

Milos Tanurdzic

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

4,157
citations

236833

25
h-index

360920

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.	0.8	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.	1.8	36
3	Profiling the endosperm, one nucleus at a time. <i>Nature Plants</i> , 2021, 7, 710-711.	4.7	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.	1.0	4
5	De novo transcriptome assembly and annotation for gene discovery in avocado, macadamia and mango. <i>Scientific Data</i> , 2020, 7, 9.	2.4	22
6	SDG8-Mediated Histone Methylation and RNA Processing Function in the Response to Nitrate Signaling. <i>Plant Physiology</i> , 2020, 182, 215-227.	2.3	30
7	Juvenility and Vegetative Phase Transition in Tropical/Subtropical Tree Crops. <i>Frontiers in Plant Science</i> , 2019, 10, 729.	1.7	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.	1.9	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.	3.1	135
10	De Novo Plant Transcriptome Assembly and Annotation Using Illumina RNA-Seq Reads. <i>Methods in Molecular Biology</i> , 2019, 1933, 265-275.	0.4	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.	1.5	14
12	Sponge Long Non-Coding RNAs Are Expressed in Specific Cell Types and Conserved Networks. <i>Non-coding RNA</i> , 2018, 4, 6.	1.3	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.	0.8	22
14	Sirtuins in the phylum Basidiomycota: A role in virulence in <i>Cryptococcus neoformans</i> . <i>Scientific Reports</i> , 2017, 7, 46567.	1.6	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.	1.2	24
16	Origin and evolution of the metazoan non-coding regulatory genome. <i>Developmental Biology</i> , 2017, 427, 193-202.	0.9	42
17	Convergent microevolution of <i>Cryptococcus neoformans</i> hypervirulence in the laboratory and the clinic. <i>Scientific Reports</i> , 2017, 7, 17918.	1.6	34
18	Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. <i>ELife</i> , 2017, 6, .	2.8	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.	3.5	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.	3.8	91
21	Differential sRNA Regulation in Leaves and Roots of Sugarcane under Water Depletion. <i>PLoS ONE</i> , 2014, 9, e93822.	1.1	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.	1.2	76
23	Computational identification and analysis of novel sugarcane microRNAs. <i>BMC Genomics</i> , 2012, 13, 290.	1.2	63
24	Origins of Novel Phenotypic Variation in Polyploids. , 2012, , 57-76.		15
25	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. <i>Science</i> , 2011, 332, 960-963.	6.0	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.	1.5	65
28	Epigenetic Reprogramming and Small RNA Silencing of Transposable Elements in Pollen. <i>Cell</i> , 2009, 136, 461-472.	13.5	908
29	ABAP1 is a novel plant Armadillo BTB protein involved in DNA replication and transcription. <i>EMBO Journal</i> , 2008, 27, 2746-2756.	3.5	71
30	Epigenetic Inheritance and Reprogramming in Plants and Fission Yeast. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2008, 73, 265-271.	2.0	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.	3.3	333
32	Epigenomic Consequences of Immortalized Plant Cell Suspension Culture. <i>PLoS Biology</i> , 2008, 6, e302.	2.6	179
33	Epigenetic Natural Variation in <i>Arabidopsis thaliana</i> . <i>PLoS Biology</i> , 2007, 5, e174.	2.6	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.	1.2	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.	1.6	53
36	Replication, Repair, and Reactivation. <i>Developmental Cell</i> , 2005, 9, 724-725.	3.1	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.	1.6	51
38	Sex-Determining Mechanisms in Land Plants. Plant Cell, 2004, 16, S61-S71.	3.1	301
39	Polyglutamine-encoding microsatellite contributes to LMW GS diversity in Triticum monococcum. Cereal Research Communications, 2004, 32, 301-308.	0.8	0
40	DESIGNING MICROARRAYS. Conference on Applied Statistics in Agriculture, 0, , .	0.0	0