Belén RomÃ;n

List of Publications by Year in descending order

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RELÃON ROMÃ:N

#	Article	IF	CITATIONS
1	Gene Expression in Zucchini Fruit Development. Horticulturae, 2022, 8, 306.	2.8	2
2	Verticillium Wilt Evaluation of Olive Breeding Selections Under Semi-Controlled Conditions. Plant Disease, 2021, 105, 1781-1790.	1.4	11
3	Nucleotide diversity analysis of candidate genes for Verticillium wilt resistance in olive. Scientia Horticulturae, 2020, 274, 109653.	3.6	6
4	Candidate gene analysis of Tomato leaf curl New Delhi virus resistance in Cucumis melo. Scientia Horticulturae, 2019, 243, 12-20.	3.6	11
5	First RNA-seq approach to study fruit set and parthenocarpy in zucchini (Cucurbita pepo L.). BMC Plant Biology, 2019, 19, 61.	3.6	19
6	Genome-scale examination of NBS-encoding genes in blueberry. Scientific Reports, 2018, 8, 3429.	3.3	18
7	Auxin signalling regulation during induced and parthenocarpic fruit set in zucchini. Molecular Breeding, 2017, 37, 1.	2.1	21
8	Design and Sampling Plan Optimization for RT-qPCR Experiments in Plants: A Case Study in Blueberry. Frontiers in Plant Science, 2016, 7, 271.	3.6	9
9	Expression Profile of Carotenoid Cleavage Dioxygenase Genes in Summer Squash (Cucurbita pepo L.). Plant Foods for Human Nutrition, 2015, 70, 200-206.	3.2	21
10	Identification, cloning, and expression analysis of three phytoene synthase genes from Cucurbita pepo. Biologia Plantarum, 2015, 59, 201-210.	1.9	9
11	An improved method to obtain novel mutants in Cucurbita pepo by pollen viability. Scientia Horticulturae, 2014, 169, 14-19.	3.6	4
12	First TILLING Platform in Cucurbita pepo: A New Mutant Resource for Gene Function and Crop Improvement. PLoS ONE, 2014, 9, e112743.	2.5	40
13	Carotenogenic Gene Expression and Carotenoid Accumulation in Three Varieties of Cucurbita pepo during Fruit Development. Journal of Agricultural and Food Chemistry, 2013, 61, 6393-6403.	5.2	33
14	Population Diversity and Dynamics of Parasitic Weeds. , 2013, , 345-356.		6
15	RNA quality assessment: a view from plant qPCR studies. Journal of Experimental Botany, 2012, 63, 6069-6077.	4.8	52
16	Evaluation of Different Pulverisation Methods for RNA Extraction in Squash Fruit: Lyophilisation, Cryogenic Mill and Mortar Grinding. Phytochemical Analysis, 2012, 23, 622-626.	2.4	3
17	Development of a multiplex real-time PCR method for simultaneous detection of Salmonella enterica, Shigella flexneri and Listeria monocytogenes in processed food samples. European Food Research and Technology, 2012, 234, 571-580.	3.3	29
18	Selection of reference genes for expression studies in Cicer arietinum L.: analysis of cyp81E3 gene expression against Ascochyta rabiei. Molecular Breeding, 2012, 29, 261-274.	2.1	26

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19	Selection of Reference Genes for Gene Expression Studies in Zucchini (Cucurbita pepo) Using qPCR. Journal of Agricultural and Food Chemistry, 2011, 59, 5402-5411.	5.2	74
20	Characterization of the 3′:5′ ratio for reliable determination of RNA quality. Analytical Biochemistry, 2011, 419, 336-338.	2.4	21
21	Selection of reference genes in Hedysarum coronarium under various stresses and stages of development. Analytical Biochemistry, 2011, 409, 236-243.	2.4	28
22	Validation of QTLs for Orobanche crenata resistance in faba bean (Vicia faba L.) across environments and generations. Theoretical and Applied Genetics, 2010, 120, 909-919.	3.6	54
23	Evaluation of candidate reference genes for expression studies in Pisum sativum under different experimental conditions. Planta, 2010, 232, 145-153.	3.2	151
24	Gene expression profiling of <i>Medicago truncatula</i> roots in response to the parasitic plant <i>Orobanche crenata</i> . Weed Research, 2009, 49, 66-80.	1.7	26
25	Gene expression analysis of molecular mechanisms of defense induced in Medicago truncatula parasitized by Orobanche crenata. Plant Physiology and Biochemistry, 2009, 47, 635-641.	5.8	10
26	Population genetics in weedy species of <i>Orobanche</i> . Australasian Plant Pathology, 2009, 38, 228.	1.0	25
27	Expression analysis of Pisum sativum putative defence genes during Orobanche crenata infection. Crop and Pasture Science, 2009, 60, 490.	1.5	7
28	Confirmation of QTLs controlling Ascochyta fabae resistance in different generations of faba bean (Vicia faba L.). Crop and Pasture Science, 2009, 60, 353.	1.5	35
29	Selection of housekeeping genes for normalization by real-time RT–PCR: Analysis of Or-MYB1 gene expression in Orobanche ramosa development. Analytical Biochemistry, 2008, 379, 176-181.	2.4	46
30	Vicia faba germplasm multiplication – floral traits associated with pollen-mediated gene flow under diverse between-plot isolation strategies. Annals of Applied Biology, 2008, 152, 201-208.	2.5	17
31	Genetic Variation Among and Within <i>Uromyces</i> Species Infecting Legumes. Journal of Phytopathology, 2008, 156, 419-424.	1.0	22
32	Genetic diversity of Moroccan populations of <i>Orobanche foetida</i> : evolving from parasitising wild hosts to crop plants. Weed Research, 2008, 48, 179-186.	1.7	34
33	Control of Orobanche crenata in Vicia narbonensis by glyphosate. Crop Protection, 2008, 27, 873-876.	2.1	8
34	Isolation and expression analysis of a cobalamin-independent methionine synthase gene from the parasitic plant Orobanche ramosa. Scientia Horticulturae, 2008, 116, 337-341.	3.6	2
35	First Report of <i>Orobanche crenata</i> on Sulla (<i>Hedysarum coronarium</i>) in Andalusia, Southern Spain. Plant Disease, 2008, 92, 1709-1709.	1.4	2
36	Genetic diversity in two variants of Orobanche gracilis Sm. [var. gracilis and var. deludens (Beck) A. Pujadas] (Orobanchaceae) from different regions of Spain. Electronic Journal of Biotechnology, 2007, 10, 0-0.	2.2	10

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37	Identification by suppression subtractive hybridization and expression analysis of Medicago truncatula putative defence genes in response to Orobanche crenata parasitization. Physiological and Molecular Plant Pathology, 2007, 70, 49-59.	2.5	37
38	Host differentiation in Orobanche foetida Poir. Flora: Morphology, Distribution, Functional Ecology of Plants, 2007, 202, 201-208.	1.2	35
39	Plant resistance to parasitic plants: molecular approaches to an old foe. New Phytologist, 2007, 173, 703-712.	7.3	89
40	DetectingOrobanche species by using cpDNA diagnostic markers. Phytoparasitica, 2007, 35, 129-135.	1.2	9
41	Faba bean breeding for resistance against biotic stresses: Towards application of marker technology. Euphytica, 2006, 147, 67-80.	1.2	104
42	Screening techniques and sources of resistance against parasitic weeds in grain legumes. Euphytica, 2006, 147, 187-199.	1.2	137
43	First Report of Orobanche foetida on Common Vetch (Vicia sativa) in Morocco. Plant Disease, 2005, 89, 528-528.	1.4	36
44	Locating quantitative trait loci associated with Orobanche crenata resistance in pea. Weed Research, 2004, 44, 323-328.	1.7	53
45	Development of a composite map in Vicia faba, breeding applications and future prospects. Theoretical and Applied Genetics, 2004, 108, 1079-1088.	3.6	58
46	Genetic Relationships among Orobanche Species as Revealed by RAPD Analysis. Annals of Botany, 2003, 91, 637-642.	2.9	45
47	Locating genes associated with Ascochyta fabae resistance in Vicia faba. Australian Journal of Agricultural Research, 2003, 54, 85.	1.5	61
48	Variation Among and Within Populations of the Parasitic Weed Orobanche crenata from Spain and Israel Revealed by Inter Simple Sequence Repeat Markers. Phytopathology, 2002, 92, 1262-1266.	2.2	46
49	Mapping of quantitative trait loci controlling broomrape (Orobanche crenataForsk.) resistance in faba bean (Vicia fabaL.). Genome, 2002, 45, 1057-1063.	2.0	103
50	Development and Characterization of Microsatellite Markers from Chromosome 1-Specific DNA Libraries of Vicia Faba. Biologia Plantarum, 2002, 45, 337-345.	1.9	87
51	Genetic diversity in Orobanche crenata populations from southern Spain. Theoretical and Applied Genetics, 2001, 103, 1108-1114.	3.6	42