

Milos Tanurdzic

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6015114/publications.pdf>

Version: 2024-02-01

40
papers

4,157
citations

236925

25
h-index

361022

35
g-index

43
all docs

43
docs citations

43
times ranked

6316
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Parallel introgression contributes to parallel differentiation and contrasting hybridization outcomes between invasive and native marine mussels. <i>Journal of Evolutionary Biology</i> , 2021, 34, 175-192. | 1.7 | 10 |
| 2 | Loss of Small-RNA-Directed DNA Methylation in the Plant Cell Cycle Promotes Germline Reprogramming and Somaclonal Variation. <i>Current Biology</i> , 2021, 31, 591-600.e4. | 3.9 | 36 |
| 3 | Profiling the endosperm, one nucleus at a time. <i>Nature Plants</i> , 2021, 7, 710-711. | 9.3 | 0 |
| 4 | An optimised chromatin immunoprecipitation (ChIP) method for starchy leaves of <i>Nicotiana benthamiana</i> to study histone modifications of an allotetraploid plant. <i>Molecular Biology Reports</i> , 2020, 47, 9499-9509. | 2.3 | 4 |
| 5 | De novo transcriptome assembly and annotation for gene discovery in avocado, macadamia and mango. <i>Scientific Data</i> , 2020, 7, 9. | 5.3 | 22 |
| 6 | SDG8-Mediated Histone Methylation and RNA Processing Function in the Response to Nitrate Signaling. <i>Plant Physiology</i> , 2020, 182, 215-227. | 4.8 | 30 |
| 7 | Juvenility and Vegetative Phase Transition in Tropical/Subtropical Tree Crops. <i>Frontiers in Plant Science</i> , 2019, 10, 729. | 3.6 | 38 |
| 8 | A phenol/chloroform-free method to extract nucleic acids from recalcitrant, woody tropical species for gene expression and sequencing. <i>Plant Methods</i> , 2019, 15, 62. | 4.3 | 67 |
| 9 | Identification of Molecular Integrators Shows that Nitrogen Actively Controls the Phosphate Starvation Response in Plants. <i>Plant Cell</i> , 2019, 31, 1171-1184. | 6.6 | 135 |
| 10 | De Novo Plant Transcriptome Assembly and Annotation Using Illumina RNA-Seq Reads. <i>Methods in Molecular Biology</i> , 2019, 1933, 265-275. | 0.9 | 9 |
| 11 | Long non-coding regulatory RNAs in sponges and insights into the origin of animal multicellularity. <i>RNA Biology</i> , 2018, 15, 1-7. | 3.1 | 14 |
| 12 | Sponge Long Non-Coding RNAs Are Expressed in Specific Cell Types and Conserved Networks. <i>Non-coding RNA</i> , 2018, 4, 6. | 2.6 | 8 |
| 13 | Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2205-2214. | 1.8 | 22 |
| 14 | Sirtuins in the phylum Basidiomycota: A role in virulence in <i>Cryptococcus neoformans</i> . <i>Scientific Reports</i> , 2017, 7, 46567. | 3.3 | 27 |
| 15 | De novo transcriptome assembly reveals high transcriptional complexity in <i>Pisum sativum</i> axillary buds and shows rapid changes in expression of diurnally regulated genes. <i>BMC Genomics</i> , 2017, 18, 221. | 2.8 | 24 |
| 16 | Origin and evolution of the metazoan non-coding regulatory genome. <i>Developmental Biology</i> , 2017, 427, 193-202. | 2.0 | 42 |
| 17 | Convergent microevolution of <i>Cryptococcus neoformans</i> hypervirulence in the laboratory and the clinic. <i>Scientific Reports</i> , 2017, 7, 17918. | 3.3 | 34 |
| 18 | Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. <i>ELife</i> , 2017, 6, . | 6.0 | 51 |

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|----|---|------|-----------|
| 19 | Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. <i>Molecular Biology and Evolution</i> , 2015, 32, 2367-2382. | 8.9 | 66 |
| 20 | The histone methyltransferase SDG8 mediates the epigenetic modification of light and carbon responsive genes in plants. <i>Genome Biology</i> , 2015, 16, 79. | 8.8 | 91 |
| 21 | Differential sRNA Regulation in Leaves and Roots of Sugarcane under Water Depletion. <i>PLoS ONE</i> , 2014, 9, e93822. | 2.5 | 37 |
| 22 | Integrated RNA-seq and sRNA-seq analysis identifies novel nitrate-responsive genes in <i>Arabidopsis thaliana</i> roots. <i>BMC Genomics</i> , 2013, 14, 701. | 2.8 | 76 |
| 23 | Computational identification and analysis of novel sugarcane microRNAs. <i>BMC Genomics</i> , 2012, 13, 290. | 2.8 | 63 |
| 24 | Origins of Novel Phenotypic Variation in Polyploids. , 2012, , 57-76. | | 15 |
| 25 | The <i>Selaginella</i> Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963. | 12.6 | 794 |
| 26 | Targeted Isolation Sequence Assembly and Characterization of White Spruce. , 2011, , 23-38. | | 0 |
| 27 | <i>Arabidopsis thaliana</i> Chromosome 4 Replicates in Two Phases That Correlate with Chromatin State. <i>PLoS Genetics</i> , 2010, 6, e1000982. | 3.5 | 65 |
| 28 | Epigenetic Reprogramming and Small RNA Silencing of Transposable Elements in Pollen. <i>Cell</i> , 2009, 136, 461-472. | 28.9 | 908 |
| 29 | ABAP1 is a novel plant Armadillo BTB protein involved in DNA replication and transcription. <i>EMBO Journal</i> , 2008, 27, 2746-2756. | 7.8 | 71 |
| 30 | Epigenetic Inheritance and Reprogramming in Plants and Fission Yeast. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2008, 73, 265-271. | 1.1 | 31 |
| 31 | Systems approach identifies an organic nitrogen-responsive gene network that is regulated by the master clock control gene <i>CCA1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4939-4944. | 7.1 | 333 |
| 32 | Epigenomic Consequences of Immortalized Plant Cell Suspension Culture. <i>PLoS Biology</i> , 2008, 6, e302. | 5.6 | 179 |
| 33 | Epigenetic Natural Variation in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2007, 5, e174. | 5.6 | 400 |
| 34 | Functional analysis and comparative genomics of expressed sequence tags from the lycophyte <i>Selaginella moellendorffii</i> . <i>BMC Genomics</i> , 2005, 6, 85. | 2.8 | 38 |
| 35 | Construction of a bacterial artificial chromosome library from the spikemoss <i>Selaginella moellendorffii</i> : a new resource for plant comparative genomics. <i>BMC Plant Biology</i> , 2005, 5, 10. | 3.6 | 53 |
| 36 | Replication, Repair, and Reactivation. <i>Developmental Cell</i> , 2005, 9, 724-725. | 7.0 | 3 |

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|----|---|-----|-----------|
| 37 | A systemic gene silencing method suitable for high throughput, reverse genetic analyses of gene function in fern gametophytes. BMC Plant Biology, 2004, 4, 6. | 3.6 | 51 |
| 38 | Sex-Determining Mechanisms in Land Plants. Plant Cell, 2004, 16, S61-S71. | 6.6 | 301 |
| 39 | Polyglutamine-encoding microsatellite contributes to LMW GS diversity in Triticum monococcum. Cereal Research Communications, 2004, 32, 301-308. | 1.6 | 0 |
| 40 | DESIGNING MICROARRAYS. Conference on Applied Statistics in Agriculture, 0, , . | 0.0 | 0 |