Igor Pacheco Cruz

List of Publications by Year
in descending order

28 papers	1,091 citations	687363 13 h-index	552781 26 g-index
30 all docs	30 docs citations	30 times ranked	913 citing authors

#	Article	IF	Citations
1	An Upgraded, Highly Saturated Linkage Map of Japanese Plum (Prunus salicina Lindl.), and Identification of a New Major Locus Controlling the Flavan-3-ol Composition in Fruits. Frontiers in Plant Science, 2022, 13, 805744.	3.6	2
2	Transcriptomic Analysis of Sex-Associated DEGs in Female and Male Flowers of Kiwifruit (Actinidia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.8	0
3	Insights into gene expression responses to infections in teleosts using microarray data: a systematic review. Reviews in Aquaculture, 2021, 13, 18-42.	9.0	2
4	Detection of Quantitative Trait Loci Controlling the Content of Phenolic Compounds in an Asian Plum (Prunus salicina L.) F1 Population. Frontiers in Plant Science, 2021, 12, 679059.	3.6	7
5	Transcriptome analysis and postharvest behavior of the kiwifruit â€˜Actinidia deliciosaâ€™ reveal the role of ethylene-related phytohormones during fruit ripening. Tree Genetics and Genomes, 2021, 17, 1.	1.6	15
6	Identification of loci controlling phenology, fruit quality and post-harvest quantitative parameters in Japanese plum (Prunus salicina Lindl.). Postharvest Biology and Technology, 2020, 169, 111292.	6.0	14
7	The Multisite PeachRefPop Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. Plant Physiology, 2020, 184, 632-646.	4.8	12
8	Do Consumers Evaluate New and Existing Fruit Varieties in the Same Way? Modeling the Role of Search and Experience Intrinsic Attributes. Journal of Food Products Marketing, 2020, 26, 521-534.	3.3	6
9	Hydroethanolic Extract of Lampaya Medicinalis Phil. (Verbenaceae) Decreases Proinflammatory Marker Expression in Palmitic Acid-exposed Macrophages. Endocrine, Metabolic and Immune Disorders - Drug Targets, 2020, 20, 1309-1320.	1.2	4
10	Development and applicability of GBS approach for genomic studies in Japanese plum (Prunus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.9	7
11	Linkage and association mapping for the slow softening (SwS) trait in peach (P. persica L. Batsch) fruit. Tree Genetics and Genomes, 2018, 14, 1.	1.6	9
12	Deletion of the miR172 target site in a <scp>TOE</scp>â€type gene is a strong candidate variant for dominant doubleâ€flower trait in Rosaceae. Plant Journal, 2018, 96, 358-371.	5.7	43
13	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. BMC Genomics, 2017, 18, 432.	2.8	44
14	Exploring and exploiting phenotypic and genetic diversity in peach: identification of major genes and QTLs by GWAS. Acta Horticulturae, 2017, , 419-424.	0.2	1
15	Preliminary results on effectiveness of marker-assisted seedling selection applied to Mendelian traits in peach. Acta Horticulturae, 2017, , 425-430.	0.2	2
16	Genotyping by Sequencing for SNP-Based Linkage Analysis and Identification of QTLs Linked to Fruit Quality Traits in Japanese Plum (Prunus salicina Lindl.). Frontiers in Plant Science, 2017, 8, 476.	3.6	74
17	Identifying SNP markers tightly associated with six major genes in peach [Prunus persica (L.) Batsch] using a high-density SNP array with an objective of marker-assisted selection (MAS). Tree Genetics and Genomes, 2016, 12, 1.	1.6	28
18	Brown Rot Strikes Prunus Fruit: An Ancient Fight Almost Always Lost. Journal of Agricultural and Food Chemistry, 2016, 64, 4029-4047.	5.2	72

#	Article	IF	Citations
19	GENETIC VARIABILITY AND POPULATION STRUCTURE OF PEACH ACCESSIONS FROM MAS.PES GERMPLASM BANK. Acta Horticulturae, 2015, , 233-239.	0.2	0
20	TOWARDS FASTER PHENOTYPING METHODS FOR BROWN ROT SUSCEPTIBILITY BY ARTIFICIAL INOCULATION IN THE ORCHARD. Acta Horticulturae, 2015, , 367-374.	0.2	2
21	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. PLoS ONE, 2015, 10, e0136803.	2.5	98
22	Genetic dissection of fruit weight and size in an F2 peach (Prunus persica (L.) Batsch) progeny. Molecular Breeding, 2015, 35, 1.	2.1	48
23	QTL mapping for brown rot (Monilinia fructigena) resistance in an intraspecific peach (Prunus persica) Tj ETQq1 1 0.784314 rgBT /Ov	1.6	64
24	A Unique Mutation in a MYB Gene Cosegregates with the Nectarine Phenotype in Peach. PLoS ONE, 2014, 9, e90574.	2.5	86
25	Fine mapping and identification of a candidate gene for a major locus controlling maturity date in peach. BMC Plant Biology, 2013, 13, 166.	3.6	113
26	Genetic dissection of aroma volatile compounds from the essential oil of peach fruit: QTL analysis and identification of candidate genes using dense SNP maps. Tree Genetics and Genomes, 2013, 9, 189-204.	1.6	105
27	QTL analysis of fruit quality traits in two peach intraspecific populations and importance of maturity date pleiotropic effect. Tree Genetics and Genomes, 2011, 7, 323-335.	1.6	154
28	Identification of woolliness response genes in peach fruit after post-harvest treatments. Journal of Experimental Botany, 2008, 59, 1973-1986.	4.8	78