

Pamela J Green

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

10,558
citations

81900

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48
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52
all docs

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docs citations

52
times ranked

10890
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative Analysis of Gene Expression and miRNAs Reveal Biological Pathways Associated with Bud Paradormancy and Endodormancy in Grapevine. <i>Plants</i> , 2021, 10, 669.	3.5	5
2	RNA degradomes reveal substrates and importance for dark and nitrogen stress responses of <i>Arabidopsis XRN4</i> . <i>Nucleic Acids Research</i> , 2019, 47, 9216-9230.	14.5	30
3	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.	3.3	35
4	Analysis of <i>Brachypodium</i> miRNA targets: evidence for diverse control during stress and conservation in bioenergy crops. <i>BMC Genomics</i> , 2018, 19, 547.	2.8	17
5	An miRNA Expression Signature for the Human Colonic Stem Cell Niche Distinguishes Malignant from Normal Epithelia. <i>Cancer Research</i> , 2017, 77, 3778-3790.	0.9	18
6	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, 1571-1589.	2.5	50
7	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	27.8	460
8	Heat-induced ribosome pausing triggers mRNA co-translational decay in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2015, 43, 4121-4132.	14.5	104
9	<i>AtCCR4a</i> and <i>AtCCR4b</i> 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, 863-874.	3.1	32
10	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, 309-323.	14.5	90
11	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.	5.7	69
12	Sample sequencing of vascular plants demonstrates widespread conservation and divergence of microRNAs. <i>Nature Communications</i> , 2014, 5, 3722.	12.8	224
13	The role of rice microRNAs in abiotic stress responses. <i>Journal of Plant Biology</i> , 2013, 56, 187-197.	2.1	83
14	XRN 5'â€²3'â€² exoribonucleases: Structure, mechanisms and functions. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 590-603.	1.9	290
15	Comprehensive Investigation of MicroRNAs Enhanced by Analysis of Sequence Variants, Expression Patterns, ARGONAUTE Loading, and Target Cleavage. <i>Plant Physiology</i> , 2013, 162, 1225-1245.	4.8	61
16	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.	9.6	67
17	Methods for validation of miRNA sequence variants and the cleavage of their targets. <i>Methods</i> , 2012, 58, 135-143.	3.8	22
18	Roles of DCL4 and DCL3b in rice phased small RNA biogenesis. <i>Plant Journal</i> , 2012, 69, 462-474.	5.7	289

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19	MAJOR DEVELOPMENTAL REGULATORS AND THEIR EXPRESSION IN TWO CLOSELY RELATED SPECIES OF <i>PORPHYRA</i> (RHODOPHYTA). <i>Journal of Phycology</i> , 2012, 48, 883-896.	2.3	19
20	Analysis of Small RNAs Associated with Plant Senescence. <i>FASEB Journal</i> , 2012, 26, 952.7.	0.5	0
21	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, 2540-2553.	5.9	668
22	Evidence that XRN4, an <i>Arabidopsis</i> homolog of exoribonuclease XRN1, preferentially impacts transcripts with certain sequences or in particular functional categories. <i>Rna</i> , 2011, 17, 501-511.	3.5	76
23	Massive Analysis of Rice Small RNAs: Mechanistic Implications of Regulated MicroRNAs and Variants for Differential Target RNA Cleavage. <i>Plant Cell</i> , 2011, 23, 4185-4207.	6.6	341
24	Nitrate-responsive miR393/ AFB3 regulatory module controls root system architecture in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4477-4482.	7.1	556
25	Uridylation of mature miRNAs and siRNAs by the MUT68 nucleotidyltransferase promotes their degradation in <i>Chlamydomonas</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3906-3911.	7.1	122
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.	0.9	39
27	MicroRNAs Associated with Environmental Stress in <i>Arabidopsis</i> . <i>FASEB Journal</i> , 2010, 24, 500.1.	0.5	0
28	Distinct extremely abundant siRNAs associated with cosuppression in petunia. <i>Rna</i> , 2009, 15, 1965-1970.	3.5	93
29	Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. <i>Rna</i> , 2009, 15, 2147-2160.	3.5	525
30	MicroRNAs of Gallid and Meleagrid herpesviruses show generally conserved genomic locations and are virus-specific. <i>Virology</i> , 2009, 388, 128-136.	2.4	56
31	mRNA Degradation Machinery in Plants. <i>Journal of Plant Biology</i> , 2009, 52, 114-124.	2.1	61
32	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, 356-362.	12.0	301
33	Global identification of microRNA target RNA pairs by parallel analysis of RNA ends. <i>Nature Biotechnology</i> , 2008, 26, 941-946.	17.5	793
34	Diamonds in the rough: mRNA-like non-coding RNAs. <i>Trends in Plant Science</i> , 2008, 13, 329-334.	8.8	80
35	Criteria for Annotation of Plant MicroRNAs. <i>Plant Cell</i> , 2008, 20, 3186-3190.	6.6	1,158
36	Sequence Conservation and Differential Expression of Marek's Disease Virus MicroRNAs. <i>Journal of Virology</i> , 2008, 82, 12213-12220.	3.4	107

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37	Distinct size distribution of endogenous siRNAs in maize: Evidence from deep sequencing in the <i>mop1-1</i> mutant. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14958-14963.	7.1	208
38	Genome-wide analysis for discovery of rice microRNAs reveals natural antisense microRNAs (nat-miRNAs). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4951-4956.	7.1	218
39	tRNA cleavage is a conserved response to oxidative stress in eukaryotes. Rna, 2008, 14, 2095-2103.	3.5	506
40	Construction of small RNA cDNA libraries for deep sequencing. Methods, 2007, 43, 110-117.	3.8	216
41	Dissecting Arabidopsis thaliana DICER function in small RNA processing, gene silencing and DNA methylation patterning. Nature Genetics, 2006, 38, 721-725.	21.4	561
42	Sweating the small stuff: microRNA discovery in plants. Current Opinion in Biotechnology, 2006, 17, 139-146.	6.6	63
43	MicroRNAs and other small RNAs enriched in the Arabidopsis RNA-dependent RNA polymerase-2 mutant. Genome Research, 2006, 16, 1276-1288.	5.5	329
44	Marek's Disease Virus Encodes MicroRNAs That Map to <i>meq</i> and the Latency-Associated Transcript. Journal of Virology, 2006, 80, 8778-8786.	3.4	196
45	Circadian Control of Messenger RNA Stability. Association with a Sequence-Specific Messenger RNA Decay Pathway. Plant Physiology, 2005, 138, 2374-2385.	4.8	98
46	Elucidation of the Small RNA Component of the Transcriptome. Science, 2005, 309, 1567-1569.	12.6	582
47	AtPARN is an essential poly(A) ribonuclease in Arabidopsis. Gene, 2004, 328, 95-102.	2.2	61
48	AtXRN4 Degrades mRNA in Arabidopsis and Its Substrates Include Selected miRNA Targets. Molecular Cell, 2004, 15, 173-183.	9.7	369
49	Identification of unstable transcripts in Arabidopsis by cDNA microarray analysis: Rapid decay is associated with a group of touch- and specific clock-controlled genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11513-11518.	7.1	200
50	Analysis of XRN Orthologs by Complementation of Yeast Mutants and Localization of XRN-GFP Fusion Proteins. Methods in Enzymology, 2001, 342, 269-282.	1.0	10
51	The RNA World: Identifying miRNA-Target RNA Pairs as Possible Missing Links in Multi-Network Models. , 0, , 229-242.		0