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List of Publications by Year in descending order

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49
papers

4,193
citations

172457

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47
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54
all docs

54
docs citations

54
times ranked

3935
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic architecture and genomic predictive ability of apple quantitative traits across environments. Horticulture Research, 2022, 9, .	6.3	20
2	Development of molecular markers for fruit skin color in Japanese plum (<i>Prunus salicina</i> Lindl.). Acta Horticulturae, 2021, , 221-226.	0.2	2
3	Characterization of Japanese Plum (<i>Prunus salicina</i>) PsMYB10 Alleles Reveals Structural Variation and Polymorphisms Correlating With Fruit Skin Color. Frontiers in Plant Science, 2021, 12, 655267.	3.6	14
4	The apple REFPOPâ€”a reference population for genomics-assisted breeding in apple. Horticulture Research, 2020, 7, 189.	6.3	37
5	The Multisite <i>PeachRefPop</i> Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. Plant Physiology, 2020, 184, 632-646.	4.8	12
6	Fine mapping of the peach pollen sterility gene (<i>Ps/ps</i>) and detection of markers for marker-assisted selection. Molecular Breeding, 2020, 40, 1.	2.1	4
7	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. Horticulture Research, 2019, 6, 58.	6.3	121
8	An integrated approach for increasing breeding efficiency in apple and peach in Europe. Horticulture Research, 2018, 5, 11.	6.3	98
9	Survey of over 4, 500 monumental olive trees preserved on-farm in the northeast Iberian Peninsula, their genotyping and characterization. Scientia Horticulturae, 2018, 231, 253-264.	3.6	34
10	Region-wide association analysis and high-throughput resequencing strategies in peach to develop molecular markers for flat fruit marker-assisted selection. Acta Horticulturae, 2018, , 79-84.	0.2	3
11	Attention sports fans! The far-reaching contributions of bud sport mutants to horticulture and plant biology. Horticulture Research, 2018, 5, 44.	6.3	80
12	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. BMC Genomics, 2017, 18, 432.	2.8	44
13	A deletion affecting an LRR-RLK gene co-segregates with the fruit flat shape trait in peach. Scientific Reports, 2017, 7, 6714.	3.3	39
14	Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404.	2.8	75
15	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
16	Discovering peach QTLs with multiple progeny analysis. Acta Horticulturae, 2017, , 405-410.	0.2	5
17	Preliminary results on effectiveness of marker-assisted seedling selection applied to Mendelian traits in peach. Acta Horticulturae, 2017, , 425-430.	0.2	2
18	Genetic Structure of Modern Durum Wheat Cultivars and Mediterranean Landraces Matches with Their Agronomic Performance. PLoS ONE, 2016, 11, e0160983.	2.5	92

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	A PEACH GERMPLASM COLLECTION FOR INCREASING THE GENETIC DIVERSITY IN EUROPEAN BREEDING PROGRAMS. <i>Acta Horticulturae</i> , 2015, , 125-129.	0.2	6
22	High-density mapping suggests cytoplasmic male sterility with two restorer genes in almond $\tilde{\text{A}}$ — peach progenies. <i>Horticulture Research</i> , 2015, 2, 15016.	6.3	35
23	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
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	ASSIsT: an automatic SNP scoring tool for in- and outbreeding species. <i>Bioinformatics</i> , 2015, 31, 3873-3874.	4.1	45
26	THE PEACH GENOME AND ITS APPLICATIONS. <i>Acta Horticulturae</i> , 2015, , 29-33.	0.2	0
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	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
29	Peach genetic resources: diversity, population structure and linkage disequilibrium. <i>BMC Genetics</i> , 2013, 14, 84.	2.7	78
30	Diversity and Genetic Structure of a Collection of Spanish Durum Wheat Landraces. <i>Crop Science</i> , 2012, 52, 2262-2275.	1.8	41
31	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
32	Genomics of Temperate Fruit Trees. , 2012, , 155-208.		0
33	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
34	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
35	Genetic variation, population structure and linkage disequilibrium in peach commercial varieties. <i>BMC Genetics</i> , 2010, 11, 69.	2.7	139
36	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

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37	An Arabidopsis Example of Association Mapping in Structured Samples. <i>PLoS Genetics</i> , 2007, 3, e4.	3.5	625
38	A Nonparametric Test Reveals Selection for Rapid Flowering in the Arabidopsis Genome. <i>PLoS Biology</i> , 2006, 4, e137.	5.6	118
39	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
40	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
41	Genome-wide association mapping in Arabidopsis thaliana identifies previously known genes responsible for variation in flowering time and pathogen resistance. <i>PLoS Genetics</i> , 2005, preprint, e60.	3.5	3
42	A set of simple-sequence repeat (SSR) markers covering the Prunus genome. <i>Theoretical and Applied Genetics</i> , 2003, 106, 819-825.	3.6	199
43	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
44	SSR AND AFLP MARKERS FOR GERMPLASM EVALUATION AND CULTIVAR IDENTIFICATION IN PEACH. <i>Acta Horticulturae</i> , 2003, , 35-40.	0.2	4
45	SYNTENY WITHIN THE PRUNUS GENOMES DETECTED BY MOLECULAR MARKERS. <i>Acta Horticulturae</i> , 2003, , 177-187.	0.2	5
46	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
47	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
48	Development and variability analysis of microsatellite markers in peach. <i>Plant Breeding</i> , 2002, 121, 87-92.	1.9	221
49	DEVELOPMENT OF PEACH SSRS AND THEIR USE IN FINGERPRINTING PEACH AND SWEET CHERRY CULTIVARS. <i>Acta Horticulturae</i> , 2002, , 245-252.	0.2	2