

MarÃ-a Teresa Cervera

List of Publications by Year in descending order

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58
papers

3,447
citations

136740

32
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143772

57
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59
all docs

59
docs citations

59
times ranked

3690
citing authors

#	ARTICLE	IF	CITATIONS
1	Maritime Pine Genomics in Focus. Compendium of Plant Genomes, 2022, , 67-123.	0.3	4
2	Correlating the above- and belowground genotype of <i>Pinus pinaster</i> trees and rhizosphere bacterial communities under drought conditions. Science of the Total Environment, 2022, 832, 155007.	3.9	6
3	Comprehensive analysis of the <i>isomiRome</i> in the vegetative organs of the conifer <i>Pinus pinaster</i> under contrasting water availability. Plant, Cell and Environment, 2021, 44, 706-728.	2.8	9
4	Scion-rootstock interaction and drought systemic effect modulate the organ-specific terpene profiles in grafted <i>Pinus pinaster</i> Ait. Environmental and Experimental Botany, 2021, 186, 104437.	2.0	5
5	Molecular study of drought response in the Mediterranean conifer <i>Pinus pinaster</i> Ait.: Differential transcriptomic profiling reveals constitutive water deficit-independent drought tolerance mechanisms. Ecology and Evolution, 2020, 10, 9788-9807.	0.8	19
6	Genomics of Clinal Local Adaptation in <i>Pinus sylvestris</i> Under Continuous Environmental and Spatial Genetic Setting. G3: Genes, Genomes, Genetics, 2020, 10, 2683-2696.	0.8	24
7	Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. Genome Biology and Evolution, 2017, 9, 1130-1147.	1.1	75
8	Leaf metabolic response to water deficit in <i>Pinus pinaster</i> Ait. relies upon ontogeny and genotype. Environmental and Experimental Botany, 2017, 140, 41-55.	2.0	39
9	Inter-genotypic differences in drought tolerance of maritime pine are modified by elevated [CO ₂]. Annals of Botany, 2017, 120, 591-602.	1.4	13
10	Analysis of DNA Cytosine Methylation Patterns Using Methylation-Sensitive Amplification Polymorphism (MSAP). Methods in Molecular Biology, 2017, 1456, 99-112.	0.4	24
11	Organ-specific metabolic responses to drought in <i>Pinus pinaster</i> Ait.. Plant Physiology and Biochemistry, 2016, 102, 17-26.	2.8	47
12	Massive sequencing of <i>Ulmus minor</i> 's transcriptome provides new molecular tools for a genus under the constant threat of Dutch elm disease. Frontiers in Plant Science, 2015, 6, 541.	1.7	19
13	Nucleotide polymorphisms in a pine ortholog of the <i>Arabidopsis</i> degrading enzyme cellulase KORRIGAN are associated with early growth performance in <i>Pinus pinaster</i> . Tree Physiology, 2015, 35, 1000-1006.	1.4	13
14	Genetic control of functional traits related to photosynthesis and water use efficiency in <i>Pinus pinaster</i> Ait. drought response: integration of genome annotation, allele association and QTL detection for candidate gene identification. BMC Genomics, 2014, 15, 464.	1.2	64
15	<i>De novo</i> assembly of maritime pine transcriptome: implications for forest breeding and biotechnology. Plant Biotechnology Journal, 2014, 12, 286-299.	4.1	115
16	Selection of haploid cell lines from megagametophyte cultures of maritime pine as a DNA source for massive sequencing of the species. Plant Cell, Tissue and Organ Culture, 2014, 118, 147-155.	1.2	12
17	Epigenetic Variability in the Genetically Uniform Forest Tree Species <i>Pinus pinea</i> L. PLoS ONE, 2014, 9, e103145.	1.1	77
18	Molecular response to water stress in two contrasting Mediterranean pines (<i>Pinus pinaster</i> and <i>Pinus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	2.8	27

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19	Epigenetic regulation of adaptive responses of forest tree species to the environment. <i>Ecology and Evolution</i> , 2013, 3, 399-415.	0.8	271
20	DNA sequence variation of drought-response candidate genes in <i>Austrocedrus chilensis</i> . <i>Electronic Journal of Biotechnology</i> , 2013, 16, .	1.2	1
21	Functional and genetic characterization of gas exchange and intrinsic water use efficiency in a full-sib family of <i>Pinus pinaster</i> Ait. in response to drought. <i>Tree Physiology</i> , 2012, 32, 94-103.	1.4	43
22	Novel conserved segments are associated with differential expression patterns for Pinaceae dehydrins. <i>Planta</i> , 2012, 236, 1863-1874.	1.6	30
23	Towards decoding the conifer giga-genome. <i>Plant Molecular Biology</i> , 2012, 80, 555-569.	2.0	91
24	Annotated genetic linkage maps of <i>Pinus pinaster</i> Ait. from a Central Spain population using microsatellite and gene based markers. <i>BMC Genomics</i> , 2012, 13, 527.	1.2	13
25	Identification of water stress genes in <i>Pinus pinaster</i> Ait. by controlled progressive stress and suppression-subtractive hybridization. <i>Plant Physiology and Biochemistry</i> , 2012, 50, 44-53.	2.8	28
26	Genetic stability analysis of chrysanthemum (<i>Chrysanthemum x morifolium</i> Ramat) after different stages of an encapsulationâ€ dehydration cryopreservation protocol. <i>Journal of Plant Physiology</i> , 2011, 168, 158-166.	1.6	40
27	Inter-clonal variation in functional traits in response to drought for a genetically homogeneous Mediterranean conifer. <i>Environmental and Experimental Botany</i> , 2011, 70, 104-109.	2.0	37
28	EuroPineDB: a high-coverage web database for maritime pine transcriptome. <i>BMC Genomics</i> , 2011, 12, 366.	1.2	59
29	Development and implementation of a highly-multiplexed SNP array for genetic mapping in maritime pine and comparative mapping with loblolly pine. <i>BMC Genomics</i> , 2011, 12, 368.	1.2	66
30	In Vitro vs In Silico Detected SNPs for the Development of a Genotyping Array: What Can We Learn from a Non-Model Species?. <i>PLoS ONE</i> , 2010, 5, e11034.	1.1	52
31	"Contrasting Patterns of Selection at <i>Pinus pinaster</i> Ait. Drought Stress Candidate Genes as Revealed by Genetic Differentiation Analyses". <i>Molecular Biology and Evolution</i> , 2008, 25, 417-437.	3.5	198
32	A genetic analysis of seed and berry weight in grapevine. <i>Genome</i> , 2006, 49, 1572-1585.	0.9	139
33	Isolation and characterization of nuclear microsatellite loci in <i>Pinus pinaster</i> Ait. <i>Molecular Ecology Notes</i> , 2005, 5, 57-59.	1.7	21
34	Intraspecific and interspecific genetic and phylogenetic relationships in the genus <i>Populus</i> based on AFLP markers. <i>Theoretical and Applied Genetics</i> , 2005, 111, 1440-1456.	1.8	103
35	DNA methylation increases throughout <i>Arabidopsis</i> development. <i>Planta</i> , 2005, 222, 301-306.	1.6	93
36	Characterization of microsatellite loci in <i>Ulmus minor</i> Miller and cross-amplification in <i>U. glabra</i> Hudson and <i>U. laevis</i> Pall.. <i>Molecular Ecology Notes</i> , 2004, 4, 731-732.	1.7	29

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37	English elm is a 2,000-year-old Roman clone. <i>Nature</i> , 2004, 431, 1053-1053.	13.7	74
38	Cross-amplification and sequence variation of microsatellite loci in Eurasian hard pines. <i>Theoretical and Applied Genetics</i> , 2004, 109, 103-111.	1.8	60
39	Cross-species transferability and mapping of genomic and cDNA SSRs in pines. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1204-1214.	1.8	153
40	Selfing and sibship structure in a two-cohort stand of maritime pine (<i>Pinus pinaster</i> Ait.) using nuclear SSR markers. <i>Annals of Forest Science</i> , 2003, 60, 115-121.	0.8	17
41	Seed gene flow and fine-scale structure in a Mediterranean pine (<i>Pinus pinaster</i> Ait.) using nuclear microsatellite markers. <i>Theoretical and Applied Genetics</i> , 2002, 104, 1290-1297.	1.8	76
42	Analysis of DNA methylation in <i>Arabidopsis thaliana</i> based on methylation-sensitive AFLP markers. <i>Molecular Genetics and Genomics</i> , 2002, 268, 543-552.	1.0	250
43	Identification of Plum pox virus Determinants Implicated in Specific Interactions with Different <i>Prunus</i> spp.. <i>Phytopathology</i> , 2001, 91, 159-164.	1.1	41
44	Characterisation of Iberian pig genotypes using AFLP markers. <i>Animal Genetics</i> , 2000, 31, 117-122.	0.6	33
45	A genetic map of Maritime pine based on AFLP, RAPD and protein markers. <i>Theoretical and Applied Genetics</i> , 2000, 100, 39-48.	1.8	67
46	Identification of a pathogenicity determinant of Plum pox virus in the sequence encoding the C-terminal region of protein P3+6K1. <i>Journal of General Virology</i> , 2000, 81, 557-566.	1.3	95
47	Application of AFLPs to the characterization of grapevine <i>Vitis vinifera</i> L. genetic resources. A case study with accessions from Rioja (Spain). <i>Theoretical and Applied Genetics</i> , 1998, 97, 51-59.	1.8	164
48	Plum pox potyvirus resistance associated to transgene silencing that can be stabilized after different number of plant generations. <i>Gene</i> , 1998, 206, 263-272.	1.0	29
49	Engineering Resistance against Viral Diseases in Plants. <i>Sub-Cellular Biochemistry</i> , 1998, 29, 287-320.	1.0	9
50	Application of AFLP, ϕ -based molecular markers to breeding of <i>Populus</i> spp.. <i>Plant Growth Regulation</i> , 1996, 20, 47-52.	1.8	28
51	Identification of AFLP molecular markers for resistance against <i>Melampsora larici-populina</i> in <i>Populus</i> . <i>Theoretical and Applied Genetics</i> , 1996, 93-93, 733-737.	1.8	118
52	Processing of the plum pox virus polyprotein at the P3-6K1 junction is not required for virus viability. <i>Journal of General Virology</i> , 1995, 76, 951-956.	1.3	50
53	Properties of the active plum pox potyvirus RNA polymerase complex in defined glycerol gradient fractions. <i>Virus Research</i> , 1995, 37, 127-137.	1.1	37
54	Inhibitory effects of human cystatin C on plum pox potyvirus proteases. <i>Plant Molecular Biology</i> , 1993, 22, 697-701.	2.0	22

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55	3'-Terminal sequence of the plum pox virus PS and o6 isolates: evidence for RNA recombination within the potyvirus group. <i>Journal of General Virology</i> , 1993, 74, 329-334.	1.3	111
56	Intracellular localization of three non-structural plum pox potyvirus proteins by immunogold labelling. <i>Virus Research</i> , 1992, 25, 201-211.	1.1	15
57	Proteolytic processing of the plum pox potyvirus polyprotein by the N1a protease at a novel cleavage site. <i>Virology</i> , 1992, 188, 697-703.	1.1	43
58	Mutational Analysis of Plum Pox Potyvirus Polyprotein Processing By the N1a Protease in <i>Escherichia Coli</i> . <i>Journal of General Virology</i> , 1990, 71, 2773-2779.	1.3	31