Pere ArÃºs

List of Publications by Year
in descending order

145 papers	11,453 citations	28274 55 h-index	30087 103 g-index
153 all docs	153 docs citations	153 times ranked	5921 citing authors

#	Article	IF	Citations
1	Comparative QTL analysis in peach â€˜Earlygoldâ€™ F2 and backcross progenies. Scientia Horticulturae, 2022, 293, 110726.	3.6	4
2	Chromosome-level genome assemblies of four wild peach species provide insights into genome evolution and genetic basis of stress resistance. BMC Biology, 2022, 20, .	3.8	13
3	Pedigree analysis of 220 almond genotypes reveals two world mainstream breeding lines based on only three different cultivars. Horticulture Research, 2021, 8, 11.	6.3	20
4	Impacts of Use and Abuse of Nature in Catalonia with Proposals for Sustainable Management. Land, 2021, 10, 144.	2.9	2
5	Genomic analyses provide insights into peach local adaptation and responses to climate change. Genome Research, 2021, 31, 592-606.	5.5	30
6	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
7	Biochemical and genetic implications of the slow ripening phenotype in peach fruit. Scientia Horticulturae, 2020, 259, 108824.	3.6	26
8	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
9	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. Plant Journal, 2020, 101, 455-472.	5.7	94
10	Resynthesis: Marker-Based Partial Reconstruction of Elite Genotypes in Clonally-Reproducing Plant Species. Frontiers in Plant Science, 2020, 11, 1205.	3.6	5
11	Fine mapping and identification of candidate genes for the peach powdery mildew resistance gene Vr3. Horticulture Research, 2020, 7, 175.	6.3	12
12	The Multisite PeachRefPop Collection: A True Cultural Heritage and International Scientific Tool for Fruit Trees. Plant Physiology, 2020, 184, 632-646.	4.8	12
13	Inheritance and QTL analysis of chilling and heat requirements for flowering in an interspecific almond x peach (Texas x Earlygold) F2 population. Euphytica, 2020, 216, 1.	1.2	12
14	High-density genetic map and QTL analysis of soluble solid content, maturity date, and mealiness in peach using genotyping by sequencing. Scientia Horticulturae, 2019, 257, 108734.	3.6	30
15	Prunus genetics and applications after de novo genome sequencing: achievements and prospects. Horticulture Research, 2019, 6, 58.	6.3	121
16	Exploring sources of resistance to brown rot in an interspecific almond Ã— peach population. Journal of the Science of Food and Agriculture, 2019, 99, 4105-4113.	3.5	22
17	Expression QTL (eQTLs) Analyses Reveal Candidate Genes Associated With Fruit Flesh Softening Rate in Peach [Prunus persica (L.) Batsch]. Frontiers in Plant Science, 2019, 10, 1581.	3.6	41
18	CiÃ¨ncia i Tecnologia per a lâ€™Agricultura del Futur. Metode, 2019, , .	0.1	2

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19	An integrated approach for increasing breeding efficiency in apple and peach in Europe. Horticulture Research, 2018, 5, 11.	6.3	98
20	Genotyping by Sequencing in Almond: SNP Discovery, Linkage Mapping, and Marker Design. G3: Genes, Genomes, Genetics, 2018, 8, 161-172.	1.8	28
21	High-density multi-population consensus genetic linkage map for peach. PLoS ONE, 2018, 13, e0207724.	2.5	19
22	Identification of a new allele of the Dw gene causing brachytic dwarfing in peach. BMC Research Notes, 2018, 11, 386.	1.4	12
23	Genetic analysis of the slow-melting flesh character in peach. Tree Genetics and Genomes, 2017, 13, 1.	1.6	31
24	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. BMC Genomics, 2017, 18, 432.	2.8	44
25	Mapping a major gene for red skin color suppression (highlighter) in peach. Euphytica, 2017, 213, 1.	1.2	16
26	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
27	Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404.	2.8	75
28	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
29	Discovering peach QTLs with multiple progeny analysis. Acta Horticulturae, 2017, , 405-410.	0.2	5
30	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
31	A codominant diagnostic marker for the slow ripening trait in peach. Molecular Breeding, 2016, 36, 1.	2.1	44
32	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. Tree Genetics and Genomes, 2016, 12, 1.	1.6	21
33	Exploring almond genetic variability useful for peach improvement: mapping major genes and QTLs in two interspecific almondÂÃ—Âpeach populations. Molecular Breeding, 2016, 36, 1.	2.1	56
34	High-density mapping suggests cytoplasmic male sterility with two restorer genes in almond Ã— peach progenies. Horticulture Research, 2015, 2, 15016.	6.3	35
35	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. PLoS ONE, 2015, 10, e0136803.	2.5	98
36	Identification of volatile and softening-related genes using digital gene expression profiles in melting peach. Tree Genetics and Genomes, 2015, 11, 1.	1.6	31

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37	A near-isogenic line (NIL) collection in diploid strawberry and its use in the genetic analysis of morphologic, phenotypic and nutritional characters. Theoretical and Applied Genetics, 2015, 128, 1261-1275.	3.6	22
38	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
39	ASSIsT: an automatic SNP scoring tool for in- and outbreeding species. Bioinformatics, 2015, 31, 3873-3874.	4.1	45
40	Development of diagnostic markers for selection of the subacid trait in peach. Tree Genetics and Genomes, 2014, 10, 1695-1709.	1.6	24
41	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
42	Peach genetic resources: diversity, population structure and linkage disequilibrium. BMC Genetics, 2013, 14, 84.	2.7	78
43	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	21.4	1,031
44	A first insight into peach [Prunus persica (L.) Batsch] SNP variability. Tree Genetics and Genomes, 2012, 8, 1359-1369.	1.6	39
45	Whole genome comparisons of Fragaria, Prunus and Malus reveal different modes of evolution between Rosaceous subfamilies. BMC Genomics, 2012, 13, 129.	2.8	77
46	Comparison of the genetic determinism of two key phenological traits, flowering and maturity dates, in three Prunus species: peach, apricot and sweet cherry. Heredity, 2012, 109, 280-292.	2.6	139
47	Cell Wall Polysaccharide Chemistry of Peach Genotypes with Contrasted Textures and Other Fruit Traits. Journal of Agricultural and Food Chemistry, 2012, 60, 6594-6605.	5.2	19
48	The genome of melon (Cucumis melo L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	7.1	654
49	The peach genome. Tree Genetics and Genomes, 2012, 8, 531-547.	1.6	120
50	Diversity Analysis. , 2012, , 55-75.		2
51	Development and Evaluation of a 9K SNP Array for Peach by Internationally Coordinated SNP Detection and Validation in Breeding Germplasm. PLoS ONE, 2012, 7, e35668.	2.5	199
52	The genome of woodland strawberry (Fragaria vesca). Nature Genetics, 2011, 43, 109-116.	21.4	1,091
53	Saturating the Prunus (stone fruits) genome with candidate genes for fruit quality. Molecular Breeding, 2011, 28, 667-682.	2.1	53
54	Identification of quantitative trait loci associated with self-compatibility in a Prunus species. Tree Genetics and Genomes, 2011, 7, 629-639.	1.6	18

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55	Comparative analysis of rosaceous genomes and the reconstruction of a putative ancestral genome for the family. BMC Evolutionary Biology, 2011, 11, 9.	3.2	103
56	Molecular markers for kernel bitterness in almond. Tree Genetics and Genomes, 2010, 6, 237-245.	1.6	49
57	Prunus microsatellite marker transferability across rosaceous crops. Tree Genetics and Genomes, 2010, 6, 689-700.	1.6	87
58	Generation of a BAC-based physical map of the melon genome. BMC Genomics, 2010, 11, 339.	2.8	30
59	Genetic variation, population structure and linkage disequilibrium in peach commercial varieties. BMC Genetics, 2010, 11, 69.	2.7	139
60	On the Genetic Control of Heterosis for Fruit Shape in Melon (Cucumis Melo L.). Journal of Heredity, 2009, 100, 229-235.	2.4	20
61	Development and bin mapping of a Rosaceae Conserved Ortholog Set (COS) of markers. BMC Genomics, 2009, 10, 562.	2.8	61
62	A set of EST-SNPs for map saturation and cultivar identification in melon. BMC Plant Biology, 2009, 9, 90.	3.6	90
63	The development and characterisation of a bacterial artificial chromosome library for Fragaria vesca. BMC Research Notes, 2009, 2, 188.	1.4	4
64	Development of â€œuniversalâ€•gene-specific markers from Malus spp. cDNA sequences, their mapping and use in synteny studies within Rosaceae. Tree Genetics and Genomes, 2009, 5, 133-145.	1.6	30
65	Molecular characterization and genetic diversity of Prunus rootstocks. Scientia Horticulturae, 2009, 120, 237-245.	3.6	36
66	Genomics of Almond. , 2009, , 187-219.		12
67	A framework physical map for peach, a model Rosaceae species. Tree Genetics and Genomes, 2008, 4, 745-756.	1.6	72
68	Bin mapping of genomic and EST-derived SSRs in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2008, 118, 139-150.	3.6	115
69	Synteny conservation between two distantly-related Rosaceae genomes: Prunus (the stone fruits) and Fragaria(the strawberry). BMC Plant Biology, 2008, 8, 67.	3.6	58
70	Comparative Genetic Mapping Between Octoploid and Diploid Fragaria Species Reveals a High Level of Colinearity Between Their Genomes and the Essentially Disomic Behavior of the Cultivated Octoploid Strawberry. Genetics, 2008, 179, 2045-2060.	2.9	140
71	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
72	Genomic characterization of putative allergen genes in peach/almond and their synteny with apple. BMC Genomics, 2008, 9, 543.	2.8	61

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73	Multiple Models for Rosaceae Genomics. Plant Physiology, 2008, 147, 985-1003.	4.8	291
74	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
75	Genomics For Improvement Of Rosaceae Temperate Tree Fruit. , 2007, , 357-397.		3
76	Almond. , 2007, , 229-242.		27
77	Mapping major genes and quantitative trait loci controlling agronomic traits in almond. Plant Breeding, 2007, 126, 310-318.	1.9	93
78	MELOGEN: an EST database for melon functional genomics. BMC Genomics, 2007, 8, 306.	2.8	87
79	Structure of two melon regions reveals high microsynteny with sequenced plant species. Molecular Genetics and Genomics, 2007, 278, 611-622.	2.1	28
80	Creating climacteric melon fruit from nonclimacteric parentals: postharvest quality implications. , 2007, , 197-205.		8
81	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
82	Estimating the Genetic Architecture of Fruit Quality Traits in Melon Using a Genomic Library of Near Isogenic Lines. Journal of the American Society for Horticultural Science, 2007, 132, 80-89.	1.0	91
83	Mapping Fruit Susceptibility to Postharvest Physiological Disorders and Decay Using a Collection of Near-isogenic Lines of Melon. Journal of the American Society for Horticultural Science, 2007, 132, 739-748.	1.0	24
84	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. Scientia Horticulturae, 2006, 108, 310-316.	3.6	29
85	A new set of polymorphic simple sequence repeat (SSR) markers from a wild strawberry (Fragaria) Tj ETQq1 1 0.784314 rgBT /Overloc Ecology Notes, 2006, 6, 197-200.	1.7	48
86	Use of Microsatellite Polymorphisms to Develop an Identification Key for Tunisian Apricots. Genetic Resources and Crop Evolution, 2006, 53, 1699-1706.	1.6	19
87	An enhanced microsatellite map of diploid Fragaria. Theoretical and Applied Genetics, 2006, 112, 1349-1359.	3.6	112
88	Synteny conservation between the Prunus genome and both the present and ancestral Arabidopsis genomes. BMC Genomics, 2006, 7, 81.	2.8	25
89	Development and transportability across Prunus species of 42 polymorphic almond microsatellites. Molecular Ecology Notes, 2005, 5, 531-535.	1.7	84
90	'Francoli', a late flowering almond cultivar re-classified as self-compatible. Plant Breeding, 2005, 124, 502-506.	1.9	7

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91	Simple-sequence repeat markers used in merging linkage maps of melon (Cucumis melo L.). Theoretical and Applied Genetics, 2005, 110, 802-811.	3.6	170
92	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
93	A physical map covering the nsv locus that confers resistance to Melon necrotic spot virus in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2005, 111, 914-922.	3.6	27
94	Development of a genomic library of near isogenic lines (NILs) in melon (Cucumis melo L.) from the exotic accession PI161375. Theoretical and Applied Genetics, 2005, 112, 139-148.	3.6	98
95	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
96	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
97	Mapping With a Few Plants: Using Selective Mapping for Microsatellite Saturation of the Prunus Reference Map. Genetics, 2005, 171, 1305-1309.	2.9	180
98	Simple-sequence repeat (SSR) markers of Japanese plum (Prunus salicina Lindl.) are highly polymorphic and transferable to peach and almond. Molecular Ecology Notes, 2004, 4, 163-166.	1.7	137
99	Physical mapping of rDNA genes establishes the karyotype of almond. Annals of Applied Biology, 2004, 144, 219-222.	2.5	23
100	Phylogenetic relationships among Cucumis species based on the ribosomal internal transcribed spacer sequence and microsatellite markers. Plant Systematics and Evolution, 2004, 248, 191.	0.9	42
101	Identification of quantitative trait loci involved in fruit quality traits in melon (Cucumis melo L.). Theoretical and Applied Genetics, 2004, 108, 750-758.	3.6	159
102	Genetic linkage maps of two apricot cultivars (Prunus armeniaca L.) compared with the almond Texas Ã— peach Earlygold reference map for Prunus. Theoretical and Applied Genetics, 2004, 108, 1120-1130.	3.6	83
103	Self-incompatibility genotypes in almond re-evaluated by PCR, stylar ribonucleases, sequencing analysis and controlled pollinations. Theoretical and Applied Genetics, 2004, 109, 954-964.	3.6	25
104	Microsatellite genetic linkage maps of myrobalan plum and an almond-peach hybrid?location of root-knot nematode resistance genes. Theoretical and Applied Genetics, 2004, 109, 827-838.	3.6	109
105	Single-nucleotide polymorphisms detected in expressed sequence tags of melon (<i>Cucumis) Tj ETQq1 1 0.784314 rgBT /Overlock 1	2.0	45
106	Comparative mapping and marker-assisted selection in Rosaceae fruit crops. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9891-9896.	7.1	473
107	Markers in Fruit Tree Breeding: Improvement of Peach. , 2004, , 279-302.		1
108	A set of simple-sequence repeat (SSR) markers covering the Prunus genome. Theoretical and Applied Genetics, 2003, 106, 819-825.	3.6	199

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109	Microsatellite variability in peach [Prunus persica (L.) Batsch]: cultivar identification, marker mutation, pedigree inferences and population structure. Theoretical and Applied Genetics, 2003, 106, 1341-1352.	3.6	113
110	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
111	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
112	Genetic variability in melon based on microsatellite variation. Plant Breeding, 2003, 122, 153-157.	1.9	92
113	Plant genome archaeology: evidence for conserved ancestral chromosome segments in dicotyledonous plant species. Plant Biotechnology Journal, 2003, 1, 91-99.	8.3	46
114	Using Amplified Fragment-length Polymorphisms (AFLPs) to Identify Peach Cultivars. Journal of the American Society for Horticultural Science, 2003, 128, 672-677.	1.0	15
115	FITMAPS and SHOWMAP: Two Programs for Graphical Comparison and Plotting of Genetic Maps. , 2002, 93, 225-227.		3
116	Sequences of the genomic DNAs encoding theS2, S9, S10,andS23alleles from almond,Prunus dulcis. Journal of Horticultural Science and Biotechnology, 2002, 77, 387-392.	1.9	10
117	Development of microsatellite markers in peach [Prunus persica (L.) Batsch] and their use in genetic diversity analysis in peach and sweet cherry (Prunus avium L.). Theoretical and Applied Genetics, 2002, 105, 127-138.	3.6	492
118	Development and variability analysis of microsatellite markers in peach. Plant Breeding, 2002, 121, 87-92.	1.9	221
119	Cloning and mapping of resistance gene homologues in melon. Plant Science, 2001, 161, 165-172.	3.6	27
120	A reciprocal translocation between â€™Garfiâ€™ almond and â€™Nemaredâ€™ peach. Theoretical and Applied Genetics, 2001, 102, 1169-1176.	3.6	76
121	Genetic mapping of a major gene delaying blooming time in almond. Plant Breeding, 2001, 120, 268-270.	1.9	88
122	Construction of a reference linkage map for melon. Genome, 2001, 44, 836-845.	2.0	27
123	Development of a second generation linkage map for almond using RAPD and SSR markers. Genome, 2000, 43, 649-655.	2.0	52
124	Simple sequence repeats in <i>Cucumis</i> mapping and map merging. Genome, 2000, 43, 963-974.	2.0	50
125	Location of the self-incompatibility gene on the almond linkage map. Plant Breeding, 1998, 117, 69-72.	1.9	48
126	RFLP variability in apricot (Prunus armeniacaL.). Plant Breeding, 1998, 117, 153-158.	1.9	41

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127	Construction of a saturated linkage map for Prunus using an almondÃ—peach F2 progeny. Theoretical and Applied Genetics, 1998, 97, 1034-1041.	3.6	202
128	Accumulation of specific mRNAs during almond fruit development. Plant Science, 1996, 113, 185-192.	3.6	9
129	Molecular characterization of cDNAs corresponding to genes expressed during almond (Prunus) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.9	50
130	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
131	A linkage map with RFLP and isozyme markers for almond. Theoretical and Applied Genetics, 1995, 91-91, 964-971.	3.6	103
132	Genetic analysis and nomenclature for seven isozyme systems in Brassica nigra, B. oleracea and B. campestris. Plant Breeding, 1995, 114, 473-480.	1.9	28
133	Identifying Olive Cultivars by Isozyme Analysis. Journal of the American Society for Horticultural Science, 1995, 120, 318-324.	1.0	80
134	The European Prunus mapping project Progress in the almond linkage map. Euphytica, 1994, 77, 97-100.	1.2	37
135	Inheritance and linkage relationships of ten isozyme genes in hazelnut. Theoretical and Applied Genetics, 1993, 86-86, 322-328.	3.6	10
136	A highly conserved ?-tubulin sequence from Prunus amygdalus. Plant Molecular Biology, 1993, 22, 913-916.	3.9	10
137	The Extensin from Prunus amygdalus. Plant Physiology, 1992, 100, 1603-1604.	4.8	15
138	Identification of peach cultivars with pollen isozymes. Scientia Horticulturae, 1987, 31, 107-117.	3.6	33
139	Application of isozyme electrophoresis for purity testing and cultivar identification of F1 hybrids of Brassica oleracea. Euphytica, 1985, 34, 651-657.	1.2	38
140	Outcrossing in celery (Apium graveolens). Euphytica, 1984, 33, 471-480.	1.2	6
141	Inheritance patterns and linkage relationships of eight genes of celery. Journal of Heredity, 1984, 75, 11-14.	2.4	26
142	On Estimating the Sib Proportion in Seed-Purity Determinations. Biometrics, 1983, 39, 563.	1.4	6
143	Inheritance and linkage relationships of isozyme loci in Brassica oleracea. Journal of Heredity, 1983, 74, 405-412.	2.4	88
144	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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145	Construction of a collection of introgression lines of â€œTexasâ€•almond DNA fragments in the â€œEarlygoldâ€•peach genetic background. Horticulture Research, 0, , .	6.3	1