Eva Madrid

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1560746/publications.pdf Version: 2024-02-01



Ενλ Μληριη

| # | Article | IF | CITATIONS |
|----|---|--------------------|-------------|
| 1 | 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 |
| 2 | Mechanism and molecular markers associated with rust resistance in a chickpea interspecific cross (Cicer arietinum × Cicer reticulatum). European Journal of Plant Pathology, 2008, 121, 43-53. | 0.8 | 54 |
| 3 | Large-Scale Transcriptome Analysis in Faba Bean (Vicia faba L.) under Ascochyta fabae Infection. PLoS ONE, 2015, 10, e0135143. | 1.1 | 43 |
| 4 | 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 |
| 5 | Allele-specific amplification for the detection of ascochyta blight resistance in chickpea. Euphytica, 2013, 189, 183-190. | 0.6 | 38 |
| 6 | Development of chickpea near-isogenic lines for fusarium wilt. Theoretical and Applied Genetics, 2010, 121, 1519-1526. | 1.8 | 37 |
| 7 | 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 |
| 8 | 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 |
| 9 | Legume breeding for rust resistance: lessons to learn from the model Medicago truncatula. Euphytica, 2011, 180, 89-98. | 0.6 | 28 |
| 10 | Genetic and physical mapping of the QTLAR3 controlling blight resistance in chickpea (Cicer arietinum) Tj ETQqO | 0 0 rgBT /0 0.6 | Overlock 10 |
| 11 | Efficiency of marker-assisted selection for ascochyta blight in chickpea. Journal of Agricultural Science, 2015, 153, 56-67. | 0.6 | 25 |
| 12 | 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 |
| 13 | Twoâ€dimensional gel electrophoresisâ€based proteomic analysis of the <i>Medicago truncatula</i> –rust (<i>Uromyces striatus</i>) interaction. Annals of Applied Biology, 2010, 157, 243-257. | 1.3 | 19 |

| 14 | Mapping and identification of a Cicer arietinum NSP2 gene involved in nodulation pathway. Theoretical and Applied Genetics, 2014, 127, 481-488. | 1.8 | 19 |
|----|---|-----|----|
| 15 | Transcription factor profiling leading to the identification of putative transcription factors involved in the Medicago truncatula–Uromyces striatus interaction. Theoretical and Applied Genetics, 2010, 121, 1311-1321. | 1.8 | 17 |
| 16 | Gibberellins Act Downstream of <i>Arabis</i> PERPETUAL FLOWERING1 to Accelerate Floral Induction during Vernalization. Plant Physiology, 2019, 180, 1549-1563. | 2.3 | 17 |
| 17 | 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 |
| | | | |

18Detection of a new QTL/gene for growth habit in chickpea CaLG1 using wide and narrow crosses.0.61518Euphytica, 2015, 204, 473-485.0.615

Eva Madrid

| # | Article | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | Production of "super-males―of asparagus by anther culture and its detection with SSR-ESTs. Plant Cell, Tissue and Organ Culture, 2016, 124, 119-135. | 1.2 | 12 |
| 22 | Chickpea. Handbook of Plant Breeding, 2015, , 85-109. | 0.1 | 9 |
| 23 | Detection of partial resistance quantitative trait loci against Didymella pinodes in Medicago truncatula. Molecular Breeding, 2014, 33, 589-599. | 1.0 | 7 |
| 24 | Characterization of Transcription Factors Following Expression Profiling of Medicago truncatula–Botrytis spp. Interactions. Plant Molecular Biology Reporter, 2014, 32, 1030-1040. | 1.0 | 7 |
| 25 | Development of new kabuli large-seeded chickpea materials with resistance to Ascochyta blight. Crop and Pasture Science, 2017, 68, 967. | 0.7 | 6 |
| 26 | Transposition and duplication of MADS-domain transcription factor genes in annual and perennial <i>Arabis</i> species modulates flowering. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 6 |
| 27 | 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 |
| 28 | Genetic Mapping and Quantitative Trait Loci. Compendium of Plant Genomes, 2017, , 83-106. | 0.3 | 1 |