

# Ramanjulu Sunkar

## List of Publications by Citations

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

90 papers	12,915 citations	42 h-index	93 g-index
93 ext. papers	14,799 ext. citations	6.7 avg, IF	6.63 L-index

#	Paper	IF	Citations
90	Drought and Salt Tolerance in Plants. <i>Critical Reviews in Plant Sciences</i> , <b>2005</b> , 24, 23-58	5.6	1674
89	Novel and stress-regulated microRNAs and other small RNAs from Arabidopsis. <i>Plant Cell</i> , <b>2004</b> , 16, 2001-10	11.6	1475
88	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> , <b>2006</b> , 18, 2051-65	11.6	937
87	Endogenous siRNAs derived from a pair of natural cis-antisense transcripts regulate salt tolerance in Arabidopsis. <i>Cell</i> , <b>2005</b> , 123, 1279-91	56.2	887
86	Small RNAs as big players in plant abiotic stress responses and nutrient deprivation. <i>Trends in Plant Science</i> , <b>2007</b> , 12, 301-9	13.1	726
85	Functions of microRNAs in plant stress responses. <i>Trends in Plant Science</i> , <b>2012</b> , 17, 196-203	13.1	702
84	Cloning and characterization of microRNAs from rice. <i>Plant Cell</i> , <b>2005</b> , 17, 1397-411	11.6	429
83	Identification of novel and candidate miRNAs in rice by high throughput sequencing. <i>BMC Plant Biology</i> , <b>2008</b> , 8, 25	5.3	388
82	Overexpression of a stress-inducible aldehyde dehydrogenase gene from Arabidopsis thaliana in transgenic plants improves stress tolerance. <i>Plant Journal</i> , <b>2003</b> , 35, 452-64	6.9	338
81	Transcriptome-wide identification of microRNA targets in rice. <i>Plant Journal</i> , <b>2010</b> , 62, 742-59	6.9	311
80	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , <b>2015</b> , 47, 1435-42	36.3	309
79	Biotic and abiotic stress down-regulate miR398 expression in Arabidopsis. <i>Planta</i> , <b>2009</b> , 229, 1009-14	4.7	309
78	In silico identification of conserved microRNAs in large number of diverse plant species. <i>BMC Plant Biology</i> , <b>2008</b> , 8, 37	5.3	291
77	Gene regulation during cold stress acclimation in plants. <i>Methods in Molecular Biology</i> , <b>2010</b> , 639, 39-55	1.4	257
76	Novel and nodulation-regulated microRNAs in soybean roots. <i>BMC Genomics</i> , <b>2008</b> , 9, 160	4.5	248
75	Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , <b>2013</b> , 14, R41	18.3	241
74	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> , <b>1999</b> , 20, 171-82	6.9	233

73	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> , <b>2012</b> , 10, 443-52	11.6	226
72	MicroRNAs with macro-effects on plant stress responses. <i>Seminars in Cell and Developmental Biology</i> , <b>2010</b> , 21, 805-11	7.5	212
71	The role of microRNAs and other endogenous small RNAs in plant stress responses. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2008</b> , 1779, 743-8	6	211
70	Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 969-976	44.5	197
69	Deep sequencing of small RNA libraries reveals dynamic regulation of conserved and novel microRNAs and microRNA-stars during silkworm development. <i>BMC Genomics</i> , <b>2010</b> , 11, 52	4.5	154
68	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> , <b>2000</b> , 24, 533-42	6.9	153
67	Cloning and characterization of small RNAs from <i>Medicago truncatula</i> reveals four novel legume-specific microRNA families. <i>New Phytologist</i> , <b>2009</b> , 184, 85-98	9.8	143
66	Sliced microRNA targets and precise loop-first processing of MIR319 hairpins revealed by analysis of the <i>Physcomitrella patens</i> degradome. <i>Rna</i> , <b>2009</b> , 15, 2112-21	5.8	136
65	Detailed expression analysis of selected genes of the aldehyde dehydrogenase (ALDH) gene superfamily in <i>Arabidopsis thaliana</i> . <i>Plant Molecular Biology</i> , <b>2005</b> , 57, 315-32	4.6	105
64	Genome-wide identification and analysis of small RNAs originated from natural antisense transcripts in <i>Oryza sativa</i> . <i>Genome Research</i> , <b>2009</b> , 19, 70-8	9.7	95
63	Identification and characterization of endogenous small interfering RNAs from rice. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 4443-54	20.1	89
62	Cloning, characterization and expression analysis of porcine microRNAs. <i>BMC Genomics</i> , <b>2009</b> , 10, 65	4.5	84
61	SeqTar: an effective method for identifying microRNA guided cleavage sites from degradome of polyadenylated transcripts in plants. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, e28	20.1	84
60	Micro RNAs and Short-interfering RNAs in Plants. <i>Journal of Integrative Plant Biology</i> , <b>2007</b> , 49, 817-826	8.3	67
59	Characterization of drought- and heat-responsive microRNAs in switchgrass. <i>Plant Science</i> , <b>2016</b> , 242, 214-223	5.3	66
58	Non-coding small RNAs responsive to abiotic stress in wheat ( <i>Triticum aestivum</i> L.). <i>Functional and Integrative Genomics</i> , <b>2010</b> , 10, 187-90	3.8	62
57	Identification of microRNAs and their targets in switchgrass, a model biofuel plant species. <i>Journal of Plant Physiology</i> , <b>2010</b> , 167, 896-904	3.6	58
56	Redox signaling mediates the expression of a sulfate-deprivation-inducible microRNA395 in <i>Arabidopsis</i> . <i>Plant Journal</i> , <b>2014</b> , 77, 85-96	6.9	57

55	Identification and temporal expression analysis of conserved and novel microRNAs in Sorghum. <i>Genomics</i> , <b>2011</b> , 98, 460-8	4.3	56
54	High-throughput sequence analysis of small RNAs in grapevine ( <i>Vitis vinifera</i> L.) affected by grapevine leafroll disease. <i>Molecular Plant Pathology</i> , <b>2012</b> , 13, 1060-76	5.7	49
53	Identification and developmental profiling of conserved and novel microRNAs in <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , <b>2012</b> , 42, 381-95	4.5	49
52	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> , <b>2015</b> , 235, 46-57	5.3	47
51	Characterization of the small RNA component of leaves and fruits from four different cucurbit species. <i>BMC Genomics</i> , <b>2012</b> , 13, 329	4.5	45
50	Genome-wide expression profiling in leaves and roots of date palm ( <i>Phoenix dactylifera</i> L.) exposed to salinity. <i>BMC Genomics</i> , <b>2017</b> , 18, 246	4.5	43
49	Cucumis melo microRNA expression profile during aphid herbivory in a resistant and susceptible interaction. <i>Molecular Plant-Microbe Interactions</i> , <b>2012</b> , 25, 839-48	3.6	42
48	A genome-wide identification of the miRNAome in response to salinity stress in date palm ( <i>Phoenix dactylifera</i> L.). <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 946	6.2	41
47	Characterization of small RNAs and their target genes in wheat seedlings using sequencing-based approaches. <i>Plant Science</i> , <b>2013</b> , 203-204, 17-24	5.3	37
46	Genome-wide identification of the <i>Phaseolus vulgaris</i> sRNAome using small RNA and degradome sequencing. <i>BMC Genomics</i> , <b>2015</b> , 16, 423	4.5	36
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> , <b>2014</b> , 47, 12-22	4.5	31
44	Expression of small RNA in <i>Aphis gossypii</i> and its potential role in the resistance interaction with melon. <i>PLoS ONE</i> , <b>2012</b> , 7, e48579	3.7	27
43	Comparative transcriptome and translatoome analysis in contrasting rice genotypes reveals differential mRNA translation in salt-tolerant Pokkali under salt stress. <i>BMC Genomics</i> , <b>2018</b> , 19, 935	4.5	27
42	Overexpression of a Gene from Date Palm Confers Abiotic Stress Tolerance to Yeast and. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	26
41	microRNAs responsive to ozone-induced oxidative stress in <i>Arabidopsis thaliana</i> . <i>Plant Signaling and Behavior</i> , <b>2012</b> , 7, 484-91	2.5	26
40	Genome-Wide Analysis of MicroRNAs in Sacred Lotus, <i>Nelumbo nucifera</i> (Gaertn). <i>Tropical Plant Biology</i> , <b>2013</b> , 6, 117-130	1.6	24
39	Genome-wide discovery and analysis of phased small interfering RNAs in Chinese sacred lotus. <i>PLoS ONE</i> , <b>2014</b> , 9, e113790	3.7	23
38	Small RNA profiles in soybean primary root tips under water deficit. <i>BMC Systems Biology</i> , <b>2016</b> , 10, 126	3.5	22

37	Metabolomic analysis of date palm seedlings exposed to salinity and silicon treatments. <i>Plant Signaling and Behavior</i> , <b>2019</b> , 14, 1663112	2.5	20
36	Global and local perturbation of the tomato microRNA pathway by a trans-activated DICER-LIKE 1 mutant. <i>Journal of Experimental Botany</i> , <b>2014</b> , 65, 725-39	7	20
35	Sex specific expression and distribution of small RNAs in papaya. <i>BMC Genomics</i> , <b>2014</b> , 15, 20	4.5	20
34	Asymmetric purine-pyrimidine distribution in cellular small RNA population of papaya. <i>BMC Genomics</i> , <b>2012</b> , 13, 682	4.5	19
33	Identification of microRNAs, phasiRNAs and Their Targets in Pineapple. <i>Tropical Plant Biology</i> , <b>2016</b> , 9, 176-186	1.6	18
32	Epigenetics and epigenomics: underlying mechanisms, relevance, and implications in crop improvement. <i>Functional and Integrative Genomics</i> , <b>2020</b> , 20, 739-761	3.8	18
31	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> , <b>2016</b> , 11, e0166216	3.7	18
30	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> , <b>2017</b> , 7, 9418	4.9	14
29	Determining Glutathione Levels in Plants. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1631, 273-277	1.4	12
28	The Effect of Drought on Transcriptome and Hormonal Profiles in Barley Genotypes With Contrasting Drought Tolerance. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 618491	6.2	12
27	Genome-wide identification and comprehensive analysis of microRNAs and phased small interfering RNAs in watermelon. <i>BMC Genomics</i> , <b>2018</b> , 19, 111	4.5	11
26	Analysis of microRNAs, phased small interfering RNAs and their potential targets in <i>Rosmarinus officinalis</i> L. <i>BMC Genomics</i> , <b>2019</b> , 19, 983	4.5	10
25	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> , <b>2014</b> , 20, 57-67	2.8	10
24	Nutrient- and other stress-responsive microRNAs in plants: Role for thiol-based redox signaling. <i>Plant Signaling and Behavior</i> , <b>2015</b> , 10, e1010916	2.5	10
23	Genotype- and tissue-specific miRNA profiles and their targets in three alfalfa ( <i>Medicago sativa</i> L.) genotypes. <i>BMC Genomics</i> , <b>2018</b> , 19, 913	4.5	10
22	Effect of high temperature on yield associated parameters and vascular bundle development in five potato cultivars. <i>Scientia Horticulturae</i> , <b>2017</b> , 225, 134-140	4.1	9
21	The neglected other half - role of the pistil in plant heat stress responses. <i>Plant, Cell and Environment</i> , <b>2021</b> , 44, 2200-2210	8.4	9
20	Water-deficit responsive microRNAs in the primary root growth zone of maize. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 447	5.3	8

19	MicroRNA dynamics in a wild and cultivated species of Convolvulaceae exposed to drought stress. <i>Physiology and Molecular Biology of Plants</i> , <b>2017</b> , 23, 291-300	2.8	7
18	Cloning of stress-responsive microRNAs and other small RNAs from plants. <i>Methods in Molecular Biology</i> , <b>2010</b> , 639, 239-51	1.4	7
17	Dynamic Regulation of Novel and Conserved miRNAs Across Various Tissues of Diverse Cucurbit Species. <i>Plant Molecular Biology Reporter</i> , <b>2013</b> , 31, 335-343	1.7	5
16	Global identification of small RNA targets in plants by sequencing sliced ends of messenger RNAs. <i>Methods in Molecular Biology</i> , <b>2013</b> , 956, 119-29	1.4	5
15	Role of microRNAs in Plant Adaptation to Environmental Stresses. <i>Signaling and Communication in Plants</i> , <b>2012</b> , 219-232	1	5
14	Zymographic Method for Distinguishing Different Classes of Superoxide Dismutases in Plants. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1631, 221-227	1.4	5
13	Comparative Water Relations of Two Contrasting Date Palm Genotypes under Salinity. <i>International Journal of Agronomy</i> , <b>2019</b> , 2019, 1-16	1.9	5
12	Characterizing microRNAs and their targets in different organs of <i>Camellia sinensis</i> var. <i>assamica</i> . <i>Genomics</i> , <b>2021</b> , 113, 159-170	4.3	4
11	Molecular Characterization of a Date Palm Vascular Highway 1-Interacting Kinase () Under Abiotic Stresses. <i>Genes</i> , <b>2020</b> , 11,	4.2	3
10	MicroRNA expression profiles in the emerging tillers and inflorescence of switchgrass, a major feedstock for biofuel production. <i>Indian Journal of Plant Physiology</i> , <b>2017</b> , 22, 558-565		2
9	Splice Variants of Superoxide Dismutases in Rice and Their Expression Profiles under Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	2
8	Impact of Climate Change on MicroRNA Expression in Plants <b>2013</b> , 507-520		1
7	ChIP-Seq Analysis for Identifying Genome-Wide Histone Modifications Associated with Stress-Responsive Genes in Plants. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1631, 139-149	1.4	1
6	Isolation of Polysomal RNA for Analyzing Stress-Responsive Genes Regulated at the Translational Level in Plants. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1631, 151-161	1.4	1
5	MicroRNA profiles in Sorghum exposed to individual drought or heat or their combination. <i>Journal of Plant Biochemistry and Biotechnology</i> , <b>2021</b> , 30, 848	1.6	1
4	An improved method of constructing degradome library suitable for sequencing using Illumina platform. <i>Plant Methods</i> , <b>2019</b> , 15, 134	5.8	1
3	MicroRNAs, tasiRNAs, phasiRNAs, and Their Potential Functions in Pineapple. <i>Plant Genetics and Genomics: Crops and Models</i> , <b>2018</b> , 167-182	0.2	1
2	A high resolution single molecule sequencing-based Arabidopsis transcriptome using novel methods of Iso-seq analysis		1

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| 1 | Molecular basis of priming-induced acquired tolerance to multiple abiotic stresses in plants..<br><i>Journal of Experimental Botany</i> , <b>2022</b> , | 7 | 1 |
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