Fernando Andres

List of Publications by Year in descending order

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24 papers	2,814 citations	430874 18 h-index	642732 23 g-index
25 all docs	25 docs citations	25 times ranked	4042 citing authors

#	Article	IF	Citations
1	Unraveling the role of MADS transcription factor complexes in apple tree dormancy. New Phytologist, 2021, 232, 2071-2088.	7.3	31
2	The Identification of Small RNAs Differentially Expressed in Apple Buds Reveals a Potential Role of the Mir159-MYB Regulatory Module during Dormancy. Plants, 2021, 10, 2665.	3.5	9
3	An efficient protocol for functional studies of apple transcription factors using a glucocorticoid receptor fusion system. Applications in Plant Sciences, 2020, 8, e11396.	2.1	3
4	Functional Divergence of the Arabidopsis Florigen-Interacting bZIP Transcription Factors FD and FDP. Cell Reports, 2020, 31, 107717.	6.4	49
5	Mutagenesis of a Quintuple Mutant Impaired in Environmental Responses Reveals Roles for CHROMATIN REMODELING4 in the Arabidopsis Floral Transition. Plant Cell, 2020, 32, 1479-1500.	6.6	17
6	The sugar transporter SWEET10 acts downstream of FLOWERING LOCUS T during floral transition of Arabidopsis thaliana. BMC Plant Biology, 2020, 20, 53.	3.6	59
7	I Want to (Bud) Break Free: The Potential Role of DAM and SVP-Like Genes in Regulating Dormancy Cycle in Temperate Fruit Trees. Frontiers in Plant Science, 2018, 9, 1990.	3.6	129
8	Copper and ectopic expression of the Arabidopsis transport protein COPT1 alter iron homeostasis in rice (Oryza sativa L.). Plant Molecular Biology, 2017, 95, 17-32.	3.9	19
9	Sample Preparation of Arabidopsis thaliana Shoot Apices for Expression Studies of Photoperiod-Induced Genes. Methods in Molecular Biology, 2016, 1398, 81-91.	0.9	0
10	The dynamics of <scp>FLOWERING LOCUS</scp> T expression encodes longâ€day information. Plant Journal, 2015, 83, 952-961.	5.7	33
11	Floral induction in Arabidopsis thaliana by FLOWERING LOCUS T requires direct repression of BLADE-ON-PETIOLE genes by homeodomain protein PENNYWISE. Plant Physiology, 2015, 169, pp.00960.2015.	4.8	51
12	Arabidopsis florigen FT binds to diurnally oscillating phospholipids that accelerate flowering. Nature Communications, 2014, 5, 3553.	12.8	143
13	SHORT VEGETATIVE PHASE reduces gibberellin biosynthesis at the Arabidopsis shoot apex to regulate the floral transition. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2760-9.	7.1	132
14	Diurnal and circadian expression profiles of glycerolipid biosynthetic genes inArabidopsis. Plant Signaling and Behavior, 2014, 9, e29715.	2.4	21
15	Flowering responses to seasonal cues: what's new?. Current Opinion in Plant Biology, 2014, 21, 120-127.	7.1	91
16	Identification of pathways directly regulated by SHORT VEGETATIVE PHASE during vegetative and reproductive development in Arabidopsis. Genome Biology, 2013, 14, R56.	8.8	134
17	Analysis of the Arabidopsis Shoot Meristem Transcriptome during Floral Transition Identifies Distinct Regulatory Patterns and a Leucine-Rich Repeat Protein That Promotes Flowering. Plant Cell, 2012, 24, 444-462.	6.6	178
18	The genetic basis of flowering responses to seasonal cues. Nature Reviews Genetics, 2012, 13, 627-639.	16.3	1,200

#	Article	IF	Citations
19	Sensitivity to high salinity in tetraploid citrus seedlings increases with water availability and correlates with expression of candidate genes. Functional Plant Biology, 2010, 37, 674.	2.1	72
20	Analysis of PHOTOPERIOD SENSITIVITY5 Sheds Light on the Role of Phytochromes in Photoperiodic Flowering in Rice Â. Plant Physiology, 2009, 151, 681-690.	4.8	73
21	Constitutive Expression of OsGH3.1 Reduces Auxin Content and Enhances Defense Response and Resistance to a Fungal Pathogen in Rice. Molecular Plant-Microbe Interactions, 2009, 22, 201-210.	2.6	179
22	Analysis of 13000 unique Citrus clusters associated with fruit quality, production and salinity tolerance. BMC Genomics, 2007, 8, 31.	2.8	64
23	Rice cv. Bahia mutagenized population: a new resource for rice breeding in the Mediterranean basin. Spanish Journal of Agricultural Research, 2007, 5, 341.	0.6	22
24	Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies. Plant Molecular Biology, 2005, 57, 375-391.	3.9	104