

Molly Megraw

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,810
citations

430874

18
h-index

395702

33
g-index

41
all docs

41
docs citations

41
times ranked

4930
citing authors

#	ARTICLE	IF	CITATIONS
1	A guide through present computational approaches for the identification of mammalian microRNA targets. <i>Nature Methods</i> , 2006, 3, 881-886.	19.0	525
2	Frequency and fate of microRNA editing in human brain. <i>Nucleic Acids Research</i> , 2008, 36, 5270-5280.	14.5	298
3	miRGen: a database for the study of animal microRNA genomic organization and function. <i>Nucleic Acids Research</i> , 2007, 35, D149-D155.	14.5	272
4	Alternative splicing in plants: directing traffic at the crossroads of adaptation and environmental stress. <i>Current Opinion in Plant Biology</i> , 2015, 24, 125-135.	7.1	215
5	Editing of Epstein-Barr Virus-encoded BART6 MicroRNAs Controls Their Dicer Targeting and Consequently Affects Viral Latency*. <i>Journal of Biological Chemistry</i> , 2010, 285, 33358-33370.	3.4	200
6	MicroRNA promoter element discovery in <i>Arabidopsis</i> . <i>Rna</i> , 2006, 12, 1612-1619.	3.5	175
7	A stele-enriched gene regulatory network in the <i>Arabidopsis</i> root. <i>Molecular Systems Biology</i> , 2011, 7, 459.	7.2	145
8	Environmental Stresses Modulate Abundance and Timing of Alternatively Spliced Circadian Transcripts in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2015, 8, 207-227.	8.3	142
9	The protein expression landscape of the <i>Arabidopsis</i> root. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6811-6818.	7.1	140
10	miRGen 2.0: a database of microRNA genomic information and regulation. <i>Nucleic Acids Research</i> , 2010, 38, D137-D141.	14.5	130
11	Paired-End Analysis of Transcription Start Sites in <i>Arabidopsis</i> Reveals Plant-Specific Promoter Signatures. <i>Plant Cell</i> , 2014, 26, 2746-2760.	6.6	112
12	A comparative study of ripening among berries of the grape cluster reveals an altered transcriptional programme and enhanced ripening rate in delayed berries. <i>Journal of Experimental Botany</i> , 2014, 65, 5889-5902.	4.8	59
13	The cyclophilin A <i>DIAGEOTROPICA</i> gene affects auxin transport in both root and shoot to control lateral root formation. <i>Development (Cambridge)</i> , 2015, 142, 712-21.	2.5	57
14	A transcription factor affinity-based code for mammalian transcription initiation. <i>Genome Research</i> , 2009, 19, 644-656.	5.5	54
15	Establishment of Expression in the <i>SHORTROOT-SCARECROW</i> Transcriptional Cascade through Opposing Activities of Both Activators and Repressors. <i>Developmental Cell</i> , 2016, 39, 585-596.	7.0	54
16	NanoCAGE-XL and CapFilter: an approach to genome wide identification of high confidence transcription start sites. <i>BMC Genomics</i> , 2015, 16, 597.	2.8	38
17	Small Genetic Circuits and MicroRNAs: Big Players in Polymerase II Transcriptional Control in Plants. <i>Plant Cell</i> , 2016, 28, 286-303.	6.6	38
18	MicroRNA Promoter Analysis. <i>Methods in Molecular Biology</i> , 2010, 592, 149-161.	0.9	22

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19	Improved DNase-seq protocol facilitates high resolution mapping of DNase I hypersensitive sites in roots in <i>Arabidopsis thaliana</i> . <i>Plant Methods</i> , 2015, 11, 42.	4.3	20
20	Sustained-input switches for transcription factors and microRNAs are central building blocks of eukaryotic gene circuits. <i>Genome Biology</i> , 2013, 14, R85.	9.6	16
21	<i>Arabidopsis</i> bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109.	1.9	14
22	Isoform specific gene auto-regulation via miRNAs: a case study on miR-128b and ARPP-21. <i>Theoretical Chemistry Accounts</i> , 2010, 125, 593-598.	1.4	13
23	Quality control and evaluation of plant epigenomics data. <i>Plant Cell</i> , 2022, 34, 503-513.	6.6	13
24	The Next Generation of Training for <i>Arabidopsis</i> Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509.	4.8	11
25	Environmental Stresses Modulate Abundance and Timing of Alternatively Spliced Circadian Transcripts in <i>Arabidopsis</i> . <i>Molecular Plant</i> , 2014, , .	8.3	9
26	Identification of transcription factors from NF-Y, NAC, and SPL families responding to osmotic stress in multiple tomato varieties. <i>Plant Science</i> , 2018, 274, 441-450.	3.6	9
27	IndeCut evaluates performance of network motif discovery algorithms. <i>Bioinformatics</i> , 2018, 34, 1514-1521.	4.1	7
28	Computational Identification of Regulatory Factors Involved in MicroRNA Transcription. <i>Lecture Notes in Computer Science</i> , 2005, , 457-468.	1.3	5
29	Metabolomics analysis reveals both plant variety and choice of hormone treatment modulate vinca alkaloid production in <i>Catharanthus roseus</i> . <i>Plant Direct</i> , 2020, 4, e00267.	1.9	5
30	TIPR: transcription initiation pattern recognition on a genome scale. <i>Bioinformatics</i> , 2015, 31, 3725-3732.	4.1	4
31	Computational approaches to elucidate miRNA biology. , 2007, , 187-198.		2
32	NanoCAGE-XL: An Approach to High-Confidence Transcription Start Site Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1830, 225-237.	0.9	2
33	RNA-Seq analysis of genes affected by Cyclophilin A/DIAGEOTROPICA (DGT) in tomato root development. <i>F1000Research</i> , 2020, 9, 1175.	1.6	2
34	DNase I SIM: A Simplified In-Nucleus Method for DNase I Hypersensitive Site Sequencing. <i>Methods in Molecular Biology</i> , 2017, 1629, 141-154.	0.9	1
35	Convmd: Convolutional Matrix Decomposition For Classification Of Matrix Data. , 2018, , .		0
36	A Suite of Resources for the Study of microRNA Ontology and Function. , 2009, , 45-56.		0