Jordi Garcia-Mas

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/1006058/publications.pdf

Version: 2024-02-01

91 papers	6,914 citations	44042 48 h-index	62565 80 g-index
98 all docs	98 docs citations	98 times ranked	5752 citing authors

#	Article	IF	Citations
1	A cryptic variation in a member of the Ovate Family Proteins is underlying the melon fruit shape QTL fsqs8.1. Theoretical and Applied Genetics, 2022, 135, 785-801.	1.8	12
2	CRISPR/Cas9 gene editing uncovers the roles of CONSTITUTIVE TRIPLE RESPONSE 1 and REPRESSOR OF SILENCING 1 in melon fruit ripening and epigenetic regulation. Journal of Experimental Botany, 2022, 73, 4022-4033.	2.4	21
3	QTLs and candidate genes analyses for fruit size under domestication and differentiation in melon (Cucumis melo L.) based on high resolution maps. BMC Plant Biology, 2021, 21, 126.	1.6	25
4	A novel introgression line collection to unravel the genetics of climacteric ripening and fruit quality in melon. Scientific Reports, 2021, 11, 11364.	1.6	14
5	Genetic dissection of aroma biosynthesis in melon and its relationship with climacteric ripening. Food Chemistry, 2021, 353, 129484.	4.2	24
6	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	2.8	94
7	Genetic dissection of climacteric fruit ripening in a melon population segregating for ripening behavior. Horticulture Research, 2020, 7, 187.	2.9	29
8	Editorial: Translational Research for Cucurbit Molecular Breeding: Traits, Markers, and Genes. Frontiers in Plant Science, 2020, 11, 615346.	1.7	1
9	Linking sensory and proton transfer reactionâ€“mass spectrometry analyses for the assessment of melon fruit (Cucumis melo L.) quality traits. European Food Research and Technology, 2020, 246, 1439-1457.	1.6	2
10	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. Nature Genetics, 2019, 51, 1607-1615.	9.4	153
11	Mapping Cucumber Vein Yellowing Virus Resistance in Cucumber (Cucumis sativus L.) by Using BSA-seq Analysis. Frontiers in Plant Science, 2019, 10, 1583.	1.7	23
12	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. Nucleic Acids Research, 2019, 47, D1128-D1136.	6.5	177
13	An Improved Melon Reference Genome With Single-Molecule Sequencing Uncovers a Recent Burst of Transposable Elements With Potential Impact on Genes. Frontiers in Plant Science, 2019, 10, 1815.	1.7	48
14	QTL mapping of melon fruit quality traits using a high-density GBS-based genetic map. BMC Plant Biology, 2018, 18, 324.	1.6	82
15	Genome encode analyses reveal the basis of convergent evolution of fleshy fruit ripening. Nature Plants, 2018, 4, 784-791.	4.7	256
16	An improved assembly and annotation of the melon (Cucumis melo L.) reference genome. Scientific Reports, 2018, 8, 8088.	1.6	81
17	The Evolutionary Consequences of Transposon-Related Pericentromer Expansion in Melon. Genome Biology and Evolution, 2018, 10, 1584-1595.	1.1	20
18	<scp>ETHQV</scp>6.3 is involved in melon climacteric fruit ripening and is encoded by a <scp>NAC</scp> domain transcription factor. Plant Journal, 2017, 91, 671-683.	2.8	71

#	Article	IF	Citations
19	Quantitative trait loci analysis of melon (Cucumis melo L.) domestication-related traits. Theoretical and Applied Genetics, 2017, 130, 1837-1856.	1.8	37
20	Nonâ€invasive quantification of ethylene in attached fruit headspace at 1Âp.p.b. by gas chromatographyâ€“mass spectrometry. Plant Journal, 2017, 91, 172-183.	2.8	26
21	A mutation in the melon Vacuolar Protein Sorting 41prevents systemic infection of Cucumber mosaic virus. Scientific Reports, 2017, 7, 10471.	1.6	51
22	QTL Analyses in Multiple Populations Employed for the Fine Mapping and Identification of Candidate Genes at a Locus Affecting Sugar Accumulation in Melon (Cucumis melo L.). Frontiers in Plant Science, 2017, 8, 1679.	1.7	32
23	Genome-Wide Differentiation of Various Melon Horticultural Groups for Use in GWAS for Fruit Firmness and Construction of a High Resolution Genetic Map. Frontiers in Plant Science, 2016, 7, 1437.	1.7	98
24	The Melon Genome. Plant Genetics and Genomics: Crops and Models, 2016, , 173-181.	0.3	3
25	The carrot genome sequence brings colors out of the dark. Nature Genetics, 2016, 48, 589-590.	9.4	5
26	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. Genome Biology, 2016, 17, 32.	3.8	166
27	Pentatricopeptide repeat 336 as the candidate gene for paternal sorting of mitochondria (Psm) in cucumber. Theoretical and Applied Genetics, 2016, 129, 1951-1959.	1.8	8
28	Textural properties of different melon (Cucumis melo L.) fruit types: Sensory and physical-chemical evaluation. Scientia Horticulturae, 2016, 201, 46-56.	1.7	56
29	Melon Genome Sequence. Biotechnology in Agriculture and Forestry, 2016, , 15-29.	0.2	0
30	Genomics of Ecological Adaptation in Cactophilic Drosophila. Genome Biology and Evolution, 2015, 7, 349-366.	1.1	51
31	Combined use of genetic and genomics resources to understand virus resistance and fruit quality traits in melon. Physiologia Plantarum, 2015, 155, 4-11.	2.6	26
32	Use of targeted SNP selection for an improved anchoring of the melon (Cucumis melo L.) scaffold genome assembly. BMC Genomics, 2015, 16, 4.	1.2	67
33	Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. Molecular Biology and Evolution, 2015, 32, 2760-2774.	3.5	80
34	Anchoring the consensus ICuGI genetic map to the melon (Cucumis melo L.) genome. Molecular Breeding, 2015, 35, 1.	1.0	24
35	Comparative transcriptional profiling analysis of developing melon (Cucumis melo L.) fruit from climacteric and non-climacteric varieties. BMC Genomics, 2015, 16, 440.	1.2	62
36	The 2-C-methylerythritol 4-phosphate pathway in melon is regulated by specialized isoforms for the first and last steps. Journal of Experimental Botany, 2014, 65, 5077-5092.	2.4	54

#	Article	IF	Citations
37	The complex resistance to cucumber mosaic cucumovirus (CMV) in the melon accession PI161375 is governed by one gene and at least two quantitative trait loci. Molecular Breeding, 2014, 34, 351-362.	1.0	31
38	Nextâ€generation sequencing, <scp>FISH</scp> mapping and syntenyâ€based modeling reveal mechanisms of decreasing dysploidy in <scp>C</scp>ucumis. Plant Journal, 2014, 77, 16-30.	2.8	90
39	A 1,681-locus consensus genetic map of cultivated cucumber including 67 NB-LRR resistance gene homolog and ten gene loci. BMC Plant Biology, 2013, 13, 53.	1.6	58
40	Interaction between QTLs induces an advance in ethylene biosynthesis during melon fruit ripening. Theoretical and Applied Genetics, 2013, 126, 1531-1544.	1.8	56
41	SNP genotyping in melons: genetic variation, population structure, and linkage disequilibrium. Theoretical and Applied Genetics, 2013, 126, 1285-1303.	1.8	85
42	Effect of cold storage and 1-MCP treatment on ethylene perception, signalling and synthesis: Influence on the development of the evergreen behaviour in â€˜Conferenceâ€™ pears. Postharvest Biology and Technology, 2013, 86, 212-220.	2.9	60
43	The genome of melon (Cucumis melo L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	3.3	654
44	Melon Transcriptome Characterization: Simple Sequence Repeats and Single Nucleotide Polymorphisms Discovery for High Throughput Genotyping across the Species. Plant Genome, 2011, 4, 118-131.	1.6	53
45	Drought-resistant fungi control soil organic matter decomposition and its response to temperature. Global Change Biology, 2011, 17, 1475-1486.	4.2	335
46	A consensus linkage map for molecular markers and Quantitative Trait Loci associated with economically important traits in melon (Cucumis meloL.). BMC Plant Biology, 2011, 11, 111.	1.6	156
47	Towards a TILLING platform for functional genomics in Piel de Sapo melons. BMC Research Notes, 2011, 4, 289.	0.6	59
48	Analysis of expressed sequence tags generated from full-length enriched cDNA libraries of melon. BMC Genomics, 2011, 12, 252.	1.2	49
49	Analysis of the melon (Cucumis melo) small RNAome by high-throughput pyrosequencing. BMC Genomics, 2011, 12, 393.	1.2	58
50	Syntenic relationships between cucumber (Cucumis sativus L.) and melon (C. melo L.) chromosomes as revealed by comparative genetic mapping. BMC Genomics, 2011, 12, 396.	1.2	69
51	Determination of the melon chloroplast and mitochondrial genome sequences reveals that the largest reported mitochondrial genome in plants contains a significant amount of DNA having a nuclear origin. BMC Genomics, 2011, 12, 424.	1.2	118
52	Shaping melons: agronomic and genetic characterization of QTLs that modify melon fruit morphology. Theoretical and Applied Genetics, 2010, 121, 931-940.	1.8	39
53	Molecular markers for kernel bitterness in almond. Tree Genetics and Genomes, 2010, 6, 237-245.	0.6	49
54	Prunus microsatellite marker transferability across rosaceous crops. Tree Genetics and Genomes, 2010, 6, 689-700.	0.6	87

#	Article	IF	Citations
55	Generation of a BAC-based physical map of the melon genome. BMC Genomics, 2010, 11, 339.	1.2	30
56	Genome-wide BAC-end sequencing of Cucumis melo using two BAC libraries. BMC Genomics, 2010, 11, 618.	1.2	26
57	Sequencing of 6.7 Mb of the melon genome using a BAC pooling strategy. BMC Plant Biology, 2010, 10, 246.	1.6	30
58	An oligo-based microarray offers novel transcriptomic approaches for the analysis of pathogen resistance and fruit quality traits in melon (Cucumis melo L.). BMC Genomics, 2009, 10, 467.	1.2	61
59	A set of EST-SNPs for map saturation and cultivar identification in melon. BMC Plant Biology, 2009, 9, 90.	1.6	90
60	Dissection of the oligogenic resistance to Cucumber mosaic virus in the melon accession PI 161375. Theoretical and Applied Genetics, 2009, 118, 275-284.	1.8	47
61	Candidate genes and QTLs for fruit ripening and softening in melon. Theoretical and Applied Genetics, 2008, 116, 589-602.	1.8	97
62	Exploiting synteny in Cucumis for mapping of Psm: a unique locus controlling paternal mitochondrial sorting. Theoretical and Applied Genetics, 2008, 117, 523-529.	1.8	13
63	Bin mapping of genomic and EST-derived SSRs in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2008, 118, 139-150.	1.8	115
64	Construction of a fosmid library of cucumber (Cucumis sativus) and comparative analyses of the eIF4E and eIF(iso)4E regions from cucumber and melon (Cucumis melo). Molecular Genetics and Genomics, 2008, 279, 473-480.	1.0	25
65	Climacteric or non-climacteric behavior in melon fruit. Postharvest Biology and Technology, 2008, 49, 27-37.	2.9	126
66	Climacteric and non-climacteric behavior in melon fruit. Postharvest Biology and Technology, 2008, 50, 125-134.	2.9	34
67	EcoTILLING for the identification of allelic variants of melon eIF4E, a factor that controls virus susceptibility. BMC Plant Biology, 2007, 7, 34.	1.6	123
68	MELOGEN: an EST database for melon functional genomics. BMC Genomics, 2007, 8, 306.	1.2	87
69	Structure of two melon regions reveals high microsynteny with sequenced plant species. Molecular Genetics and Genomics, 2007, 278, 611-622.	1.0	28
70	AneIF4Eallele confers resistance to an uncapped and non-polyadenylated RNA virus in melon. Plant Journal, 2006, 48, 452-462.	2.8	203
71	Development and transportability across Prunus species of 42 polymorphic almond microsatellites. Molecular Ecology Notes, 2005, 5, 531-535.	1.7	84
72	Simple-sequence repeat markers used in merging linkage maps of melon (Cucumis melo L.). Theoretical and Applied Genetics, 2005, 110, 802-811.	1.8	170

#	Article	IF	Citations
73	Looking into flowering time in almond (Prunus dulcis (Mill) D. A. Webb): the candidate gene approach. Theoretical and Applied Genetics, 2005, 110, 959-968.	1.8	64
74	A physical map covering the nsv locus that confers resistance to Melon necrotic spot virus in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2005, 111, 914-922.	1.8	27
75	Analysis of the melon genome in regions encompassing TIR-NBS-LRR resistance genes. Molecular Genetics and Genomics, 2005, 273, 240-251.	1.0	38
76	Advances in understanding recessive resistance to plant viruses. Molecular Plant Pathology, 2004, 5, 223-233.	2.0	157
77	Simple-sequence repeat (SSR) markers of Japanese plum (Prunus salicina Lindl.) are highly polymorphic and transferable to peach and almond. Molecular Ecology Notes, 2004, 4, 163-166.	1.7	137
78	Phylogenetic relationships among Cucumis species based on the ribosomal internal transcribed spacer sequence and microsatellite markers. Plant Systematics and Evolution, 2004, 248, 191.	0.3	42
79	Single-nucleotide polymorphisms detected in expressed sequence tags of melon (<i>Cucumis) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.9	45
80	Genetic variability in melon based on microsatellite variation. Plant Breeding, 2003, 122, 153-157.	1.0	92
81	Development and variability analysis of microsatellite markers in peach. Plant Breeding, 2002, 121, 87-92.	1.0	221
82	Marker Saturation of the Region Flanking the Gene NSV Conferring Resistance to the Melon Necrotic Spot Carmovirus (MNSV) in Melon. Journal of the American Society for Horticultural Science, 2002, 127, 540-544.	0.5	15
83	Cloning and mapping of resistance gene homologues in melon. Plant Science, 2001, 161, 165-172.	1.7	27
84	Comparing AFLP, RAPD and RFLP markers for measuring genetic diversity in melon. Theoretical and Applied Genetics, 2000, 101, 860-864.	1.8	170
85	Molecular mapping of the potato virus Y resistance gene Rysto in potato. Theoretical and Applied Genetics, 1997, 94, 198-203.	1.8	130
86	Accumulation of specific mRNAs during almond fruit development. Plant Science, 1996, 113, 185-192.	1.7	9
87	Molecular characterization of cDNAs corresponding to genes expressed during almond (Prunus) Tj ETQq1 1 0.784314 rgBT /Overlock	2.0	50
88	A linkage map with RFLP and isozyme markers for almond. Theoretical and Applied Genetics, 1995, 91-91, 964-971.	1.8	103
89	A highly conserved ?-tubulin sequence from Prunus amygdalus. Plant Molecular Biology, 1993, 22, 913-916.	2.0	10
90	The Extensin from Prunus amygdalus. Plant Physiology, 1992, 100, 1603-1604.	2.3	15

#	Article	IF	Citations
91	Knock-Out of CmNAC-NOR Affects Melon Climacteric Fruit Ripening. Frontiers in Plant Science, 0, 13, .	1.7	14