Eva Madrid

List of Publications by Year
in descending order

28 papers	726 citations	567144 15 h-index	552653 26 g-index
29 all docs	29 docs citations	29 times ranked	1000 citing authors

#	Article	IF	Citations
1	Gene regulatory networks controlled by FLOWERING LOCUS C that confer variation in seasonal flowering and life history. Journal of Experimental Botany, 2021, 72, 4-14.	2.4	41
2	Transposition and duplication of MADS-domain transcription factor genes in annual and perennial Arabis species modulates flowering. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	6
3	Cloning and characterization of a putative orthologue of the wheat vernalization (VRN1) gene in perennial wheatgrass (Agropyron cristatum). Plant Breeding, 2020, 139, 1290-1298.	1.0	4
4	Gibberellins Act Downstream of Arabis PERPETUAL FLOWERING1 to Accelerate Floral Induction during Vernalization. Plant Physiology, 2019, 180, 1549-1563.	2.3	17
5	Saturation of genomic region implicated in resistance to Fusarium oxysporum f. sp. ciceris race 5 in chickpea. Molecular Breeding, 2019, 39, 1.	1.0	13
6	Improving and correcting the contiguity of long-read genome assemblies of three plant species using optical mapping and chromosome conformation capture data. Genome Research, 2017, 27, 778-786.	2.4	155
7	Saturation mapping of regions determining resistance to Ascochyta blight and broomrape in faba bean using transcriptome-based SNP genotyping. Theoretical and Applied Genetics, 2017, 130, 2271-2282.	1.8	24
8	Genetic Mapping and Quantitative Trait Loci. Compendium of Plant Genomes, 2017, , 83-106.	0.3	1
9	Development of new kabuli large-seeded chickpea materials with resistance to Ascochyta blight. Crop and Pasture Science, 2017, 68, 967.	0.7	6
10	Identification of the target region including the Foc0 1 /foc0 1 gene and development of near isogenic lines for resistance to Fusarium Wilt race 0 in chickpea. Euphytica, 2016, 210, 119-133.	0.6	15
11	Production of â€œsuper-malesâ€•of asparagus by anther culture and its detection with SSR-ESTs. Plant Cell, Tissue and Organ Culture, 2016, 124, 119-135.	1.2	12
12	AutoFlow, a Versatile Workflow Engine Illustrated by Assembling an Optimised de novo Transcriptome for a Non-Model Species, such as Faba Bean (Vicia faba). Current Bioinformatics, 2016, 11, 440-450.	0.7	17
13	Large-Scale Transcriptome Analysis in Faba Bean (Vicia faba L.) under Ascochyta fabae Infection. PLoS ONE, 2015, 10, e0135143.	1.1	43
14	Detection of a new QTL/gene for growth habit in chickpea CaLG1 using wide and narrow crosses. Euphytica, 2015, 204, 473-485.	0.6	15
15	Efficiency of marker-assisted selection for ascochyta blight in chickpea. Journal of Agricultural Science, 2015, 153, 56-67.	0.6	25
16	Chickpea. Handbook of Plant Breeding, 2015, , 85-109.	0.1	9
17	Molecular and cytogenetic characterization of a common wheat-Agropyron cristatum chromosome translocation conferring resistance to leaf rust. Euphytica, 2015, 201, 89-95.	0.6	35
18	Genetic and physical mapping of the QTLAR3 controlling blight resistance in chickpea (Cicer arietinum) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.6	27

#	Article	IF	Citations
19	Mapping and identification of a Cicer arietinum NSP2 gene involved in nodulation pathway. Theoretical and Applied Genetics, 2014, 127, 481-488.	1.8	19
20	Detection of partial resistance quantitative trait loci against Didymella pinodes in Medicago truncatula. Molecular Breeding, 2014, 33, 589-599.	1.0	7
21	Characterization of Transcription Factors Following Expression Profiling of Medicago truncatulaâ€“Botrytis spp. Interactions. Plant Molecular Biology Reporter, 2014, 32, 1030-1040.	1.0	7
22	Allele-specific amplification for the detection of ascochyta blight resistance in chickpea. Euphytica, 2013, 189, 183-190.	0.6	38
23	Characterization and genetic analysis of an EIN4-like sequence (CaETR-1) located in QTLAR1 implicated in ascochyta blight resistance in chickpea. Plant Cell Reports, 2012, 31, 1033-1042.	2.8	33
24	Legume breeding for rust resistance: lessons to learn from the model Medicago truncatula. Euphytica, 2011, 180, 89-98.	0.6	28
25	Transcription factor profiling leading to the identification of putative transcription factors involved in the Medicago truncatulaâ€“Uromyces striatus interaction. Theoretical and Applied Genetics, 2010, 121, 1311-1321.	1.8	17
26	Development of chickpea near-isogenic lines for fusarium wilt. Theoretical and Applied Genetics, 2010, 121, 1519-1526.	1.8	37
27	Twoâ€dimensional gel electrophoresisâ€based proteomic analysis of the Medicago truncatulaâ€“rust (Uromyces striatus) interaction. Annals of Applied Biology, 2010, 157, 243-257.	1.3	19
28	Mechanism and molecular markers associated with rust resistance in a chickpea interspecific cross (Cicer arietinum Ã— Cicer reticulatum). European Journal of Plant Pathology, 2008, 121, 43-53.	0.8	54