.6 | 12 |
| 25 | Temporal, Environmental, and Biological Drivers of the Mucosal Microbiome in a Wild Marine Fish, Scomber japonicus. <i>MSphere</i> , 2020 , 5, | 5 | 11 |
| 24 | Selective inheritance of target genes from only one parent of sexually reproduced F1 progeny in Arabidopsis. <i>Nature Communications</i> , 2021 , 12, 3854 | 17.4 | 11 |
| 23 | The Arabidopsis circadian system. <i>The Arabidopsis Book</i> , 2002 , 1, e0044 | 3 | 10 |
| 22 | Comparative genomic analysis of Genlisea (corkscrew plants-Lentibulariaceae) chloroplast genomes reveals an increasing loss of the ndh genes. <i>PLoS ONE</i> , 2018 , 13, e0190321 | 3.7 | 9 |
| 21 | The Terrestrial Carnivorous Plant Sheds Light on Environmental and Life-Form Genome Plasticity. <i>International Journal of Molecular Sciences</i> , 2019 , 21, | 6.3 | 8 |
| 20 | Improved Spirodela polyrhiza genome and proteomic analyses reveal a conserved chromosomal structure with high abundance of chloroplastic proteins favoring energy production. <i>Journal of Experimental Botany</i> , 2021 , 72, 2491-2500 | 7 | 8 |
| 19 | High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell | | 7 |

| 18 | Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation. <i>New Phytologist</i> , 2020 , 227, 1709-1724 | 9.8 | 6 |
|------------------|--|-------|-------------|
| 17 | Sequence-guided approach to genotyping plant clones and species using polymorphic NB-ARC-related genes. <i>Plant Molecular Biology</i> , 2018 , 98, 219-231 | 4.6 | 6 |
| 16 | A new Spirodela polyrhiza genome and proteome reveal a conserved chromosomal structure with high abundances of proteins favoring energy production | | 4 |
| 15 | Development of microsatellite markers for the carnivorous plant Genlisea aurea (Lentibulariaceae) using genomics data of NGS. <i>Molecular Biology Reports</i> , 2018 , 45, 57-61 | 2.8 | 3 |
| 14 | The complete chloroplast genome sequence of the leafy bladderwort, Utricularia foliosa L. (Lentibulariaceae). <i>Conservation Genetics Resources</i> , 2017 , 9, 213-216 | 0.8 | 3 |
| 13 | Underwater CAM photosynthesis elucidated by Isoetes genome. <i>Nature Communications</i> , 2021 , 12, 6348 | 817.4 | 3 |
| 12 | Large structural variations in the haplotype-resolved African cassava genome. Plant Journal, 2021, | 6.9 | 2 |
| 11 | Horizontal[Iransfer and Levolution of Iwall Leichoic Lacid Legene Leassettes in I F1000Research, 2021, 10, 354 | 3.6 | 2 |
| 10 | Scalable Biosynthesis of the Seaweed Neurochemical, Kainic Acid. <i>Angewandte Chemie</i> , 2019 , 131, 8542 | 3.6 | 1 |
| | | | |
| 9 | The complex architecture of plant transgene insertions | | 1 |
| 9 | The complex architecture of plant transgene insertions Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation | | 1 |
| | Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon | | |
| 8 | Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation Genome and time-of-day transcriptome of Wolffia australiana link morphological extreme | 3.6 | 1 |
| 8 | Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation Genome and time-of-day transcriptome of Wolffia australiana link morphological extreme minimization with un-gated plant growth | 3.6 | 1 |
| 8 7 6 | Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation Genome and time-of-day transcriptome of Wolffia australiana link morphological extreme minimization with un-gated plant growth A pan-genome method to determine core regions of the and genomes. F1000Research, 2021, 10, 286 | 3.6 | 1 1 |
| 8 7 6 5 | Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation Genome and time-of-day transcriptome of Wolffia australiana link morphological extreme minimization with un-gated plant growth A pan-genome method to determine core regions of the and genomes. F1000Research, 2021, 10, 286 Large structural variations in the haplotype-resolved African cassava genome A pan-genome method to determine core regions of the Bacillus subtilis and Escherichia coli | | 1 1 1 |
| 8 7 6 5 | Changes in ambient temperature are the prevailing cue in determining Brachypodium distachyon diurnal gene regulation Genome and time-of-day transcriptome of Wolffia australiana link morphological extreme minimization with un-gated plant growth A pan-genome method to determine core regions of the and genomes. F1000Research, 2021, 10, 286 Large structural variations in the haplotype-resolved African cassava genome A pan-genome method to determine core regions of the Bacillus subtilis and Escherichia coli genomes. F1000Research, 2021, 10, 286 Contrasting a reference cranberry genome to a crop wild relative provides insights into adaptation, | 3.6 | 1 1 1 1 1 |