

# 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	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
2	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. <i>Horticulture Research</i> , 2019, 6, 58.	6.3	121
3	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
4	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
5	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
6	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
7	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
8	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
9	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
10	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
11	QTL mapping for brown rot ( <i>Monilinia fructigena</i> ) resistance in an intraspecific peach ( <i>Prunus persica</i> ) Tj ETQq1 1 0,784314 rgBT /Overl	1.6	64
12	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
13	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
14	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
15	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
16	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
17	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
18	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

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19	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
20	A codominant diagnostic marker for the slow ripening trait in peach. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	44
21	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
22	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
23	Genetic analysis of the slow-melting flesh character in peach. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	31
24	Biochemical and genetic implications of the slow ripening phenotype in peach fruit. <i>Scientia Horticulturae</i> , 2020, 259, 108824.	3.6	26
25	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
26	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
27	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
28	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
29	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
30	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
31	Mapping a major gene for red skin color suppression (highlighter) in peach. <i>Euphytica</i> , 2017, 213, 1.	1.2	16
32	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
33	Identification of a new allele of the Dw gene causing brachytic dwarfing in peach. <i>BMC Research Notes</i> , 2018, 11, 386.	1.4	12
34	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
35	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
36	Inheritance and QTL analysis of chilling and heat requirements for flowering in an interspecific almond × peach (Texas × Earlygold) F2 population. <i>Euphytica</i> , 2020, 216, 1.	1.2	12

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37	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
38	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
39	Reuteran and levan as carbohydrate sinks in transgenic sugarcane. <i>Planta</i> , 2012, 236, 1803-1815.	3.2	4
40	Fine mapping of the peach pollen sterility gene (Ps/ps) and detection of markers for marker-assisted selection. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	4
41	Comparative QTL analysis in peach "Earlygold"™ F2 and backcross progenies. <i>Scientia Horticulturae</i> , 2022, 293, 110726.	3.6	4
42	STATISTICAL MULTIVARIATE ANALYSIS OF MELON SHAPE: A CASE STUDY USING NEAR ISOGENIC LINES. <i>Acta Horticulturae</i> , 2005, , 537-544.	0.2	2
43	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
44	HORTICULTURAL AND MOLECULAR CHARACTERIZATION OF LANDRACES OF INDIAN SNAPMELON (CUCUMIS) Tj ETQq0 0 0 rgBT /Overl	0.2	1
45	A qPCR-based method for the detection and quantification of the peach powdery mildew ( <i>Podosphaera</i> ) Tj ETQq1 1 0.784314 rgBT /O	1.7	1
46	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
47	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
48	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
49	Genomics of Temperate Fruit Trees. , 2012, , 155-208.		0
50	THE PEACH GENOME AND ITS APPLICATIONS. <i>Acta Horticulturae</i> , 2015, , 29-33.	0.2	0