

Teresa Millan

List of Publications by Year in descending order

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59
papers

3,403
citations

186209

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143943

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times ranked

2579
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#	ARTICLE	IF	CITATIONS
1	The <i>SINGLE FLOWER (SFL)</i> gene encodes a MYB transcription factor that regulates the number of flowers produced by the inflorescence of chickpea. <i>New Phytologist</i> , 2022, 234, 827-836.	3.5	6
2	Aldehyde Dehydrogenase 3 Is an Expanded Gene Family with Potential Adaptive Roles in Chickpea. <i>Plants</i> , 2021, 10, 2429.	1.6	3
3	Genetic diversity and population structure of Algerian chickpea (<i>Cicer arietinum</i>) genotypes: use of agro-morphological traits and molecular markers linked or not linked to the gene or QTL of interest. <i>Crop and Pasture Science</i> , 2020, 71, 155.	0.7	9
4	Genetic analysis reveals PDH1 as a candidate gene for control of pod dehiscence in chickpea. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	14
5	Altered Expression of an FT Cluster Underlies a Major Locus Controlling Domestication-Related Changes to Chickpea Phenology and Growth Habit. <i>Frontiers in Plant Science</i> , 2019, 10, 824.	1.7	38
6	Candidate genes expression profiling during wilting in chickpea caused by <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> race 5. <i>PLoS ONE</i> , 2019, 14, e0224212.	1.1	18
7	Saturation of genomic region implicated in resistance to <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> race 5 in chickpea. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	13
8	Genome-wide identification of the auxin response factor gene family in <i>Cicer arietinum</i> . <i>BMC Genomics</i> , 2018, 19, 301.	1.2	40
9	Assessment of genetic diversity in Iranian <i>Asparagus</i> spp. related to garden asparagus. <i>Acta Horticulturae</i> , 2018, , 39-44.	0.1	4
10	STMS (sequence tagged microsatellite site) molecular markers as a valuable tool to confirm controlled crosses in chickpea (<i>Cicer arietinum</i> L.) breeding programs. <i>Euphytica</i> , 2018, 214, 1.	0.6	9
11	Segmental and Tandem Duplications Driving the Recent NBS-LRR Gene Expansion in the <i>Asparagus</i> Genome. <i>Genes</i> , 2018, 9, 568.	1.0	18
12	Integration of Genetic and Cytogenetic Maps and Identification of Sex Chromosome in Garden <i>Asparagus</i> (<i>Asparagus officinalis</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1068.	1.7	18
13	Genetic Mapping and Quantitative Trait Loci. <i>Compendium of Plant Genomes</i> , 2017, , 83-106.	0.3	1
14	Development of new kabuli large-seeded chickpea materials with resistance to <i>Ascochyta</i> blight. <i>Crop and Pasture Science</i> , 2017, 68, 967.	0.7	6
15	Identification of the target region including the <i>Foc0 1 /foc0 1</i> gene and development of near isogenic lines for resistance to <i>Fusarium</i> Wilt race 0 in chickpea. <i>Euphytica</i> , 2016, 210, 119-133.	0.6	15
16	Fine mapping for double podding gene in chickpea. <i>Theoretical and Applied Genetics</i> , 2016, 129, 77-86.	1.8	21
17	TOWARDS THE ROSE GENOME SEQUENCE AND ITS USE IN RESEARCH AND BREEDING. <i>Acta Horticulturae</i> , 2015, , 167-175.	0.1	11
18	Genetic control of inflorescence architecture in legumes. <i>Frontiers in Plant Science</i> , 2015, 6, 543.	1.7	76

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19	Detection of a new QTL/gene for growth habit in chickpea CaLG1 using wide and narrow crosses. <i>Euphytica</i> , 2015, 204, 473-485.	0.6	15
20	Efficiency of marker-assisted selection for ascochyta blight in chickpea. <i>Journal of Agricultural Science</i> , 2015, 153, 56-67.	0.6	25
21	Chickpea. <i>Handbook of Plant Breeding</i> , 2015, , 85-109.	0.1	9
22	Genetic and physical mapping of the QTLAR3 controlling blight resistance in chickpea (<i>Cicer arietinum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 27	0.6	27
23	Mapping and identification of a <i>Cicer arietinum</i> NSP2 gene involved in nodulation pathway. <i>Theoretical and Applied Genetics</i> , 2014, 127, 481-488.	1.8	19
24	A chromosomal genomics approach to assess and validate the <i>desi</i> and <i>kabuli</i> draft chickpea genome assemblies. <i>Plant Biotechnology Journal</i> , 2014, 12, 778-786.	4.1	54
25	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	9.4	1,049
26	Allele-specific amplification for the detection of ascochyta blight resistance in chickpea. <i>Euphytica</i> , 2013, 189, 183-190.	0.6	38
27	Sort communication. Genotype × environment interaction analysis in two chickpea RIL populations. <i>Spanish Journal of Agricultural Research</i> , 2013, 11, 808.	0.3	1
28	Characterization and genetic analysis of an EIN4-like sequence (CaETR-1) located in QTLAR1 implicated in ascochyta blight resistance in chickpea. <i>Plant Cell Reports</i> , 2012, 31, 1033-1042.	2.8	33
29	Identification of chickpea cultivars by microsatellite markers. <i>Journal of Agricultural Science</i> , 2011, 149, 451-460.	0.6	7
30	A segregation distortion locus located on linkage group 4 of the chickpea genetic map. <i>Euphytica</i> , 2011, 179, 515-523.	0.6	16
31	Integration of genetic and physical maps of the chickpea (<i>Cicer arietinum</i> L.) genome using flow-sorted chromosomes. <i>Chromosome Research</i> , 2011, 19, 729-739.	1.0	34
32	Transcription factor profiling leading to the identification of putative transcription factors involved in the <i>Medicago truncatula</i> – <i>Uromyces striatus</i> interaction. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1311-1321.	1.8	17
33	Development of chickpea near-isogenic lines for fusarium wilt. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1519-1526.	1.8	37
34	A consensus genetic map of chickpea (<i>Cicer arietinum</i> L.) based on 10 mapping populations. <i>Euphytica</i> , 2010, 175, 175-189.	0.6	101
35	Tagging and mapping a second resistance gene for Fusarium wilt race 0 in chickpea. <i>European Journal of Plant Pathology</i> , 2009, 124, 87-92.	0.8	38
36	Integration of new CAPS and dCAPS-RGA markers into a composite chickpea genetic map and their association with disease resistance. <i>Theoretical and Applied Genetics</i> , 2009, 118, 671-682.	1.8	30

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37	The marker SCK13603 associated with resistance to ascochyta blight in chickpea is located in a region of a putative retrotransposon. <i>Plant Cell Reports</i> , 2009, 28, 53-60.	2.8	15
38	Resistance in chickpea (<i>Cicer arietinum</i>) to <i>Fusarium</i> wilt race 0 TM . <i>Plant Breeding</i> , 2009, 129, 563.	1.0	6
39	Genetic analysis of agronomic traits in a wide cross of chickpea. <i>Field Crops Research</i> , 2009, 111, 130-136.	2.3	108
40	Mechanism and molecular markers associated with rust resistance in a chickpea interspecific cross (<i>Cicer arietinum</i> × <i>Cicer reticulatum</i>). <i>European Journal of Plant Pathology</i> , 2008, 121, 43-53.	0.8	54
41	Validation of a QTL for resistance to ascochyta blight linked to resistance to fusarium wilt race 5 in chickpea (<i>Cicer arietinum</i> L.). , 2007, , 29-37.		7
42	Genetic analysis of seed size, yield and days to flowering in a chickpea recombinant inbred line population derived from a Kabuli × Desi cross. <i>Annals of Applied Biology</i> , 2007, 151, 33-42.	1.3	69
43	Validation of a QTL for resistance to ascochyta blight linked to resistance to fusarium wilt race 5 in chickpea (<i>Cicer arietinum</i> L.). <i>European Journal of Plant Pathology</i> , 2007, 119, 29-37.	0.8	67
44	A new QTL for Ascochyta blight resistance in an RIL population derived from an interspecific cross in chickpea. <i>Euphytica</i> , 2006, 149, 105-111.	0.6	70
45	Chickpea molecular breeding: New tools and concepts. <i>Euphytica</i> , 2006, 147, 81-103.	0.6	135
46	Ploidic and Molecular Analysis of 'Morado de Huetor' Asparagus (<i>Asparagus officinale</i> L.) Population; A Spanish Tetraploid Landrace. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 729-736.	0.8	51
47	Detection of two quantitative trait loci for resistance to ascochyta blight in an intra-specific cross of chickpea (<i>Cicer arietinum</i> L.): development of SCAR markers associated with resistance. <i>Theoretical and Applied Genetics</i> , 2006, 112, 278-287.	1.8	107
48	A linkage map of chickpea (<i>Cicer arietinum</i> L.) based on populations from Kabuli × Desi crosses: location of genes for resistance to fusarium wilt race 0. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1347-1353.	1.8	106
49	Genetic mapping of QTLs controlling horticultural traits in diploid roses. <i>Theoretical and Applied Genetics</i> , 2005, 111, 511-520.	1.8	88
50	Two genes and linked RAPD markers involved in resistance to <i>Fusarium oxysporum</i> f. sp. <i>Ciceris</i> race 0 in chickpea. <i>Plant Breeding</i> , 2003, 122, 188-191.	1.0	59
51	Markers associated with Ascochyta blight resistance in chickpea and their potential in marker-assisted selection. <i>Field Crops Research</i> , 2003, 84, 373-384.	2.3	71
52	Phylogenetic analysis in the genus <i>Cicer</i> and cultivated chickpea using RAPD and ISSR markers. <i>Theoretical and Applied Genetics</i> , 2002, 104, 643-651.	1.8	148
53	Physical mapping of ribosomal DNA on several species of the subgenus <i>Rosa</i> . <i>Theoretical and Applied Genetics</i> , 2001, 103, 835-838.	1.8	30
54	VARIETAL IDENTIFICATION IN ROSA BY USING ISOZYME AND RAPD MARKERS. <i>Acta Horticulturae</i> , 1996, , 261-264.	0.1	6

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55	Using RAPDs to study phylogenetic relationships in Rosa. Theoretical and Applied Genetics, 1996, 92, 273-277.	1.8	28
56	Comparative RFLP maps of the homoeologous group-2 chromosomes of wheat, rye and barley. Theoretical and Applied Genetics, 1993, 85-85, 784-792.	1.8	239
57	Chromosomal location and RFLP utility in wheat and barley of a wheat gene with homology to a 7S storage-globulin sequence. Theoretical and Applied Genetics, 1992, 85, 387-388.	1.8	5
58	Effects of Hordeum chilense and Triticum Cytoplasm on Agronomical Traits in Hexaploid Tritordeum. Plant Breeding, 1992, 108, 328-331.	1.0	12
59	Tritordeum: A New Allopolyploid of Potential Importance as a Protein Source Crop 1. Crop Science, 1986, 26, 1186-1190.	0.8	50