

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 | Quality control and evaluation of plant epigenomics data. <i>Plant Cell</i> , 2022, 34, 503-513. | 6.6 | 13 |
| 2 | 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 |
| 3 | RNA-Seq analysis of genes affected by Cyclophilin A/DIAGEOTROPICA (DGT) in tomato root development. <i>F1000Research</i> , 2020, 9, 1175. | 1.6 | 2 |
| 4 | Arabidopsis bioinformatics resources: The current state, challenges, and priorities for the future. <i>Plant Direct</i> , 2019, 3, e00109. | 1.9 | 14 |
| 5 | IndeCut evaluates performance of network motif discovery algorithms. <i>Bioinformatics</i> , 2018, 34, 1514-1521. | 4.1 | 7 |
| 6 | Convmd: Convolutional Matrix Decomposition For Classification Of Matrix Data. , 2018, , . | | 0 |
| 7 | 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 |
| 8 | NanoCAGE-XL: An Approach to High-Confidence Transcription Start Site Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1830, 225-237. | 0.9 | 2 |
| 9 | 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 |
| 10 | The Next Generation of Training for Arabidopsis Researchers: Bioinformatics and Quantitative Biology. <i>Plant Physiology</i> , 2017, 175, 1499-1509. | 4.8 | 11 |
| 11 | Establishment of Expression in the SHORTROOT-SCARECROW Transcriptional Cascade through Opposing Activities of Both Activators and Repressors. <i>Developmental Cell</i> , 2016, 39, 585-596. | 7.0 | 54 |
| 12 | 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 |
| 13 | 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 |
| 14 | 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 |
| 15 | The cyclophilin A DIAGEOTROPICA 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 |
| 16 | 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 |
| 17 | TIPR: transcription initiation pattern recognition on a genome scale. <i>Bioinformatics</i> , 2015, 31, 3725-3732. | 4.1 | 4 |
| 18 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Environmental Stresses Modulate Abundance and Timing of Alternatively Spliced Circadian Transcripts in Arabidopsis. <i>Molecular Plant</i> , 2014, , . | 8.3 | 9 |
| 20 | 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 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | A stele-enriched gene regulatory network in the Arabidopsis root. <i>Molecular Systems Biology</i> , 2011, 7, 459. | 7.2 | 145 |
| 25 | 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 |
| 26 | miRGen 2.0: a database of microRNA genomic information and regulation. <i>Nucleic Acids Research</i> , 2010, 38, D137-D141. | 14.5 | 130 |
| 27 | 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 |
| 28 | MicroRNA Promoter Analysis. <i>Methods in Molecular Biology</i> , 2010, 592, 149-161. | 0.9 | 22 |
| 29 | A transcription factor affinity-based code for mammalian transcription initiation. <i>Genome Research</i> , 2009, 19, 644-656. | 5.5 | 54 |
| 30 | A Suite of Resources for the Study of microRNA Ontology and Function. , 2009, , 45-56. | | 0 |
| 31 | Frequency and fate of microRNA editing in human brain. <i>Nucleic Acids Research</i> , 2008, 36, 5270-5280. | 14.5 | 298 |
| 32 | 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 |
| 33 | Computational approaches to elucidate miRNA biology. , 2007, , 187-198. | | 2 |
| 34 | A guide through present computational approaches for the identification of mammalian microRNA targets. <i>Nature Methods</i> , 2006, 3, 881-886. | 19.0 | 525 |
| 35 | MicroRNA promoter element discovery in Arabidopsis. <i>Rna</i> , 2006, 12, 1612-1619. | 3.5 | 175 |
| 36 | Computational Identification of Regulatory Factors Involved in MicroRNA Transcription. <i>Lecture Notes in Computer Science</i> , 2005, , 457-468. | 1.3 | 5 |