

# Ramanjulu Sunkar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3359052/publications.pdf>

Version: 2024-02-01

91  
papers

16,086  
citations

50276

46  
h-index

43889

91  
g-index

94  
all docs

94  
docs citations

94  
times ranked

13307  
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular basis of priming-induced acquired tolerance to multiple abiotic stresses in plants. <i>Journal of Experimental Botany</i> , 2022, 73, 3355-3371.	4.8	18
2	Molecular and Biochemical Analysis of Duplicated Cytosolic CuZn Superoxide Dismutases of Rice and in silico Analysis in Plants. <i>Frontiers in Plant Science</i> , 2022, 13, .	3.6	1
3	<scp>mRNA N<sup>6</sup></scp>â€methyladenosine is critical for cold tolerance in Arabidopsis. <i>Plant Journal</i> , 2022, 111, 1052-1068.	5.7	23
4	Characterizing microRNAs and their targets in different organs of <i>Camellia sinensis</i> var. <i>assamica</i> . <i>Genomics</i> , 2021, 113, 159-170.	2.9	10
5	Splice Variants of Superoxide Dismutases in Rice and Their Expression Profiles under Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3997.	4.1	9
6	The neglected other half â€role of the pistil in plant heat stress responses. <i>Plant, Cell and Environment</i> , 2021, 44, 2200-2210.	5.7	28
7	MicroRNA profiles in <i>Sorghum</i> exposed to individual drought or heat or their combination. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 848-861.	1.7	4
8	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , 2020, 20, 739-761.	3.5	37
9	The Effect of Drought on Transcriptome and Hormonal Profiles in Barley Genotypes With Contrasting Drought Tolerance. <i>Frontiers in Plant Science</i> , 2020, 11, 618491.	3.6	33
10	Molecular Characterization of a Date Palm Vascular Highway 1-Interacting Kinase (PdVIK) under Abiotic Stresses. <i>Genes</i> , 2020, 11, 568.	2.4	6
11	Overexpression of a Metallothionein 2A Gene from Date Palm Confers Abiotic Stress Tolerance to Yeast and <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 2871.	4.1	51
12	Water-deficit responsive microRNAs in the primary root growth zone of maize. <i>BMC Plant Biology</i> , 2019, 19, 447.	3.6	18
13	Metabolomic analysis of date palm seedlings exposed to salinity and silicon treatments. <i>Plant Signaling and Behavior</i> , 2019, 14, 1663112.	2.4	31
14	Analysis of microRNAs, phased small interfering RNAs and their potential targets in <i>Rosarugosa Thunb.</i> . <i>BMC Genomics</i> , 2019, 19, 983.	2.8	13
15	Comparative Water Relations of Two Contrasting Date Palm Genotypes under Salinity. <i>International Journal of Agronomy</i> , 2019, 2019, 1-16.	1.2	16
16	An improved method of constructing degradome library suitable for sequencing using Illumina platform. <i>Plant Methods</i> , 2019, 15, 134.	4.3	4
17	Comparative transcriptome and translome analysis in contrasting rice genotypes reveals differential mRNA translation in salt-tolerant Pokkali under salt stress. <i>BMC Genomics</i> , 2018, 19, 935.	2.8	66
18	Genotype- and tissue-specific miRNA profiles and their targets in three alfalfa ( <i>Medicago sativa</i> L) genotypes. <i>BMC Genomics</i> , 2018, 19, 913.	2.8	27

#	ARTICLE	IF	CITATIONS
19	MicroRNAs, tasiRNAs, phasiRNAs, and Their Potential Functions in Pineapple. <i>Plant Genetics and Genomics: Crops and Models</i> , 2018, , 167-182.	0.3	1
20	Genome-wide identification and comprehensive analysis of microRNAs and phased small interfering RNAs in watermelon. <i>BMC Genomics</i> , 2018, 19, 111.	2.8	14
21	Genome-wide expression profiling in leaves and roots of date palm ( <i>Phoenix dactylifera</i> L.) exposed to salinity. <i>BMC Genomics</i> , 2017, 18, 246.	2.8	80
22	MicroRNA dynamics in a wild and cultivated species of Convolvulaceae exposed to drought stress. <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 291-300.	3.1	13
23	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , 2017, 35, 969-976.	17.5	356
24	Small RNA profiles from <i>Panax notoginseng</i> roots differing in sizes reveal correlation between miR156 abundances and root biomass levels. <i>Scientific Reports</i> , 2017, 7, 9418.	3.3	21
25	Determining Glutathione Levels in Plants. <i>Methods in Molecular Biology</i> , 2017, 1631, 273-277.	0.9	28
26	ChIP-Seq Analysis for Identifying Genome-Wide Histone Modifications Associated with Stress-Responsive Genes in Plants. <i>Methods in Molecular Biology</i> , 2017, 1631, 139-149.	0.9	2
27	Isolation of Polysomal RNA for Analyzing Stress-Responsive Genes Regulated at the Translational Level in Plants. <i>Methods in Molecular Biology</i> , 2017, 1631, 151-161.	0.9	2
28	Effect of high temperature on yield associated parameters and vascular bundle development in five potato cultivars. <i>Scientia Horticulturae</i> , 2017, 225, 134-140.	3.6	13
29	Small RNAs: regulators of plant development and climate resilience. <i>Indian Journal of Plant Physiology</i> , 2017, 22, 369-370.	0.8	3
30	MicroRNA expression profiles in the emerging tillers and inflorescence of switchgrass, a major feedstock for biofuel production. <i>Indian Journal of Plant Physiology</i> , 2017, 22, 558-565.	0.8	4
31	Zymographic Method for Distinguishing Different Classes of Superoxide Dismutases in Plants. <i>Methods in Molecular Biology</i> , 2017, 1631, 221-227.	0.9	6
32	Identification of Reference Genes for Quantitative Real-Time PCR in Date Palm ( <i>Phoenix dactylifera</i> L.) Subjected to Drought and Salinity. <i>PLoS ONE</i> , 2016, 11, e0166216.	2.5	24
33	Small RNA profiles in soybean primary root tips under water deficit. <i>BMC Systems Biology</i> , 2016, 10, 126.	3.0	33
34	Identification of microRNAs, phasiRNAs and Their Targets in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 176-186.	1.9	32
35	Characterization of drought- and heat-responsive microRNAs in switchgrass. <i>Plant Science</i> , 2016, 242, 214-223.	3.6	81
36	A genome-wide identification of the miRNAome in response to salinity stress in date palm ( <i>Phoenix</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	3.6	54

#	ARTICLE	IF	CITATIONS
37	Genome-wide identification of the <i>Phaseolus vulgaris</i> sRNAome using small RNA and degradome sequencing. <i>BMC Genomics</i> , 2015, 16, 423.	2.8	49
38	High throughput sequencing of small RNA component of leaves and inflorescence revealed conserved and novel miRNAs as well as phasiRNA loci in chickpea. <i>Plant Science</i> , 2015, 235, 46-57.	3.6	53
39	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	21.4	472
40	Nutrient- and other stress-responsive microRNAs in plants: Role for thiol-based redox signaling. <i>Plant Signaling and Behavior</i> , 2015, 10, e1010916.	2.4	11
41	Genome-Wide Discovery and Analysis of Phased Small Interfering RNAs in Chinese Sacred Lotus. <i>PLoS ONE</i> , 2014, 9, e113790.	2.5	28
42	Global and local perturbation of the tomato microRNA pathway by a trans-activated DICER-LIKE 1 mutant. <i>Journal of Experimental Botany</i> , 2014, 65, 725-739.	4.8	27
43	Sex specific expression and distribution of small RNAs in papaya. <i>BMC Genomics</i> , 2014, 15, 20.	2.8	28
44	Redox signaling mediates the expression of a sulfate deprivation-inducible microRNA 395 in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2014, 77, 85-96.	5.7	82
45	Identification of conserved and novel microRNAs in <i>Manduca sexta</i> and their possible roles in the expression regulation of immunity-related genes. <i>Insect Biochemistry and Molecular Biology</i> , 2014, 47, 12-22.	2.7	50
46	Analysis of biochemical variations and microRNA expression in wild ( <i>Ipomoea campanulata</i> ) and cultivated ( <i>Jacquemontia pentantha</i> ) species exposed to in vivo water stress. <i>Physiology and Molecular Biology of Plants</i> , 2014, 20, 57-67.	3.1	14
47	Dynamic Regulation of Novel and Conserved miRNAs Across Various Tissues of Diverse Cucurbit Species. <i>Plant Molecular Biology Reporter</i> , 2013, 31, 335-343.	1.8	6
48	Genome-Wide Analysis of MicroRNAs in Sacred Lotus, <i>Nelumbo nucifera</i> (Gaertn.). <i>Tropical Plant Biology</i> , 2013, 6, 117-130.	1.9	25
49	Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	9.6	329
50	Global Identification of Small RNA Targets in Plants by Sequencing Sliced Ends of Messenger RNAs. <i>Methods in Molecular Biology</i> , 2013, 956, 119-129.	0.9	6
51	Characterization of small RNAs and their target genes in wheat seedlings using sequencing-based approaches. <i>Plant Science</i> , 2013, 203-204, 17-24.	3.6	53
52	SeqTar: an effective method for identifying microRNA guided cleavage sites from degradome of polyadenylated transcripts in plants. <i>Nucleic Acids Research</i> , 2012, 40, e28-e28.	14.5	94
53	microRNAs responsive to ozone-induced oxidative stress in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , 2012, 7, 484-491.	2.4	34
54	Functions of microRNAs in plant stress responses. <i>Trends in Plant Science</i> , 2012, 17, 196-203.	8.8	900

#	ARTICLE	IF	CITATIONS
55	Identification and developmental profiling of conserved and novel microRNAs in <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 381-395.	2.7	58
56	Characterization of the small RNA component of leaves and fruits from four different cucurbit species. <i>BMC Genomics</i> , 2012, 13, 329.	2.8	72
57	<i>Cucumis melo</i> MicroRNA Expression Profile During Aphid Herbivory in a Resistant and Susceptible Interaction. <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 839-848.	2.6	51
58	Asymmetric purine-pyrimidine distribution in cellular small RNA population of papaya. <i>BMC Genomics</i> , 2012, 13, 682.	2.8	41
59	Expression of Small RNA in <i>Aphis gossypii</i> and Its Potential Role in the Resistance Interaction with Melon. <i>PLoS ONE</i> , 2012, 7, e48579.	2.5	40
60	Role of microRNAs in Plant Adaptation to Environmental Stresses. <i>Signaling and Communication in Plants</i> , 2012, , 219-232.	0.7	5
61	High-throughput sequence analysis of small RNA's in grapevine ( <i>Vitis</i> ) Tj ETQq1 1 0.784314 rgBT /Overl 1060-1076.	4.2	74
62	Overexpression of miR156 in switchgrass ( <i>Panicum virgatum</i> L.) results in various morphological alterations and leads to improved biomass production. <i>Plant Biotechnology Journal</i> , 2012, 10, 443-452.	8.3	293
63	Identification and temporal expression analysis of conserved and novel microRNAs in Sorghum. <i>Genomics</i> , 2011, 98, 460-468.	2.9	88
64	Non-coding small RNAs responsive to abiotic stress in wheat ( <i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , 2010, 10, 187-190.	3.5	69
65	Deep sequencing of small RNA libraries reveals dynamic regulation of conserved and novel microRNAs and microRNA-stars during silkworm development. <i>BMC Genomics</i> , 2010, 11, 52.	2.8	178
66	Transcriptome-wide identification of microRNA targets in rice. <i>Plant Journal</i> , 2010, 62, 742-759.	5.7	370
67	Gene Regulation During Cold Stress Acclimation in Plants. <i>Methods in Molecular Biology</i> , 2010, 639, 39-55.	0.9	339
68	Identification of microRNAs and their targets in switchgrass, a model biofuel plant species. <i>Journal of Plant Physiology</i> , 2010, 167, 896-904.	3.5	66
69	MicroRNAs with macro-effects on plant stress responses. <i>Seminars in Cell and Developmental Biology</i> , 2010, 21, 805-811.	5.0	240
70	Cloning of Stress-Responsive MicroRNAs and other Small RNAs from Plants. <i>Methods in Molecular Biology</i> , 2010, 639, 239-251.	0.9	9
71	Sliced microRNA targets and precise loop-first processing of <i>MIR319</i> hairpins revealed by analysis of the <i>Physcomitrella patens</i> degradome. <i>Rna</i> , 2009, 15, 2112-2121.	3.5	186
72	Cloning, characterization and expression analysis of porcine microRNAs. <i>BMC Genomics</i> , 2009, 10, 65.	2.8	94

#	ARTICLE	IF	CITATIONS
73	Biotic and abiotic stress down-regulate miR398 expression in Arabidopsis. <i>Planta</i> , 2009, 229, 1009-1014.	3.2	366
74	Cloning and characterization of small RNAs from <i>Medicago truncatula</i> reveals four novel legume-specific microRNA families. <i>New Phytologist</i> , 2009, 184, 85-98.	7.3	162
75	Novel and nodulation-regulated microRNAs in soybean roots. <i>BMC Genomics</i> , 2008, 9, 160.	2.8	283
76	Identification of novel and candidate miRNAs in rice by high throughput sequencing. <i>BMC Plant Biology</i> , 2008, 8, 25.	3.6	436
77	In silico identification of conserved microRNAs in large number of diverse plant species. <i>BMC Plant Biology</i> , 2008, 8, 37.	3.6	323
78	The role of microRNAs and other endogenous small RNAs in plant stress responses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008, 1779, 743-748.	1.9	246
79	Genome-wide identification and analysis of small RNAs originated from natural antisense transcripts in <i>Oryza sativa</i> . <i>Genome Research</i> , 2008, 19, 70-78.	5.5	107
80	Small RNAs as big players in plant abiotic stress responses and nutrient deprivation. <i>Trends in Plant Science</i> , 2007, 12, 301-309.	8.8	872
81	Micro RNAs and Short-interfering RNAs in Plants. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 817-826.	8.5	80
82	Posttranscriptional Induction of Two Cu/Zn Superoxide Dismutase Genes in Arabidopsis Is Mediated by Downregulation of miR398 and Important for Oxidative Stress Tolerance. <i>Plant Cell</i> , 2006, 18, 2051-2065.	6.6	1,118
83	Detailed expression analysis of selected genes of the aldehyde dehydrogenase (ALDH) gene superfamily in <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , 2005, 57, 315-332.	3.9	128
84	Cloning and Characterization of MicroRNAs from Rice. <i>Plant Cell</i> , 2005, 17, 1397-1411.	6.6	462
85	Identification and characterization of endogenous small interfering RNAs from rice. <i>Nucleic Acids Research</i> , 2005, 33, 4443-4454.	14.5	92
86	Endogenous siRNAs Derived from a Pair of Natural cis-Antisense Transcripts Regulate Salt Tolerance in Arabidopsis. <i>Cell</i> , 2005, 123, 1279-1291.	28.9	999
87	Drought and Salt Tolerance in Plants. <i>Critical Reviews in Plant Sciences</i> , 2005, 24, 23-58.	5.7	2,081
88	Novel and Stress-Regulated MicroRNAs and Other Small RNAs from Arabidopsis[W]. <i>Plant Cell</i> , 2004, 16, 2001-2019.	6.6	1,787
89	Overexpression of a stress-inducible aldehyde dehydrogenase gene from <i>Arabidopsis thaliana</i> in transgenic plants improves stress tolerance. <i>Plant Journal</i> , 2003, 35, 452-464.	5.7	380
90	Expression of a truncated tobacco NtCBP4 channel in transgenic plants and disruption of the homologous Arabidopsis CNGC1 gene confer Pb <sup>2+</sup> tolerance. <i>Plant Journal</i> , 2000, 24, 533-542.	5.7	173

#	ARTICLE	IF	CITATIONS
91	A tobacco plasma membrane calmodulin-binding transporter confers Ni <sup>2+</sup> tolerance and Pb <sup>2+</sup> hypersensitivity in transgenic plants. <i>Plant Journal</i> , 1999, 20, 171-182.	5.7	288