

Pere ArÃ³s

List of Publications by Year in descending order

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145
papers

11,453
citations

28274
55
h-index

30087
103
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153
all docs

153
docs citations

153
times ranked

5921
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011, 43, 109-116.	21.4	1,091
2	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,031
3	The genome of melon (<i>Cucumis melo</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11872-11877.	7.1	654
4	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
5	Comparative mapping and marker-assisted selection in Rosaceae fruit crops. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9891-9896.	7.1	473
6	Multiple Models for Rosaceae Genomics. <i>Plant Physiology</i> , 2008, 147, 985-1003.	4.8	291
7	Development and variability analysis of microsatellite markers in peach. <i>Plant Breeding</i> , 2002, 121, 87-92.	1.9	221
8	Construction of a saturated linkage map for <i>Prunus</i> using an almond–peach F2 progeny. <i>Theoretical and Applied Genetics</i> , 1998, 97, 1034-1041.	3.6	202
9	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
10	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
11	Mapping With a Few Plants: Using Selective Mapping for Microsatellite Saturation of the <i>Prunus</i> Reference Map. <i>Genetics</i> , 2005, 171, 1305-1309.	2.9	180
12	Simple-sequence repeat markers used in merging linkage maps of melon (<i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2005, 110, 802-811.	3.6	170
13	Identification of quantitative trait loci involved in fruit quality traits in melon (<i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2004, 108, 750-758.	3.6	159
14	Comparative Genetic Mapping Between Octoploid and Diploid <i>Fragaria</i> Species Reveals a High Level of Colinearity Between Their Genomes and the Essentially Disomic Behavior of the Cultivated Octoploid Strawberry. <i>Genetics</i> , 2008, 179, 2045-2060.	2.9	140
15	Genetic variation, population structure and linkage disequilibrium in peach commercial varieties. <i>BMC Genetics</i> , 2010, 11, 69.	2.7	139
16	Comparison of the genetic determinism of two key phenological traits, flowering and maturity dates, in three <i>Prunus</i> species: peach, apricot and sweet cherry. <i>Heredity</i> , 2012, 109, 280-292.	2.6	139
17	Simple-sequence repeat (SSR) markers of Japanese plum (<i>Prunus salicina</i> Lindl.) are highly polymorphic and transferable to peach and almond. <i>Molecular Ecology Notes</i> , 2004, 4, 163-166.	1.7	137
18	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. <i>Horticulture Research</i> , 2019, 6, 58.	6.3	121

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19	The peach genome. <i>Tree Genetics and Genomes</i> , 2012, 8, 531-547.	1.6	120
20	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
21	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
22	An enhanced microsatellite map of diploid <i>Fragaria</i> . <i>Theoretical and Applied Genetics</i> , 2006, 112, 1349-1359.	3.6	112
23	Microsatellite genetic linkage maps of myrobalan plum and an almond-peach hybrid?location of root-knot nematode resistance genes. <i>Theoretical and Applied Genetics</i> , 2004, 109, 827-838.	3.6	109
24	A linkage map with RFLP and isozyme markers for almond. <i>Theoretical and Applied Genetics</i> , 1995, 91-91, 964-971.	3.6	103
25	Comparative analysis of rosaceous genomes and the reconstruction of a putative ancestral genome for the family. <i>BMC Evolutionary Biology</i> , 2011, 11, 9.	3.2	103
26	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
27	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
28	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11.	6.3	98
29	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. <i>Plant Journal</i> , 2020, 101, 455-472.	5.7	94
30	Mapping major genes and quantitative trait loci controlling agronomic traits in almond. <i>Plant Breeding</i> , 2007, 126, 310-318.	1.9	93
31	Genetic variability in melon based on microsatellite variation. <i>Plant Breeding</i> , 2003, 122, 153-157.	1.9	92
32	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
33	A set of EST-SNPs for map saturation and cultivar identification in melon. <i>BMC Plant Biology</i> , 2009, 9, 90.	3.6	90
34	Inheritance and linkage relationships of isozyme loci in <i>Brassica oleracea</i> . <i>Journal of Heredity</i> , 1983, 74, 405-412.	2.4	88
35	Genetic mapping of a major gene delaying blooming time in almond. <i>Plant Breeding</i> , 2001, 120, 268-270.	1.9	88
36	MELOGEN: an EST database for melon functional genomics. <i>BMC Genomics</i> , 2007, 8, 306.	2.8	87

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37	Prunus microsatellite marker transferability across rosaceous crops. Tree Genetics and Genomes, 2010, 6, 689-700.	1.6	87
38	Development and transportability across Prunus species of 42 polymorphic almond microsatellites. Molecular Ecology Notes, 2005, 5, 531-535.	1.7	84
39	Genetic linkage maps of two apricot cultivars (Prunus armeniaca L.) compared with the almond Texas Å— peach Earlygold reference map for Prunus. Theoretical and Applied Genetics, 2004, 108, 1120-1130.	3.6	83
40	Identifying Olive Cultivars by Isozyme Analysis. Journal of the American Society for Horticultural Science, 1995, 120, 318-324.	1.0	80
41	Peach genetic resources: diversity, population structure and linkage disequilibrium. BMC Genetics, 2013, 14, 84.	2.7	78
42	Whole genome comparisons of Fragaria, Prunus and Malus reveal different modes of evolution between Rosaceous subfamilies. BMC Genomics, 2012, 13, 129.	2.8	77
43	A reciprocal translocation between â€™Garfiâ€™ almond and â€™Nemaredâ€™ peach. Theoretical and Applied Genetics, 2001, 102, 1169-1176.	3.6	76
44	Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404.	2.8	75
45	A framework physical map for peach, a model Rosaceae species. Tree Genetics and Genomes, 2008, 4, 745-756.	1.6	72
46	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. Euphytica, 2015, 205, 627-636.	1.2	72
47	Candidate gene database and transcript map for peach, a model species for fruit trees. Theoretical and Applied Genetics, 2005, 110, 1419-1428.	3.6	71
48	Looking into flowering time in almond (Prunus dulcis (Mill) D. A. Webb): the candidate gene approach. Theoretical and Applied Genetics, 2005, 110, 959-968.	3.6	64
49	The development of a bin mapping population and the selective mapping of 103 markers in the diploid Fragaria reference map. Genome, 2008, 51, 120-127.	2.0	61
50	Genomic characterization of putative allergen genes in peach/almond and their synteny with apple. BMC Genomics, 2008, 9, 543.	2.8	61
51	Development and bin mapping of a Rosaceae Conserved Ortholog Set (COS) of markers. BMC Genomics, 2009, 10, 562.	2.8	61
52	Mapping of a gene determining linolenic acid concentration in rapeseed with DNA-based markers. Theoretical and Applied Genetics, 1995, 90, 258-262.	3.6	60
53	The potential of Prunus davidiana for introgression into peach [Prunus persica (L.) Batsch] assessed by comparative mapping. Theoretical and Applied Genetics, 2003, 107, 227-238.	3.6	60
54	Identification of Melon Fruit Quality Quantitative Trait Loci Using Near-isogenic Lines. Journal of the American Society for Horticultural Science, 2008, 133, 139-151.	1.0	59

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55	Syteny conservation between two distantly-related Rosaceae genomes: Prunus (the stone fruits) and Fragaria(the strawberry). BMC Plant Biology, 2008, 8, 67.	3.6	58
56	Identification of incompatibility genotypes in almond (Prunus dulcis Mill.) using specific primers based on the introns of the S-alleles. Plant Breeding, 2003, 122, 164-168.	1.9	57
57	Exploring almond genetic variability useful for peach improvement: mapping major genes and QTLs in two interspecific almond—Peach populations. Molecular Breeding, 2016, 36, 1.	2.1	56
58	Saturating the Prunus (stone fruits) genome with candidate genes for fruit quality. Molecular Breeding, 2011, 28, 667-682.	2.1	53
59	Combining linkage and association mapping to search for markers linked to the flat fruit character in peach. Euphytica, 2013, 190, 279-288.	1.2	53
60	Development of a second generation linkage map for almond using RAPD and SSR markers. Genome, 2000, 43, 649-655.	2.0	52
61	Molecular characterization of cDNAs corresponding to genes expressed during almond (Prunus) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222	3.9	50
62	Simple sequence repeats in <i>Cucumis</i>; mapping and map merging. Genome, 2000, 43, 963-974.	2.0	50
63	Molecular markers for kernel bitterness in almond. Tree Genetics and Genomes, 2010, 6, 237-245.	1.6	49
64	Location of the self-incompatibility gene on the almond linkage map. Plant Breeding, 1998, 117, 69-72.	1.9	48
65	Inheritance mode of fruit traits in melon: Heterosis for fruit shape and its correlation with genetic distance. Euphytica, 2005, 144, 31-38.	1.2	48
66	A new set of polymorphic simple sequence repeat (SSR) markers from a wild strawberry (Fragaria) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 Ecology Notes, 2006, 6, 197-200.	1.7	48
67	Plant genome archaeology: evidence for conserved ancestral chromosome segments in dicotyledonous plant species. Plant Biotechnology Journal, 2003, 1, 91-99.	8.3	46
68	Single-nucleotide polymorphisms detected in expressed sequence tags of melon (<i>Cucumis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222	2.0	45
69	ASSIsT: an automatic SNP scoring tool for in- and outbreeding species. Bioinformatics, 2015, 31, 3873-3874.	4.1	45
70	A codominant diagnostic marker for the slow ripening trait in peach. Molecular Breeding, 2016, 36, 1.	2.1	44
71	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. BMC Genomics, 2017, 18, 432.	2.8	44
72	Electrophoretic variation as a tool for determining seed purity and for breeding hybrid varieties of Brassica oleracea. Euphytica, 1982, 31, 417-428.	1.2	42

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73	Phylogenetic relationships among Cucumis species based on the ribosomal internal transcribed spacer sequence and microsatellite markers. <i>Plant Systematics and Evolution</i> , 2004, 248, 191.	0.9	42
74	RFLP variability in apricot (<i>Prunus armeniaca</i> L.). <i>Plant Breeding</i> , 1998, 117, 153-158.	1.9	41
75	Expression QTL (eQTLs) Analyses Reveal Candidate Genes Associated With Fruit Flesh Softening Rate in Peach [<i>Prunus persica</i> (L.) Batsch]. <i>Frontiers in Plant Science</i> , 2019, 10, 1581.	3.6	41
76	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
77	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
78	Application of isozyme electrophoresis for purity testing and cultivar identification of F1 hybrids of <i>Brassica oleracea</i> . <i>Euphytica</i> , 1985, 34, 651-657.	1.2	38
79	The European <i>Prunus</i> mapping project Progress in the almond linkage map. <i>Euphytica</i> , 1994, 77, 97-100.	1.2	37
80	Molecular characterization and genetic diversity of <i>Prunus</i> rootstocks. <i>Scientia Horticulturae</i> , 2009, 120, 237-245.	3.6	36
81	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
82	Identification of peach cultivars with pollen isozymes. <i>Scientia Horticulturae</i> , 1987, 31, 107-117.	3.6	33
83	Identification of volatile and softening-related genes using digital gene expression profiles in melting peach. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	31
84	Genetic analysis of the slow-melting flesh character in peach. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	31
85	Development of “universal” gene-specific markers from <i>Malus</i> spp. cDNA sequences, their mapping and use in synteny studies within Rosaceae. <i>Tree Genetics and Genomes</i> , 2009, 5, 133-145.	1.6	30
86	Generation of a BAC-based physical map of the melon genome. <i>BMC Genomics</i> , 2010, 11, 339.	2.8	30
87	High-density genetic map and QTL analysis of soluble solid content, maturity date, and mealiness in peach using genotyping by sequencing. <i>Scientia Horticulturae</i> , 2019, 257, 108734.	3.6	30
88	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	5.5	30
89	Comparison of SSR polymorphisms using automated capillary sequencers, and polyacrylamide and agarose gel electrophoresis: Implications for the assessment of genetic diversity and relatedness in almond. <i>Scientia Horticulturae</i> , 2006, 108, 310-316.	3.6	29
90	Genetic analysis and nomenclature for seven isozyme systems in <i>Brassica nigra</i> , <i>B. oleracea</i> and <i>B. campestris</i> . <i>Plant Breeding</i> , 1995, 114, 473-480.	1.9	28

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91	Structure of two melon regions reveals high microsynteny with sequenced plant species. <i>Molecular Genetics and Genomics</i> , 2007, 278, 611-622.	2.1	28
92	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
93	Genotyping by Sequencing in Almond: SNP Discovery, Linkage Mapping, and Marker Design. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 161-172.	1.8	28
94	Cloning and mapping of resistance gene homologues in melon. <i>Plant Science</i> , 2001, 161, 165-172.	3.6	27
95	A physical map covering the nsv locus that confers resistance to Melon necrotic spot virus in melon (<i>Cucumis melo</i> L.). <i>Theoretical and Applied Genetics</i> , 2005, 111, 914-922.	3.6	27
96	Almond. , 2007, , 229-242.		27
97	Construction of a reference linkage map for melon. <i>Genome</i> , 2001, 44, 836-845.	2.0	27
98	Inheritance patterns and linkage relationships of eight genes of celery. <i>Journal of Heredity</i> , 1984, 75, 11-14.	2.4	26
99	Biochemical and genetic implications of the slow ripening phenotype in peach fruit. <i>Scientia Horticulturae</i> , 2020, 259, 108824.	3.6	26
100	Self-incompatibility genotypes in almond re-evaluated by PCR, stylar ribonucleases, sequencing analysis and controlled pollinations. <i>Theoretical and Applied Genetics</i> , 2004, 109, 954-964.	3.6	25
101	Synten conservation between the <i>Prunus</i> genome and both the present and ancestral <i>Arabidopsis</i> genomes. <i>BMC Genomics</i> , 2006, 7, 81.	2.8	25
102	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
103	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
104	Physical mapping of rDNA genes establishes the karyotype of almond. <i>Annals of Applied Biology</i> , 2004, 144, 219-222.	2.5	23
105	A near-isogenic line (NIL) collection in diploid strawberry and its use in the genetic analysis of morphologic, phenotypic and nutritional characters. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1261-1275.	3.6	22
106	Exploring sources of resistance to brown rot in an interspecific almond Ã— peach population. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 4105-4113.	3.5	22
107	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
108	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

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109	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
110	Use of Microsatellite Polymorphisms to Develop an Identification Key for Tunisian Apricots. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 1699-1706.	1.6	19
111	Cell Wall Polysaccharide Chemistry of Peach Genotypes with Contrasted Textures and Other Fruit Traits. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 6594-6605.	5.2	19
112	High-density multi-population consensus genetic linkage map for peach. <i>PLoS ONE</i> , 2018, 13, e0207724.	2.5	19
113	Identification of quantitative trait loci associated with self-compatibility in a <i>Prunus</i> species. <i>Tree Genetics and Genomes</i> , 2011, 7, 629-639.	1.6	18
114	Mapping a major gene for red skin color suppression (highlighter) in peach. <i>Euphytica</i> , 2017, 213, 1.	1.2	16
115	The Extensin from <i>Prunus amygdalus</i> . <i>Plant Physiology</i> , 1992, 100, 1603-1604.	4.8	15
116	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
117	Chromosome-level genome assemblies of four wild peach species provide insights into genome evolution and genetic basis of stress resistance. <i>BMC Biology</i> , 2022, 20, .	3.8	13
118	Genomics of Almond. , 2009, , 187-219.		12
119	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
120	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
121	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
122	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
123	Inheritance and linkage relationships of ten isozyme genes in hazelnut. <i>Theoretical and Applied Genetics</i> , 1993, 86-86, 322-328.	3.6	10
124	A highly conserved β -tubulin sequence from <i>Prunus amygdalus</i> . <i>Plant Molecular Biology</i> , 1993, 22, 913-916.	3.9	10
125	Sequences of the genomic DNAs encoding the <i>S2</i> , <i>S9</i> , <i>S10</i> , and <i>S23</i> alleles from almond, <i>Prunus dulcis</i> . <i>Journal of Horticultural Science and Biotechnology</i> , 2002, 77, 387-392.	1.9	10
126	Accumulation of specific mRNAs during almond fruit development. <i>Plant Science</i> , 1996, 113, 185-192.	3.6	9

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127	Creating climacteric melon fruit from nonclimacteric parents: postharvest quality implications. , 2007, , 197-205.		8
128	'Francoli', a late flowering almond cultivar re-classified as self-compatible. Plant Breeding, 2005, 124, 502-506.	1.9	7
129	On Estimating the Sib Proportion in Seed-Purity Determinations. Biometrics, 1983, 39, 563.	1.4	6
130	Outcrossing in celery (<i>Apium graveolens</i>). Euphytica, 1984, 33, 471-480.	1.2	6
131	Discovering peach QTLs with multiple progeny analysis. Acta Horticulturae, 2017, , 405-410.	0.2	5
132	Resynthesis: Marker-Based Partial Reconstruction of Elite Genotypes in Clonally-Reproducing Plant Species. Frontiers in Plant Science, 2020, 11, 1205.	3.6	5
133	The development and characterisation of a bacterial artificial chromosome library for <i>Fragaria vesca</i> . BMC Research Notes, 2009, 2, 188.	1.4	4
134	Selection of Pru p 3 hypoallergenic peach and nectarine varieties. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 1256-1260.	5.7	4
135	Tri-/Hexanucleotide Microsatellite Markers in Peach Derived from Enriched Genomic Libraries and Their Application in Rosaceae. Breeding Science, 2007, 57, 289-296.	1.9	4
136	Comparative QTL analysis in peach 'Earlygold'™ F2 and backcross progenies. Scientia Horticulturae, 2022, 293, 110726.	3.6	4
137	FITMAPS and SHOWMAP: Two Programs for Graphical Comparison and Plotting of Genetic Maps. , 2002, 93, 225-227.		3
138	Genomics For Improvement Of Rosaceae Temperate Tree Fruit. , 2007, , 357-397.		3
139	Peach allergen Pru p 1 content is generally low in fruit but with large variation in different varieties. Clinical and Translational Allergy, 2021, 11, e12034.	3.2	3
140	Impacts of Use and Abuse of Nature in Catalonia with Proposals for Sustainable Management. Land, 2021, 10, 144.	2.9	2
141	Diversity Analysis. , 2012, , 55-75.		2
142	Ciència i Tecnologia per a l'Agricultura del Futur. Metode, 2019, , .	0.1	2
143	Markers in Fruit Tree Breeding: Improvement of Peach. , 2004, , 279-302.		1
144	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

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145	Construction of a collection of introgression lines of “Texas”almond DNA fragments in the “Earlygold”peach genetic background. Horticulture Research, 0, , .	6.3	1