

Federico D Ariel

List of Publications by Year in descending order

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55
papers

4,141
citations

159358

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161609

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63
all docs

63
docs citations

63
times ranked

4927
citing authors

#	ARTICLE	IF	CITATIONS
1	The lncRNA MARS modulates the epigenetic reprogramming of the maternal cluster in response to ABA. <i>Molecular Plant</i> , 2022, 15, 840-856.	3.9	25
2	<scp>TCP15</scp> interacts with <scp>GOLDEN2â€œLIKE</scp> 1 to control cotyledon opening in Arabidopsis. <i>Plant Journal</i> , 2022, 110, 748-763.	2.8	13
3	Apoplastic class III peroxidases PRX62 and PRX69 promote Arabidopsis root hair growth at low temperature. <i>Nature Communications</i> , 2022, 13, 1310.	5.8	25
4	Non-B DNA structures emerging from plant genomes. <i>Trends in Plant Science</i> , 2022, , .	4.3	4
5	R-loops at microRNA encoding loci promote co-transcriptional processing of pri-miRNAs in plants. <i>Nature Plants</i> , 2022, 8, 402-418.	4.7	47
6	Cytochrome <i>c</i> and the transcription factor ABI4 establish a molecular link between mitochondria and ABAâ€œdependent seed germination. <i>New Phytologist</i> , 2022, 235, 1780-1795.	3.5	4
7	Functional classification of plant long noncoding RNAs: a transcript is known by the company it keeps. <i>New Phytologist</i> , 2021, 229, 1251-1260.	3.5	48
8	Class I TCP proteins TCP14 and TCP15 are required for elongation and gene expression responses to auxin. <i>Plant Molecular Biology</i> , 2021, 105, 147-159.	2.0	31
9	When junk DNA turns functional: transposon-derived non-coding RNAs in plants. <i>Journal of Experimental Botany</i> , 2021, 72, 4132-4143.	2.4	23
10	Plant Long Noncoding RNAs: New Players in the Field of Post-Transcriptional Regulations. <i>Non-coding RNA</i> , 2021, 7, 12.	1.3	18
11	The lncRNA <i>APOLO</i> and the transcription factor WRKY42 target common cell wall EXTENSIN encoding genes to trigger root hair cell elongation. <i>Plant Signaling and Behavior</i> , 2021, 16, 1920191.	1.2	19
12	The lncRNA APOLO interacts with the transcription factor WRKY42 to trigger root hair cell expansion in response to cold. <i>Molecular Plant</i> , 2021, 14, 937-948.	3.9	72
13	Polycomb-dependent differential chromatin compartmentalization determines gene coregulation in <i>Arabidopsis</i> . <i>Genome Research</i> , 2021, 31, 1230-1244.	2.4	36
14	ChronoRoot: High-throughput phenotyping by deep segmentation networks reveals novel temporal parameters of plant root system architecture. <i>GigaScience</i> , 2021, 10, .	3.3	13
15	Deep Learning for the discovery of new pre-miRNAs: Helping the fight against COVID-19. <i>Machine Learning With Applications</i> , 2021, 6, 100150.	3.0	11
16	CURLY LEAF Regulates MicroRNA Activity by Controlling ARGONAUTE 1 Degradation in Plants. <i>Molecular Plant</i> , 2020, 13, 72-87.	3.9	24
17	The <i>Arabidopsis</i> lncRNA <i>ASCO</i> modulates the transcriptome through interaction with splicing factors. <i>EMBO Reports</i> , 2020, 21, e48977.	2.0	57
18	Long noncoding RNAs shape transcription in plants. <i>Transcription</i> , 2020, 11, 160-171.	1.7	24

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19	Class I TCP transcription factors regulate trichome branching and cuticle development in Arabidopsis. <i>Journal of Experimental Botany</i> , 2020, 71, 5438-5453.	2.4	26
20	Evolution of the Small Family of Alternative Splicing Modulators Nuclear Speckle RNA-Binding Proteins in Plants. <i>Genes</i> , 2020, 11, 207.	1.0	10
21	R-Loop Mediated trans Action of the APOLO Long Noncoding RNA. <i>Molecular Cell</i> , 2020, 77, 1055-1065.e4.	4.5	164
22	Lateral root development differs between main and secondary roots and depends on the ecotype. <i>Plant Signaling and Behavior</i> , 2020, 15, 1755504.	1.2	9
23	Class-I TCP Transcription Factors Activate the <i>SAUR63</i> Gene Subfamily in Gibberellin-Dependent Stamen Filament Elongation. <i>Plant Physiology</i> , 2020, 182, 2096-2110.	2.3	42
24	Dynamic regulation of chromatin topology and transcription by inverted repeat-derived small RNAs in sunflower. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17578-17583.	3.3	29
25	Eiger/TNF \pm -mediated Dilp8 and ROS production coordinate intra-organ growth in Drosophila. <i>PLoS Genetics</i> , 2019, 15, e1008133.	1.5	33
26	Class I TCP Transcription Factors Target the Gibberellin Biosynthesis Gene <i>GA20ox1</i> and the Growth-Promoting Genes <i>HBI1</i> and <i>PRE6</i> during Thermomorphogenic Growth in <i>Arabidopsis</i> . <i>Plant and Cell Physiology</i> , 2019, 60, 1633-1645.	1.5	49
27	AtHB23 participates in the gene regulatory network controlling root branching, and reveals differences between secondary and tertiary roots. <i>Plant Journal</i> , 2019, 100, 1224-1236.	2.8	24
28	Splicing regulation by long noncoding RNAs. <i>Nucleic Acids Research</i> , 2018, 46, 2169-2184.	6.5	226
29	Nuclear Speckle RNA Binding Proteins Remodel Alternative Splicing and the Non-coding Arabidopsis Transcriptome to Regulate a Cross-Talk Between Auxin and Immune Responses. <i>Frontiers in Plant Science</i> , 2018, 9, 1209.	1.7	41
30	Ploidy-dependent changes in the epigenome of symbiotic cells correlate with specific patterns of gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4543-4548.	3.3	50
31	Plant Epigenetics: Non-coding RNAs as Emerging Regulators. <i>RNA Technologies</i> , 2017, , 129-147.	0.2	0
32	Alternative splicing: The lord of the rings. <i>Nature Plants</i> , 2017, 3, 17065.	4.7	5
33	Class I and Class II TCP Transcription Factors Modulate SOC1-Dependent Flowering at Multiple Levels. <i>Molecular Plant</i> , 2017, 10, 1571-1574.	3.9	56
34	The Nuclear Ribonucleoprotein Smd1 Interplays with Splicing, RNA Quality Control, and Posttranscriptional Gene Silencing in Arabidopsis. <i>Plant Cell</i> , 2016, 28, 426-438.	3.1	46
35	The chloroplastic DEVH ϵ RNA helicase <i>INCREASED SIZE EXCLUSION LIMIT 2</i> involved in plasmodesmata regulation is required for group II intron splicing. <i>Plant, Cell and Environment</i> , 2016, 39, 165-173.	2.8	36
36	Put your 3D glasses on: plant chromatin is on show. <i>Journal of Experimental Botany</i> , 2016, 67, 3205-3221.	2.4	59

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37	Chromatin architecture: A new dimension in the dynamic control of gene expression. <i>Plant Signaling and Behavior</i> , 2016, 11, e1232224.	1.2	1
38	LHP1 Regulates H3K27me3 Spreading and Shapes the Three-Dimensional Conformation of the Arabidopsis Genome. <i>PLoS ONE</i> , 2016, 11, e0158936.	1.1	97
39	A SWI/SNF Chromatin Remodelling Protein Controls Cytokinin Production through the Regulation of Chromatin Architecture. <i>PLoS ONE</i> , 2015, 10, e0138276.	1.1	25
40	Battles and hijacks: noncoding transcription in plants. <i>Trends in Plant Science</i> , 2015, 20, 362-371.	4.3	176
41	A phylogenetically conserved group of NF-Y transcription factors interact to control nodulation in legumes. <i>Plant Physiology</i> , 2015, 169, pp.01144.2015.	2.3	72
42	Long Noncoding RNA Modulates Alternative Splicing Regulators in Arabidopsis. <i>Developmental Cell</i> , 2014, 30, 166-176.	3.1	311
43	The BAF60 Subunit of the SWI/SNF Chromatin-Remodeling Complex Directly Controls the Formation of a Gene Loop at <i>FLOWERING LOCUS C</i> in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2014, 26, 538-551.	3.1	82
44	Noncoding Transcription by Alternative RNA Polymerases Dynamically Regulates an Auxin-Driven Chromatin Loop. <i>Molecular Cell</i> , 2014, 55, 383-396.	4.5	330
45	Two <i>CCAAT</i> -box binding transcription factors redundantly regulate early steps of the legume-rhizobia endosymbiosis. <i>Plant Journal</i> , 2014, 79, 757-768.	2.8	105
46	Two Direct Targets of Cytokinin Signaling Regulate Symbiotic Nodulation in <i>Medicago truncatula</i> . <i>Plant Cell</i> , 2012, 24, 3838-3852.	3.1	136
47	Dual involvement of a <i>Medicago truncatula</i> NAC transcription factor in root abiotic stress response and symbiotic nodule senescence. <i>Plant Journal</i> , 2012, 70, 220-230.	2.8	111
48	Dual RNAs in plants. <i>Biochimie</i> , 2011, 93, 1950-1954.	1.3	41
49	MtCRE1-dependent cytokinin signaling integrates bacterial and plant cues to coordinate symbiotic nodule organogenesis in <i>Medicago truncatula</i> . <i>Plant Journal</i> , 2011, 65, 622-633.	2.8	257
50	The LOB-like transcription factor MtLBD1 controls <i>Medicago truncatula</i> root architecture under salt stress. <i>Plant Signaling and Behavior</i> , 2010, 5, 1666-1668.	1.2	39
51	Transcriptional Control of a Plant Stem Cell Niche. <i>Developmental Cell</i> , 2010, 18, 841-853.	3.1	221
52	Environmental Regulation of Lateral Root Emergence in <i>Medicago truncatula</i> Requires the HD-Zip I Transcription Factor HB1. <i>Plant Cell</i> , 2010, 22, 2171-2183.	3.1	156
53	Two ABREs, two redundant root-specific and one W-box cis-acting elements are functional in the sunflower HAHB4 promoter. <i>Plant Physiology and Biochemistry</i> , 2008, 46, 860-867.	2.8	21
54	The sunflower HD-Zip transcription factor HAHB4 is up-regulated in darkness, reducing the transcription of photosynthesis-related genes. <i>Journal of Experimental Botany</i> , 2008, 59, 3143-3155.	2.4	36

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55	The true story of the HD-Zip family. Trends in Plant Science, 2007, 12, 419-426.	4.3	508