

Pamela J Green

List of Publications by Year in Descending Order

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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.

52
papers

8,592
citations

37
h-index

52
g-index

52
ext. papers

9,921
ext. citations

11.1
avg, IF

5.53
L-index

#	Paper	IF	Citations
52	Integrative Analysis of Gene Expression and miRNAs Reveal Biological Pathways Associated with Bud Paradormancy and Endodormancy in Grapevine. <i>Plants</i> , 2021 , 10,	4.5	2
51	RNA degradomes reveal substrates and importance for dark and nitrogen stress responses of Arabidopsis XRN4. <i>Nucleic Acids Research</i> , 2019 , 47, 9216-9230	20.1	16
50	Analysis of Brachypodium miRNA targets: evidence for diverse control during stress and conservation in bioenergy crops. <i>BMC Genomics</i> , 2018 , 19, 547	4.5	9
49	The RNA World: Identifying miRNA-Target RNA Pairs as Possible Missing Links in Multi-Network Models 2018 , 229-242		
48	Murine Oviductosomes (OVS) microRNA profiling during the estrous cycle: Delivery of OVS-borne microRNAs to sperm where miR-34c-5p localizes at the centrosome. <i>Scientific Reports</i> , 2018 , 8, 16094	4.9	26
47	An miRNA Expression Signature for the Human Colonic Stem Cell Niche Distinguishes Malignant from Normal Epithelia. <i>Cancer Research</i> , 2017 , 77, 3778-3790	10.1	11
46	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016 , 530, 331-5	50.4	276
45	Opsin Repertoire and Expression Patterns in Horseshoe Crabs: Evidence from the Genome of <i>Limulus polyphemus</i> (Arthropoda: Chelicerata). <i>Genome Biology and Evolution</i> , 2016 , 8, 1571-89	3.9	33
44	Identification of SMG6 cleavage sites and a preferred RNA cleavage motif by global analysis of endogenous NMD targets in human cells. <i>Nucleic Acids Research</i> , 2015 , 43, 309-23	20.1	71
43	Differential expression of miRNAs and their target genes in senescing leaves and siliques: insights from deep sequencing of small RNAs and cleaved target RNAs. <i>Plant, Cell and Environment</i> , 2015 , 38, 188-200	8.4	42
42	Heat-induced ribosome pausing triggers mRNA co-translational decay in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2015 , 43, 4121-32	20.1	57
41	AtCCR4a and AtCCR4b are Involved in Determining the Poly(A) Length of Granule-bound starch synthase 1 Transcript and Modulating Sucrose and Starch Metabolism in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2015 , 56, 863-74	4.9	25
40	Sample sequencing of vascular plants demonstrates widespread conservation and divergence of microRNAs. <i>Nature Communications</i> , 2014 , 5, 3722	17.4	138
39	The role of rice microRNAs in abiotic stress responses 2013 , 56, 187-197		78
38	XRN 5VBVexoribonucleases: structure, mechanisms and functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013 , 1829, 590-603	6	210
37	Comprehensive investigation of microRNAs enhanced by analysis of sequence variants, expression patterns, ARGONAUTE loading, and target cleavage. <i>Plant Physiology</i> , 2013 , 162, 1225-45	6.6	54
36	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of <i>Brachypodium distachyon</i> . <i>Genome Biology</i> , 2013 , 14, R145	18.3	56

35	MAJOR DEVELOPMENTAL REGULATORS AND THEIR EXPRESSION IN TWO CLOSELY RELATED SPECIES OF PORPHYRA (RHODOPHYTA)(1). <i>Journal of Phycology</i> , 2012 , 48, 883-96	3	16
34	Methods for validation of miRNA sequence variants and the cleavage of their targets. <i>Methods</i> , 2012 , 58, 135-43	4.6	19
33	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. <i>Plant Journal</i> , 2012 , 69, 462-74	6.9	224
32	Analysis of Small RNAs Associated with Plant Senescence. <i>FASEB Journal</i> , 2012 , 26, 952.7	0.9	
31	MicroRNAs as master regulators of the plant NB-LRR defense gene family via the production of phased, trans-acting siRNAs. <i>Genes and Development</i> , 2011 , 25, 2540-53	12.6	510
30	Evidence that XRN4, an Arabidopsis homolog of exoribonuclease XRN1, preferentially impacts transcripts with certain sequences or in particular functional categories. <i>Rna</i> , 2011 , 17, 501-11	5.8	60
29	Massive analysis of rice small RNAs: mechanistic implications of regulated microRNAs and variants for differential target RNA cleavage. <i>Plant Cell</i> , 2011 , 23, 4185-207	11.6	274
28	Nitrate-responsive miR393/AFB3 regulatory module controls root system architecture in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 4477-82	11.5	446
27	Uridylation of mature miRNAs and siRNAs by the MUT68 nucleotidyltransferase promotes their degradation in Chlamydomonas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 3906-11	11.5	111
26	Methods for isolation of total RNA to recover miRNAs and other small RNAs from diverse species. <i>Methods in Molecular Biology</i> , 2010 , 592, 31-50	1.4	35
25	MicroRNAs Associated with Environmental Stress in Arabidopsis. <i>FASEB Journal</i> , 2010 , 24, 500.1	0.9	
24	Distinct extremely abundant siRNAs associated with cosuppression in petunia. <i>Rna</i> , 2009 , 15, 1965-70	5.8	75
23	Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. <i>Rna</i> , 2009 , 15, 2147-60	5.8	433
22	MicroRNAs of Gallid and Meleagrid herpesviruses show generally conserved genomic locations and are virus-specific. <i>Virology</i> , 2009 , 388, 128-36	3.6	50
21	mRNA Degradation Machinery in Plants 2009 , 52, 114-124		50
20	Construction of Parallel Analysis of RNA Ends (PARE) libraries for the study of cleaved miRNA targets and the RNA degradome. <i>Nature Protocols</i> , 2009 , 4, 356-62	18.8	250
19	Global identification of microRNA-target RNA pairs by parallel analysis of RNA ends. <i>Nature Biotechnology</i> , 2008 , 26, 941-6	44.5	668
18	Diamonds in the rough: mRNA-like non-coding RNAs. <i>Trends in Plant Science</i> , 2008 , 13, 329-34	13.1	73

17	Criteria for annotation of plant MicroRNAs. <i>Plant Cell</i> , 2008 , 20, 3186-90	11.6	992
16	Sequence conservation and differential expression of Marek disease virus microRNAs. <i>Journal of Virology</i> , 2008 , 82, 12213-20	6.6	100
15	Distinct size distribution of endogeneous siRNAs in maize: Evidence from deep sequencing in the mop1-1 mutant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 14958-63	11.5	165
14	Genome-wide analysis for discovery of rice microRNAs reveals natural antisense microRNAs (nat-miRNAs). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 4951-6	11.5	190
13	tRNA cleavage is a conserved response to oxidative stress in eukaryotes. <i>Rna</i> , 2008 , 14, 2095-103	5.8	393
12	Construction of small RNA cDNA libraries for deep sequencing. <i>Methods</i> , 2007 , 43, 110-7	4.6	194
11	MicroRNAs and other small RNAs enriched in the Arabidopsis RNA-dependent RNA polymerase-2 mutant. <i>Genome Research</i> , 2006 , 16, 1276-88	9.7	281
10	Marek disease virus encodes MicroRNAs that map to meq and the latency-associated transcript. <i>Journal of Virology</i> , 2006 , 80, 8778-86	6.6	179
9	Dissecting Arabidopsis thaliana DICER function in small RNA processing, gene silencing and DNA methylation patterning. <i>Nature Genetics</i> , 2006 , 38, 721-5	36.3	470
8	Sweating the small stuff: microRNA discovery in plants. <i>Current Opinion in Biotechnology</i> , 2006 , 17, 139-46	11.4	60
7	Elucidation of the small RNA component of the transcriptome. <i>Science</i> , 2005 , 309, 1567-9	33.3	544
6	Circadian control of messenger RNA stability. Association with a sequence-specific messenger RNA decay pathway. <i>Plant Physiology</i> , 2005 , 138, 2374-85	6.6	89
5	AtPARN is an essential poly(A) ribonuclease in Arabidopsis. <i>Gene</i> , 2004 , 328, 95-102	3.8	58
4	AtXRN4 degrades mRNA in Arabidopsis and its substrates include selected miRNA targets. <i>Molecular Cell</i> , 2004 , 15, 173-83	17.6	295
3	Identification of unstable transcripts in Arabidopsis by cDNA microarray analysis: rapid decay is associated with a group of touch- and specific clock-controlled genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 11513-8	11.5	174
2	Analysis of XRN orthologs by complementation of yeast mutants and localization of XRN-GFP fusion proteins. <i>Methods in Enzymology</i> , 2001 , 342, 269-82	1.7	10
1	The RNA World: Identifying miRNA-Target RNA Pairs as Possible Missing Links in Multi-Network Models	229-242	