

Iban Eduardo

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

1,968
citations

257450

24
h-index

254184

43
g-index

52
all docs

52
docs citations

52
times ranked

1433
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative QTL analysis in peach "Earlygold"™ F2 and backcross progenies. <i>Scientia Horticulturae</i> , 2022, 293, 110726.	3.6	4
2	Pedigree analysis of 220 almond genotypes reveals two world mainstream breeding lines based on only three different cultivars. <i>Horticulture Research</i> , 2021, 8, 11.	6.3	20
3	MAGNA and BLANQ Series: Two Yellow-fleshed and Three White-fleshed Nectarines. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2021, 56, 1130-1131.	1.0	1
4	Biochemical and genetic implications of the slow ripening phenotype in peach fruit. <i>Scientia Horticulturae</i> , 2020, 259, 108824.	3.6	26
5	Resynthesis: Marker-Based Partial Reconstruction of Elite Genotypes in Clonally-Reproducing Plant Species. <i>Frontiers in Plant Science</i> , 2020, 11, 1205.	3.6	5
6	Fine mapping and identification of candidate genes for the peach powdery mildew resistance gene Vr3. <i>Horticulture Research</i> , 2020, 7, 175.	6.3	12
7	A qPCR-based method for the detection and quantification of the peach powdery mildew (<i>Podosphaera</i>) Tj ETQq1 1.0.784314 rgBT / Qv	1.7	1
8	The Multisite <i>PeachRefPop</i> Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. <i>Plant Physiology</i> , 2020, 184, 632-646.	4.8	12
9	A Decision Support System Based on Degree-Days to Initiate Fungicide Spray Programs for Peach Powdery Mildew in Catalonia, Spain. <i>Plant Disease</i> , 2020, 104, 2418-2425.	1.4	7
10	Fine mapping of the peach pollen sterility gene (<i>Ps/ps</i>) and detection of markers for marker-assisted selection. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	4
11	Inheritance and QTL analysis of chilling and heat requirements for flowering in an interspecific almond x peach (Texas x Earlygold) F2 population. <i>Euphytica</i> , 2020, 216, 1.	1.2	12
12	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. <i>Horticulture Research</i> , 2019, 6, 58.	6.3	121
13	Exploring sources of resistance to brown rot in an interspecific almond – peach population. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 4105-4113.	3.5	22
14	Identification of a new allele of the <i>Dw</i> gene causing brachytic dwarfing in peach. <i>BMC Research Notes</i> , 2018, 11, 386.	1.4	12
15	Genetic analysis of the slow-melting flesh character in peach. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	31
16	Investigation of the aroma of commercial peach (<i>Prunus persica</i> L. Batsch) types by Proton Transfer Reaction – Mass Spectrometry (PTR-MS) and sensory analysis. <i>Food Research International</i> , 2017, 99, 133-146.	6.2	51
17	Mapping a major gene for red skin color suppression (highlighter) in peach. <i>Euphytica</i> , 2017, 213, 1.	1.2	16
18	A deletion affecting an LRR-RLK gene co-segregates with the fruit flat shape trait in peach. <i>Scientific Reports</i> , 2017, 7, 6714.	3.3	39

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19	Preliminary results on effectiveness of marker-assisted seedling selection applied to Mendelian traits in peach. <i>Acta Horticulturae</i> , 2017, , 425-430.	0.2	2
20	A codominant diagnostic marker for the slow ripening trait in peach. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	44
21	Marker-assisted introgression (MAI) of almond genes into the peach background: a fast method to mine and integrate novel variation from exotic sources in long intergeneration species. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	21
22	Exploring almond genetic variability useful for peach improvement: mapping major genes and QTLs in two interspecific almond-peach populations. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	56
23	High-density mapping suggests cytoplasmic male sterility with two restorer genes in almond-peach progenies. <i>Horticulture Research</i> , 2015, 2, 15016.	6.3	35
24	Mapping of a major gene for the slow ripening character in peach: co-location with the maturity date gene and development of a candidate gene-based diagnostic marker for its selection. <i>Euphytica</i> , 2015, 205, 627-636.	1.2	72
25	THE PEACH GENOME AND ITS APPLICATIONS. <i>Acta Horticulturae</i> , 2015, , 29-33.	0.2	0
26	Mapping and Introgression of QTL Involved in Fruit Shape Transgressive Segregation into "Piel de Sapo"™ Melon (<i>Cucumis melo</i> L.). <i>PLoS ONE</i> , 2014, 9, e104188.	2.5	58
27	Development of diagnostic markers for selection of the subacid trait in peach. <i>Tree Genetics and Genomes</i> , 2014, 10, 1695-1709.	1.6	24
28	QTL mapping for brown rot (<i>Monilinia fructigena</i>) resistance in an intraspecific peach (<i>Prunus persica</i>)	1.6	64
29	Combining linkage and association mapping to search for markers linked to the flat fruit character in peach. <i>Euphytica</i> , 2013, 190, 279-288.	1.2	53
30	Fine mapping and identification of a candidate gene for a major locus controlling maturity date in peach. <i>BMC Plant Biology</i> , 2013, 13, 166.	3.6	113
31	Genetic dissection of aroma volatile compounds from the essential oil of peach fruit: QTL analysis and identification of candidate genes using dense SNP maps. <i>Tree Genetics and Genomes</i> , 2013, 9, 189-204.	1.6	105
32	Genomics of Temperate Fruit Trees. , 2012, , 155-208.		0
33	Reuteran and levan as carbohydrate sinks in transgenic sugarcane. <i>Planta</i> , 2012, 236, 1803-1815.	3.2	4
34	Saturating the <i>Prunus</i> (stone fruits) genome with candidate genes for fruit quality. <i>Molecular Breeding</i> , 2011, 28, 667-682.	2.1	53
35	QTL analysis of fruit quality traits in two peach intraspecific populations and importance of maturity date pleiotropic effect. <i>Tree Genetics and Genomes</i> , 2011, 7, 323-335.	1.6	154
36	Identification of key odor volatile compounds in the essential oil of nine peach accessions. <i>Journal of the Science of Food and Agriculture</i> , 2010, 90, 1146-1154.	3.5	100

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37	On the Genetic Control of Heterosis for Fruit Shape in Melon (<i>Cucumis Melo</i> L.). <i>Journal of Heredity</i> , 2009, 100, 229-235.	2.4	20
38	Identification of QTLs related to sugar and organic acid composition in melon using near-isogenic lines. <i>Scientia Horticulturae</i> , 2009, 121, 425-433.	3.6	47
39	Bin mapping of genomic and EST-derived SSRs in melon (<i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 118, 139-150.	3.6	115
40	Identification of Melon Fruit Quality Quantitative Trait Loci Using Near-isogenic Lines. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 139-151.	1.0	59
41	HORTICULTURAL AND MOLECULAR CHARACTERIZATION OF LANDRACES OF INDIAN SNAPMELON (<i>CUCUMIS</i>) Tj ETQq1 1 0.784314 1	0.2	1
42	Diversity among landraces of Indian snapmelon (<i>Cucumis melo</i> var. <i>momordica</i>). <i>Genetic Resources and Crop Evolution</i> , 2007, 54, 1267-1283.	1.6	89
43	Estimating the Genetic Architecture of Fruit Quality Traits in Melon Using a Genomic Library of Near Isogenic Lines. <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 80-89.	1.0	91
44	Mapping Fruit Susceptibility to Postharvest Physiological Disorders and Decay Using a Collection of Near-isogenic Lines of Melon. <i>Journal of the American Society for Horticultural Science</i> , 2007, 132, 739-748.	1.0	24
45	IDENTIFICATION OF QTLs ASSOCIATED WITH COMMERCIAL POSTHARVEST QUALITY TRAITS AND DISORDERS USING A COLLECTION OF NEAR ISOGENIC LINES OF MELON. <i>Acta Horticulturae</i> , 2007, , 309-317.	0.2	1
46	STATISTICAL MULTIVARIATE ANALYSIS OF MELON SHAPE: A CASE STUDY USING NEAR ISOGENIC LINES. <i>Acta Horticulturae</i> , 2005, , 537-544.	0.2	2
47	Development of a genomic library of near isogenic lines (NILs) in melon (<i>Cucumis melo</i> L.) from the exotic accession PI161375. <i>Theoretical and Applied Genetics</i> , 2005, 112, 139-148.	3.6	98
48	Inheritance mode of fruit traits in melon: Heterosis for fruit shape and its correlation with genetic distance. <i>Euphytica</i> , 2005, 144, 31-38.	1.2	48
49	Molecular defects of the CYP21 gene in Spanish girls with isolated precocious pubarche. <i>European Journal of Endocrinology</i> , 2002, 147, 485-488.	3.7	13
50	Construction of a collection of introgression lines of "Texas" almond DNA fragments in the "Earlygold" peach genetic background. <i>Horticulture Research</i> , 0, , .	6.3	1