

Asher Pasha

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

2,464
citations

394286

19
h-index

501076

28
g-index

38
all docs

38
docs citations

38
times ranked

3919
citing authors

#	ARTICLE	IF	CITATIONS
1	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
2	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. <i>Plant Cell</i> , 2017, 29, 1806-1821.	3.1	316
3	NIN-like protein 8 is a master regulator of nitrate-promoted seed germination in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2016, 7, 13179.	5.8	147
4	High Temporal-Resolution Transcriptome Landscape of Early Maize Seed Development. <i>Plant Cell</i> , 2019, 31, 974-992.	3.1	141
5	Inference of Longevity-Related Genes from a Robust Coexpression Network of Seed Maturation Identifies Regulators Linking Seed Storability to Biotic Defense-Related Pathways. <i>Plant Cell</i> , 2015, 27, tpc.15.00632.	3.1	116
6	An updated gene atlas for maize reveals organ-specific and stress-induced genes. <i>Plant Journal</i> , 2019, 97, 1154-1167.	2.8	114
7	Expression atlas and comparative coexpression network analyses reveal important genes involved in the formation of lignified cell wall in <i>Brachypodium distachyon</i> . <i>New Phytologist</i> , 2017, 215, 1009-1025.	3.5	108
8	New <i>BAR</i> tools for mining expression data and exploring <i>Cis</i> -elements in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2016, 88, 490-504.	2.8	75
9	The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . <i>Plant Journal</i> , 2016, 88, 879-894.	2.8	60
10	Transcriptomics at Maize Embryo/Endosperm Interfaces Identifies a Transcriptionally Distinct Endosperm Subdomain Adjacent to the Embryo Scutellum. <i>Plant Cell</i> , 2020, 32, 833-852.	3.1	60
11	Regulation of Cell Type-Specific Immunity Networks in <i>Arabidopsis</i> Roots. <i>Plant Cell</i> , 2020, 32, 2742-2762.	3.1	59
12	The Transcriptional Landscape of Polyploid Wheats and Their Diploid Ancestors during Embryogenesis and Grain Development. <i>Plant Cell</i> , 2019, 31, 2888-2911.	3.1	57
13	Innovation, conservation, and repurposing of gene function in root cell type development. <i>Cell</i> , 2021, 184, 3333-3348.e19.	13.5	48
14	Tung Tree (<i>Vernicia fordii</i>) Genome Provides A Resource for Understanding Genome Evolution and Improved Oil Production. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 558-575.	3.0	43
15	An <i>eFP</i> - <i>Seq</i> Browser™ for visualizing and exploring <i>RNA</i> sequencing data. <i>Plant Journal</i> , 2019, 100, 641-654.	2.8	41
16	Nod factors potentiate auxin signaling for transcriptional regulation and lateral root formation in <i>Medicago truncatula</i> . <i>Journal of Experimental Botany</i> , 2017, 68, erw474.	2.4	40
17	Expression Atlas of <i>Selaginella moellendorffii</i> Provides Insights into the Evolution of Vasculature, Secondary Metabolism, and Roots. <i>Plant Cell</i> , 2020, 32, 853-870.	3.1	39
18	Proteome-wide, Structure-Based Prediction of Protein-Protein Interactions/New Molecular Interactions Viewer. <i>Plant Physiology</i> , 2019, 179, 1893-1907.	2.3	34

#	ARTICLE	IF	CITATIONS
19	Transcriptional landscapes of floral meristems in barley. <i>Science Advances</i> , 2021, 7, .	4.7	33
20	Araport Lives: An Updated Framework for Arabidopsis Bioinformatics. <i>Plant Cell</i> , 2020, 32, 2683-2686.	3.1	28
21	Complexity and specificity of the maize (<i>Zea mays</i> L.) root hair transcriptome. <i>Journal of Experimental Botany</i> , 2017, 68, 2175-2185.	2.4	19
22	A gene expression atlas for kiwifruit (<i>Actinidia chinensis</i>) and network analysis of transcription factors. <i>BMC Plant Biology</i> , 2021, 21, 121.	1.6	18
23	An Arabidopsis lipid map reveals differences between tissues and dynamic changes throughout development. <i>Plant Journal</i> , 2021, 107, 287-302.	2.8	18
24	Map of physical interactions between extracellular domains of Arabidopsis leucine-rich repeat receptor kinases. <i>Scientific Data</i> , 2019, 6, 190025.	2.4	17
25	Evolutionary divergence in embryo and seed coat development of Uâ€™s Triangle <i>Brassica</i> species illustrated by a spatiotemporal transcriptome atlas. <i>New Phytologist</i> , 2022, 233, 30-51.	3.5	16
26	Gene co-expression analysis of tomato seed maturation reveals tissue-specific regulatory networks and hubs associated with the acquisition of desiccation tolerance and seed vigour. <i>BMC Plant Biology</i> , 2021, 21, 124.	1.6	15
27	Light-responsive expression atlas reveals the effects of light quality and intensity in <i>Kalanchoë fedtschenkoi</i> , a plant with crassulacean acid metabolism. <i>GigaScience</i> , 2020, 9, .	3.3	11
28	Gene Slider: sequence logo interactive data-visualization for education and research. <i>Bioinformatics</i> , 2016, 32, 3670-3672.	1.8	8
29	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. <i>Frontiers in Plant Science</i> , 2021, 12, 736797.	1.7	1