

Artur Jarmolowski

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,958
citations

236925

25
h-index

265206

42
g-index

53
all docs

53
docs citations

53
times ranked

2254
citing authors

#	ARTICLE	IF	CITATIONS
1	MicroRNA biogenesis and activity in plant cell dedifferentiation stimulated by cell wall removal. <i>BMC Plant Biology</i> , 2022, 22, 9.	3.6	3
2	R-loops at microRNA encoding loci promote co-transcriptional processing of pri-miRNAs in plants. <i>Nature Plants</i> , 2022, 8, 402-418.	9.3	47
3	Quantitative Analysis of Plant Primary Transcripts. <i>Methods in Molecular Biology</i> , 2021, 2170, 53-77.	0.9	4
4	Arabidopsis Spliceosome Factor SmD3 Modulates Immunity to <i>Pseudomonas syringae</i> Infection. <i>Frontiers in Plant Science</i> , 2021, 12, 765003.	3.6	5
5	Barley microRNAs as metabolic sensors for soil nitrogen availability. <i>Plant Science</i> , 2020, 299, 110608.	3.6	9
6	The identification of differentially expressed genes in male and female gametophytes of simple thalloid liverwort <i>Pellia endiviifolia</i> sp. B using an RNA-seq approach. <i>Planta</i> , 2020, 252, 21.	3.2	3
7	mRNA adenosine methylase (MTA) deposits m ⁶ A on pri-miRNAs to modulate miRNA biogenesis in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21785-21795.	7.1	83
8	Core spliceosomal Sm proteins as constituents of cytoplasmic mRNPs in plants. <i>Plant Journal</i> , 2020, 103, 1155-1173.	5.7	4
9	SERRATE interacts with the nuclear exosome targeting (NEXT) complex to degrade primary miRNA precursors in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2020, 48, 6839-6854.	14.5	32
10	A Functional Network of Novel Barley MicroRNAs and Their Targets in Response to Drought. <i>Genes</i> , 2020, 11, 488.	2.4	5
11	miRNA Detection by Stem-Loop RT-qPCR in Studying microRNA Biogenesis and microRNA Responsiveness to Abiotic Stresses. <i>Methods in Molecular Biology</i> , 2019, 1932, 131-150.	0.9	11
12	Novel Nuclear Functions of <i>Arabidopsis</i> ARGONAUTE1: Beyond RNA Interference. <i>Plant Physiology</i> , 2019, 179, 1030-1039.	4.8	24
13	A stable tRNA-like molecule is generated from the long noncoding RNA <i>GUT15</i> in <i>Arabidopsis</i> . <i>RNA Biology</i> , 2018, 15, 1-13.	3.1	12
14	tRex: A Web Portal for Exploration of tRNA-Derived Fragments in <i>Arabidopsis thaliana</i> . <i>Plant and Cell Physiology</i> , 2018, 59, e1-e1.	3.1	27
15	Genomewide identification of genes involved in the potato response to drought indicates functional evolutionary conservation with <i>Arabidopsis</i> plants. <i>Plant Biotechnology Journal</i> , 2018, 16, 603-614.	8.3	42
16	N6-methyladenosine (m6A): Revisiting the Old with Focus on New, an <i>Arabidopsis thaliana</i> Centered Review. <i>Genes</i> , 2018, 9, 596.	2.4	30
17	A Role of U12 Intron in Proper Pre-mRNA Splicing of Plant Cap Binding Protein 20 Genes. <i>Frontiers in Plant Science</i> , 2018, 9, 475.	3.6	7
18	Regulation of Plant Microprocessor Function in Shaping microRNA Landscape. <i>Frontiers in Plant Science</i> , 2018, 9, 753.	3.6	28

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19	Post-transcriptional Regulation of MicroRNA Accumulation and Function: New Insights from Plants. <i>Molecular Plant</i> , 2018, 11, 1006-1007.	8.3	14
20	Active 5' splice sites regulate the biogenesis efficiency of Arabidopsis microRNAs derived from intron-containing genes. <i>Nucleic Acids Research</i> , 2017, 45, gkw895.	14.5	47
21	Alternative Polyadenylation of the Sense Transcript Controls Antisense Transcription of DELAY OF GERMINATION 1 in Arabidopsis. <i>Molecular Plant</i> , 2017, 10, 1349-1352.	8.3	24
22	Posttranscriptional coordination of splicing and miRNA biogenesis in plants. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1403.	6.4	72
23	MicroRNAs Are Intensively Regulated during Induction of Somatic Embryogenesis in Arabidopsis. <i>Frontiers in Plant Science</i> , 2017, 8, 18.	3.6	62
24	MicroRNA biogenesis: Epigenetic modifications as another layer of complexity to the microRNA expression regulation. <i>Acta Biochimica Polonica</i> , 2017, 63, 717-723.	0.5	25
25	Arabidopsis thaliana microRNA162 level is posttranscriptionally regulated via splicing and polyadenylation site selection.. <i>Acta Biochimica Polonica</i> , 2017, 63, 811-816.	0.5	12
26	Barley primary microRNA expression pattern is affected by soil water availability. <i>Acta Biochimica Polonica</i> , 2017, 63, 817-824.	0.5	3
27	Heat Stress Affects Pi-related Genes Expression and Inorganic Phosphate Deposition/Accumulation in Barley. <i>Frontiers in Plant Science</i> , 2016, 7, 926.	3.6	42
28	Salt Stress Reveals a New Role for ARGONAUTE1 in miRNA Biogenesis at the Transcriptional and Posttranscriptional Levels. <i>Plant Physiology</i> , 2016, 172, 297-312.	4.8	72
29	Virus-Induced Gene Silencing for Gene Function Studies in Barley. <i>Methods in Molecular Biology</i> , 2016, 1398, 293-308.	0.9	8
30	Promoter-based identification of novel non-coding RNAs reveals the presence of dicistronic snoRNA-miRNA genes in Arabidopsis thaliana. <i>BMC Genomics</i> , 2015, 16, 1009.	2.8	20
31	Arabidopsis microRNA expression regulation in a wide range of abiotic stress responses. <i>Frontiers in Plant Science</i> , 2015, 6, 410.	3.6	192
32	NTR 1 is required for transcription elongation checkpoints at alternative exons in Arabidopsis. <i>EMBO Journal</i> , 2015, 34, 544-558.	7.8	52
33	FUS/TLS contributes to replication-dependent histone gene expression by interaction with U7 snRNPs and histone-specific transcription factors. <i>Nucleic Acids Research</i> , 2015, 43, gkv794.	14.5	32
34	The liverwort <i>Pellia endiviifolia</i> shares microtranscriptomic traits that are common to green algae and land plants. <i>New Phytologist</i> , 2015, 206, 352-367.	7.3	84
35	mirEX 2.0 - an integrated environment for expression profiling of plant microRNAs. <i>BMC Plant Biology</i> , 2015, 15, 144.	3.6	68
36	Transcriptionally and post-transcriptionally regulated microRNAs in heat stress response in barley. <i>Journal of Experimental Botany</i> , 2014, 65, 6123-6135.	4.8	153

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37	The SERRATE protein is involved in alternative splicing in <i>Arabidopsis thaliana</i> . <i>Nucleic Acids Research</i> , 2014, 42, 1224-1244.	14.5	94
38	Low-Resolution Structure of the Full-Length Barley (<i>Hordeum vulgare</i>) SGT1 Protein in Solution, Obtained Using Small-Angle X-Ray Scattering. <i>PLoS ONE</i> , 2014, 9, e93313.	2.5	9
39	miR393 Is Required for Production of Proper Auxin Signalling Outputs. <i>PLoS ONE</i> , 2014, 9, e95972.	2.5	43
40	Down-regulation of <i>CBP80</i> gene expression as a strategy to engineer a drought-tolerant potato. <i>Plant Biotechnology Journal</i> , 2013, 11, 459-469.	8.3	114
41	The crosstalk between plant microRNA biogenesis factors and the spliceosome. <i>Plant Signaling and Behavior</i> , 2013, 8, e26955.	2.4	29
42	mirEX: a platform for comparative exploration of plant pri-miRNA expression data. <i>Nucleic Acids Research</i> , 2012, 40, D191-D197.	14.5	50
43	Novel genes specifically expressed during the development of the male thalli and antheridia in the dioecious liverwort <i>Pellia endiviifolia</i> . <i>Gene</i> , 2011, 485, 53-62.	2.2	13
44	Gene structures and processing of <i>Arabidopsis thaliana</i> HYL1-dependent pri-miRNAs. <i>Nucleic Acids Research</i> , 2009, 37, 3083-3093.	14.5	130
45	New polymorphic microsatellite loci developed and characterized from edible dormouse (<i>Glis glis</i>). <i>Conservation Genetics</i> , 2009, 10, 2029-2031.	1.5	8
46	The <i>Arabidopsis</i> CBP20 targets the cap-binding complex to the nucleus, and is stabilized by CBP80. <i>Plant Journal</i> , 2009, 59, 814-825.	5.7	51
47	siRNAs and miRNAs: small RNA molecules for big tasks. <i>Acta Physiologiae Plantarum</i> , 2004, 26, 363-369.	2.1	4
48	Cloning and characterization of two subunits of <i>Arabidopsis thaliana</i> nuclear cap-binding complex. <i>Gene</i> , 2002, 283, 171-183.	2.2	48