Milos Tanurdzic

List of Publications by Year
in descending order

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	Epigenetic Reprogramming and Small RNA Silencing of Transposable Elements in Pollen. Cell, 2009, 136, 461-472.	13.5	908
2	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	6.0	794
3	Epigenetic Natural Variation in Arabidopsis thaliana. PLoS Biology, 2007, 5, e174.	2.6	400
4	Systems approach identifies an organic nitrogen-responsive gene network that is regulated by the master clock control gene *CCA1*. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4939-4944.	3.3	333
5	Sex-Determining Mechanisms in Land Plants. Plant Cell, 2004, 16, S61-S71.	3.1	301
6	Epigenomic Consequences of Immortalized Plant Cell Suspension Culture. PLoS Biology, 2008, 6, e302.	2.6	179
7	Identification of Molecular Integrators Shows that Nitrogen Actively Controls the Phosphate Starvation Response in Plants. Plant Cell, 2019, 31, 1171-1184.	3.1	135
8	The histone methyltransferase SDG8 mediates the epigenetic modification of light and carbon responsive genes in plants. Genome Biology, 2015, 16, 79.	3.8	91
9	Integrated RNA-seq and sRNA-seq analysis identifies novel nitrate-responsive genes in Arabidopsis thaliana roots. BMC Genomics, 2013, 14, 701.	1.2	76
10	ABAP1 is a novel plant Armadillo BTB protein involved in DNA replication and transcription. EMBO Journal, 2008, 27, 2746-2756.	3.5	71
11	A phenol/chloroform-free method to extract nucleic acids from recalcitrant, woody tropical species for gene expression and sequencing. Plant Methods, 2019, 15, 62.	1.9	67
12	Dynamic and Widespread lncRNA Expression in a Sponge and the Origin of Animal Complexity. Molecular Biology and Evolution, 2015, 32, 2367-2382.	3.5	66
13	Arabidopsis thaliana Chromosome 4 Replicates in Two Phases That Correlate with Chromatin State. PLoS Genetics, 2010, 6, e1000982.	1.5	65
14	Computational identification and analysis of novel sugarcane microRNAs. BMC Genomics, 2012, 13, 290.	1.2	63
15	Construction of a bacterial artificial chromosome library from the spikemoss Selaginella moellendorffii: a new resource for plant comparative genomics. BMC Plant Biology, 2005, 5, 10.	1.6	53
16	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
17	Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. ELife, 2017, 6, .	2.8	51
18	Origin and evolution of the metazoan non-coding regulatory genome. Developmental Biology, 2017, 427, 193-202.	0.9	42

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19	Functional analysis and comparative genomics of expressed sequence tags from the lycophyte Selaginella moellendorffii. BMC Genomics, 2005, 6, 85.	1.2	38
20	Juvenility and Vegetative Phase Transition in Tropical/Subtropical Tree Crops. Frontiers in Plant Science, 2019, 10, 729.	1.7	38
21	Differential sRNA Regulation in Leaves and Roots of Sugarcane under Water Depletion. PLoS ONE, 2014, 9, e93822.	1.1	37
22	Loss of Small-RNA-Directed DNA Methylation in the Plant Cell Cycle Promotes Germline Reprogramming and Somaclonal Variation. Current Biology, 2021, 31, 591-600.e4.	1.8	36
23	Convergent microevolution of Cryptococcus neoformans hypervirulence in the laboratory and the clinic. Scientific Reports, 2017, 7, 17918.	1.6	34
24	Epigenetic Inheritance and Reprogramming in Plants and Fission Yeast. Cold Spring Harbor Symposia on Quantitative Biology, 2008, 73, 265-271.	2.0	31
25	SDG8-Mediated Histone Methylation and RNA Processing Function in the Response to Nitrate Signaling. Plant Physiology, 2020, 182, 215-227.	2.3	30
26	Sirtuins in the phylum Basidiomycota: A role in virulence in Cryptococcus neoformans. Scientific Reports, 2017, 7, 46567.	1.6	27
27	De novo transcriptome assembly reveals high transcriptional complexity in Pisum sativum axillary buds and shows rapid changes in expression of diurnally regulated genes. BMC Genomics, 2017, 18, 221.	1.2	24
28	Sex Determination in <i>Ceratopteris richardii</i> Is Accompanied by Transcriptome Changes That Drive Epigenetic Reprogramming of the Young Gametophyte. G3: Genes, Genomes, Genetics, 2018, 8, 2205-2214.	0.8	22
29	De novo transcriptome assembly and annotation for gene discovery in avocado, macadamia and mango. Scientific Data, 2020, 7, 9.	2.4	22
30	Origins of Novel Phenotypic Variation in Polyploids. , 2012, , 57-76.		15
31	Long non-coding regulatory RNAs in sponges and insights into the origin of animal multicellularity. RNA Biology, 2018, 15, 1-7.	1.5	14
32	Preâ€introduction introgression contributes to parallel differentiation and contrasting hybridization outcomes between invasive and native marine mussels. Journal of Evolutionary Biology, 2021, 34, 175-192.	0.8	10
33	De Novo Plant Transcriptome Assembly and Annotation Using Illumina RNA-Seq Reads. Methods in Molecular Biology, 2019, 1933, 265-275.	0.4	9
34	Sponge Long Non-Coding RNAs Are Expressed in Specific Cell Types and Conserved Networks. Non-coding RNA, 2018, 4, 6.	1.3	8
35	An optimised chromatin immunoprecipitation (ChIP) method for starchy leaves of Nicotiana benthamiana to study histone modifications of an allotetraploid plant. Molecular Biology Reports, 2020, 47, 9499-9509.	1.0	4
36	Replication, Repair, and Reactivation. Developmental Cell, 2005, 9, 724-725.	3.1	3

#	Article	IF	Citations
37	Profiling the endosperm, one nucleus at a time. Nature Plants, 2021, 7, 710-711.	4.7	0
38	DESIGNING MICROARRAYS. Conference on Applied Statistics in Agriculture, 0, , .	0.0	0
39	Polyglutamine-encoding microsatellite contributes to LMW GS diversity in Triticum monococcum. Cereal Research Communications, 2004, 32, 301-308.	0.8	0
40	Targeted Isolation Sequence Assembly and Characterization of White Spruce. , 2011, , 23-38.		0