

Maria Jose J Aranzana

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

4,193
citations

172457

29
h-index

214800

47
g-index

54
all docs

54
docs citations

54
times ranked

3935
citing authors

#	ARTICLE	IF	CITATIONS
1	An Arabidopsis Example of Association Mapping in Structured Samples. <i>PLoS Genetics</i> , 2007, 3, e4.	3.5	625
2	Development of microsatellite markers in peach [<i>Prunus persica</i> (L.) Batsch] and their use in genetic diversity analysis in peach and sweet cherry (<i>Prunus avium</i> L.). <i>Theoretical and Applied Genetics</i> , 2002, 105, 127-138.	3.6	492
3	Role of FRIGIDA and FLOWERING LOCUS C in Determining Variation in Flowering Time of Arabidopsis. <i>Plant Physiology</i> , 2005, 138, 1163-1173.	4.8	383
4	Genome-Wide Association Mapping in Arabidopsis Identifies Previously Known Flowering Time and Pathogen Resistance Genes. <i>PLoS Genetics</i> , 2005, 1, e60.	3.5	378
5	Development and variability analysis of microsatellite markers in peach. <i>Plant Breeding</i> , 2002, 121, 87-92.	1.9	221
6	A set of simple-sequence repeat (SSR) markers covering the <i>Prunus</i> genome. <i>Theoretical and Applied Genetics</i> , 2003, 106, 819-825.	3.6	199
7	Development and Evaluation of a 9K SNP Array for Peach by Internationally Coordinated SNP Detection and Validation in Breeding Germplasm. <i>PLoS ONE</i> , 2012, 7, e35668.	2.5	199
8	Genetic variation, population structure and linkage disequilibrium in peach commercial varieties. <i>BMC Genetics</i> , 2010, 11, 69.	2.7	139
9	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. <i>Horticulture Research</i> , 2019, 6, 58.	6.3	121
10	A Nonparametric Test Reveals Selection for Rapid Flowering in the Arabidopsis Genome. <i>PLoS Biology</i> , 2006, 4, e137.	5.6	118
11	Microsatellite variability in peach [<i>Prunus persica</i> (L.) Batsch]: cultivar identification, marker mutation, pedigree inferences and population structure. <i>Theoretical and Applied Genetics</i> , 2003, 106, 1341-1352.	3.6	113
12	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
13	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11.	6.3	98
14	Genetic Structure of Modern Durum Wheat Cultivars and Mediterranean Landraces Matches with Their Agronomic Performance. <i>PLoS ONE</i> , 2016, 11, e0160983.	2.5	92
15	Attention sports fans! The far-reaching contributions of bud sport mutants to horticulture and plant biology. <i>Horticulture Research</i> , 2018, 5, 44.	6.3	80
16	Peach genetic resources: diversity, population structure and linkage disequilibrium. <i>BMC Genetics</i> , 2013, 14, 84.	2.7	78
17	Integrated QTL detection for key breeding traits in multiple peach progenies. <i>BMC Genomics</i> , 2017, 18, 404.	2.8	75
18	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

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19	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
20	ASSIsT: an automatic SNP scoring tool for in- and outbreeding species. <i>Bioinformatics</i> , 2015, 31, 3873-3874.	4.1	45
21	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. <i>BMC Genomics</i> , 2017, 18, 432.	2.8	44
22	Diversity and Genetic Structure of a Collection of Spanish Durum Wheat Landraces. <i>Crop Science</i> , 2012, 52, 2262-2275.	1.8	41
23	Evaluation of the genetic diversity of Asian peach accessions using a selected set of SSR markers. <i>Scientia Horticulturae</i> , 2010, 125, 622-629.	3.6	40
24	A first insight into peach [<i>Prunus persica</i> (L.) Batsch] SNP variability. <i>Tree Genetics and Genomes</i> , 2012, 8, 1359-1369.	1.6	39
25	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
26	The apple REFPOPâ€™a reference population for genomics-assisted breeding in apple. <i>Horticulture Research</i> , 2020, 7, 189.	6.3	37
27	High-density mapping suggests cytoplasmic male sterility with two restorer genes in almond Ã— peach progenies. <i>Horticulture Research</i> , 2015, 2, 15016.	6.3	35
28	Survey of over 4, 500 monumental olive trees preserved on-farm in the northeast Iberian Peninsula, their genotyping and characterization. <i>Scientia Horticulturae</i> , 2018, 231, 253-264.	3.6	34
29	Identifying SNP markers tightly associated with six major genes in peach [<i>Prunus persica</i> (L.) Batsch] using a high-density SNP array with an objective of marker-assisted selection (MAS). <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	1.6	28
30	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
31	Genetic architecture and genomic predictive ability of apple quantitative traits across environments. <i>Horticulture Research</i> , 2022, 9, .	6.3	20
32	REVIEW OF FRUIT GENETICS AND BREEDING PROGRAMMES AND A NEW EUROPEAN INITIATIVE TO INCREASE FRUIT BREEDING EFFICIENCY. <i>Acta Horticulturae</i> , 2012, , 95-102.	0.2	18
33	Using Amplified Fragment-length Polymorphisms (AFLPs) to Identify Peach Cultivars. <i>Journal of the American Society for Horticultural Science</i> , 2003, 128, 672-677.	1.0	15
34	Characterization of Japanese Plum (<i>Prunus salicina</i>) PsMYB10 Alleles Reveals Structural Variation and Polymorphisms Correlating With Fruit Skin Color. <i>Frontiers in Plant Science</i> , 2021, 12, 655267.	3.6	14
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	A PEACH GERMPLASM COLLECTION FOR INCREASING THE GENETIC DIVERSITY IN EUROPEAN BREEDING PROGRAMS. <i>Acta Horticulturae</i> , 2015, , 125-129.	0.2	6

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37	Discovering peach QTLs with multiple progeny analysis. <i>Acta Horticulturae</i> , 2017, , 405-410.	0.2	5
38	SYNTENY WITHIN THE PRUNUS GENOMES DETECTED BY MOLECULAR MARKERS. <i>Acta Horticulturae</i> , 2003, , 177-187.	0.2	5
39	SSR AND AFLP MARKERS FOR GERMPLASM EVALUATION AND CULTIVAR IDENTIFICATION IN PEACH. <i>Acta Horticulturae</i> , 2003, , 35-40.	0.2	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	Region-wide association analysis and high-throughput resequencing strategies in peach to develop molecular markers for flat fruit marker-assisted selection. <i>Acta Horticulturae</i> , 2018, , 79-84.	0.2	3
42	Genome-wide association mapping in <i>Arabidopsis thaliana</i> identifies previously known genes responsible for variation in flowering time and pathogen resistance. <i>PLoS Genetics</i> , 2005, preprint, e60.	3.5	3
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	Development of molecular markers for fruit skin color in Japanese plum (<i>Prunus salicina</i> Lindl.). <i>Acta Horticulturae</i> , 2021, , 221-226.	0.2	2
45	DEVELOPMENT OF PEACH SSRS AND THEIR USE IN FINGERPRINTING PEACH AND SWEET CHERRY CULTIVARS. <i>Acta Horticulturae</i> , 2002, , 245-252.	0.2	2
46	Exploring and exploiting phenotypic and genetic diversity in peach: identification of major genes and QTLs by GWAS. <i>Acta Horticulturae</i> , 2017, , 419-424.	0.2	1
47	Genomics of Temperate Fruit Trees. , 2012, , 155-208.		0
48	BUILDING HIGH-DENSITY PEACH LINKAGE MAPS BASED ON THE ISPC 9K SNP CHIP FOR MAPPING MENDELIAN TRAITS AND QTLs: BENEFITS AND DRAWBACKS. <i>Acta Horticulturae</i> , 2015, , 113-118.	0.2	0
49	THE PEACH GENOME AND ITS APPLICATIONS. <i>Acta Horticulturae</i> , 2015, , 29-33.	0.2	0