

Pere ArÃ³s

List of Publications by Year in descending order

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143
papers

11,453
citations

32410

55
h-index

34195

103
g-index

153
all docs

153
docs citations

153
times ranked

6498
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative QTL analysis in peach "Earlygold"™ F2 and backcross progenies. <i>Scientia Horticulturae</i> , 2022, 293, 110726.	1.7	4
2	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, .	1.7	13
3	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.	2.9	20
4	Impacts of Use and Abuse of Nature in Catalonia with Proposals for Sustainable Management. <i>Land</i> , 2021, 10, 144.	1.2	2
5	Genomic analyses provide insights into peach local adaptation and responses to climate change. <i>Genome Research</i> , 2021, 31, 592-606.	2.4	30
6	Peach allergen Pru p 1 content is generally low in fruit but with large variation in different varieties. <i>Clinical and Translational Allergy</i> , 2021, 11, e12034.	1.4	3
7	Biochemical and genetic implications of the slow ripening phenotype in peach fruit. <i>Scientia Horticulturae</i> , 2020, 259, 108824.	1.7	26
8	Selection of Pru p 3 hypoallergenic peach and nectarine varieties. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020, 75, 1256-1260.	2.7	4
9	Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. <i>Plant Journal</i> , 2020, 101, 455-472.	2.8	94
10	Resynthesis: Marker-Based Partial Reconstruction of Elite Genotypes in Clonally-Reproducing Plant Species. <i>Frontiers in Plant Science</i> , 2020, 11, 1205.	1.7	5
11	Fine mapping and identification of candidate genes for the peach powdery mildew resistance gene Vr3. <i>Horticulture Research</i> , 2020, 7, 175.	2.9	12
12	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.	2.3	12
13	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.	0.6	12
14	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.	1.7	30
15	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. <i>Horticulture Research</i> , 2019, 6, 58.	2.9	121
16	Exploring sources of resistance to brown rot in an interspecific almond – peach population. <i>Journal of the Science of Food and Agriculture</i> , 2019, 99, 4105-4113.	1.7	22
17	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.	1.7	41
18	Ciència i Tecnologia per a l'Agricultura del Futur. <i>Metode</i> , 2019, , .	0.0	2

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19	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11.	2.9	98
20	Genotyping by Sequencing in Almond: SNP Discovery, Linkage Mapping, and Marker Design. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 161-172.	0.8	28
21	High-density multi-population consensus genetic linkage map for peach. <i>PLoS ONE</i> , 2018, 13, e0207724.	1.1	19
22	Identification of a new allele of the Dw gene causing brachytic dwarfing in peach. <i>BMC Research Notes</i> , 2018, 11, 386.	0.6	12
23	Genetic analysis of the slow-melting flesh character in peach. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	31
24	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. <i>BMC Genomics</i> , 2017, 18, 432.	1.2	44
25	Mapping a major gene for red skin color suppression (highlighter) in peach. <i>Euphytica</i> , 2017, 213, 1.	0.6	16
26	A deletion affecting an LRR-RLK gene co-segregates with the fruit flat shape trait in peach. <i>Scientific Reports</i> , 2017, 7, 6714.	1.6	39
27	Integrated QTL detection for key breeding traits in multiple peach progenies. <i>BMC Genomics</i> , 2017, 18, 404.	1.2	75
28	Exploring and exploiting phenotypic and genetic diversity in peach: identification of major genes and QTLs by GWAS. <i>Acta Horticulturae</i> , 2017, , 419-424.	0.1	1
29	Discovering peach QTLs with multiple progeny analysis. <i>Acta Horticulturae</i> , 2017, , 405-410.	0.1	5
30	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.	0.6	28
31	A codominant diagnostic marker for the slow ripening trait in peach. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	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. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	21
33	Exploring almond genetic variability useful for peach improvement: mapping major genes and QTLs in two interspecific almond—peach populations. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	56
34	High-density mapping suggests cytoplasmic male sterility with two restorer genes in almond—peach progenies. <i>Horticulture Research</i> , 2015, 2, 15016.	2.9	35
35	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	1.1	98
36	Identification of volatile and softening-related genes using digital gene expression profiles in melting peach. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	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. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1261-1275.	1.8	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. <i>Euphytica</i> , 2015, 205, 627-636.	0.6	72
39	ASSIsT: an automatic SNP scoring tool for in- and outbreeding species. <i>Bioinformatics</i> , 2015, 31, 3873-3874.	1.8	45
40	Development of diagnostic markers for selection of the subacid trait in peach. <i>Tree Genetics and Genomes</i> , 2014, 10, 1695-1709.	0.6	24
41	Combining linkage and association mapping to search for markers linked to the flat fruit character in peach. <i>Euphytica</i> , 2013, 190, 279-288.	0.6	53
42	Peach genetic resources: diversity, population structure and linkage disequilibrium. <i>BMC Genetics</i> , 2013, 14, 84.	2.7	78
43	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.	9.4	1,031
44	A first insight into peach [<i>Prunus persica</i> (L.) Batsch] SNP variability. <i>Tree Genetics and Genomes</i> , 2012, 8, 1359-1369.	0.6	39
45	Whole genome comparisons of <i>Fragaria</i> , <i>Prunus</i> and <i>Malus</i> reveal different modes of evolution between Rosaceous subfamilies. <i>BMC Genomics</i> , 2012, 13, 129.	1.2	77
46	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.	1.2	139
47	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.	2.4	19
48	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.	3.3	654
49	The peach genome. <i>Tree Genetics and Genomes</i> , 2012, 8, 531-547.	0.6	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. <i>PLoS ONE</i> , 2012, 7, e35668.	1.1	199
52	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011, 43, 109-116.	9.4	1,091
53	Saturating the <i>Prunus</i> (stone fruits) genome with candidate genes for fruit quality. <i>Molecular Breeding</i> , 2011, 28, 667-682.	1.0	53
54	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.	0.6	18

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55	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
56	Molecular markers for kernel bitterness in almond. <i>Tree Genetics and Genomes</i> , 2010, 6, 237-245.	0.6	49
57	<i>Prunus</i> microsatellite marker transferability across rosaceous crops. <i>Tree Genetics and Genomes</i> , 2010, 6, 689-700.	0.6	87
58	Generation of a BAC-based physical map of the melon genome. <i>BMC Genomics</i> , 2010, 11, 339.	1.2	30
59	Genetic variation, population structure and linkage disequilibrium in peach commercial varieties. <i>BMC Genetics</i> , 2010, 11, 69.	2.7	139
60	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.	1.0	20
61	Development and bin mapping of a Rosaceae Conserved Ortholog Set (COS) of markers. <i>BMC Genomics</i> , 2009, 10, 562.	1.2	61
62	A set of EST-SNPs for map saturation and cultivar identification in melon. <i>BMC Plant Biology</i> , 2009, 9, 90.	1.6	90
63	The development and characterisation of a bacterial artificial chromosome library for <i>Fragaria vesca</i> . <i>BMC Research Notes</i> , 2009, 2, 188.	0.6	4
64	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.	0.6	30
65	Molecular characterization and genetic diversity of <i>Prunus</i> rootstocks. <i>Scientia Horticulturae</i> , 2009, 120, 237-245.	1.7	36
66	Genomics of Almond. , 2009, , 187-219.		12
67	A framework physical map for peach, a model Rosaceae species. <i>Tree Genetics and Genomes</i> , 2008, 4, 745-756.	0.6	72
68	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.	1.8	115
69	Synten conservation between two distantly-related Rosaceae genomes: <i>Prunus</i> (the stone fruits) and <i>Fragaria</i> (the strawberry). <i>BMC Plant Biology</i> , 2008, 8, 67.	1.6	58
70	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.	1.2	140
71	The development of a bin mapping population and the selective mapping of 103 markers in the diploid <i>Fragaria</i> reference map. <i>Genome</i> , 2008, 51, 120-127.	0.9	61
72	Genomic characterization of putative allergen genes in peach/almond and their synteny with apple. <i>BMC Genomics</i> , 2008, 9, 543.	1.2	61

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73	Multiple Models for Rosaceae Genomics. <i>Plant Physiology</i> , 2008, 147, 985-1003.	2.3	291
74	Identification of Melon Fruit Quality Quantitative Trait Loci Using Near-isogenic Lines. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 139-151.	0.5	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. <i>Plant Breeding</i> , 2007, 126, 310-318.	1.0	93
78	MELOGEN: an EST database for melon functional genomics. <i>BMC Genomics</i> , 2007, 8, 306.	1.2	87
79	Structure of two melon regions reveals high microsynteny with sequenced plant species. <i>Molecular Genetics and Genomics</i> , 2007, 278, 611-622.	1.0	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. <i>Breeding Science</i> , 2007, 57, 289-296.	0.9	4
82	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.	0.5	91
83	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.	0.5	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. <i>Scientia Horticulturae</i> , 2006, 108, 310-316.	1.7	29
85	A new set of polymorphic simple sequence repeat (SSR) markers from a wild strawberry (<i>Fragaria</i>) Tj ETQq1 1 0.784314 rgBT /Overl Ecology Notes, 2006, 6, 197-200.	1.7	48
86	Use of Microsatellite Polymorphisms to Develop an Identification Key for Tunisian Apricots. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 1699-1706.	0.8	19
87	An enhanced microsatellite map of diploid <i>Fragaria</i> . <i>Theoretical and Applied Genetics</i> , 2006, 112, 1349-1359.	1.8	112
88	Synteny conservation between the <i>Prunus</i> genome and both the present and ancestral <i>Arabidopsis</i> genomes. <i>BMC Genomics</i> , 2006, 7, 81.	1.2	25
89	Development and transportability across <i>Prunus</i> species of 42 polymorphic almond microsatellites. <i>Molecular Ecology Notes</i> , 2005, 5, 531-535.	1.7	84
90	'Francoli', a late flowering almond cultivar re-classified as self-compatible. <i>Plant Breeding</i> , 2005, 124, 502-506.	1.0	7

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91	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.	1.8	170
92	Looking into flowering time in almond (<i>Prunus dulcis</i> (Mill) D. A. Webb): the candidate gene approach. <i>Theoretical and Applied Genetics</i> , 2005, 110, 959-968.	1.8	64
93	A physical map covering the <i>nsv</i> 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.	1.8	27
94	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.	1.8	98
95	Candidate gene database and transcript map for peach, a model species for fruit trees. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1419-1428.	1.8	71
96	Inheritance mode of fruit traits in melon: Heterosis for fruit shape and its correlation with genetic distance. <i>Euphytica</i> , 2005, 144, 31-38.	0.6	48
97	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.	1.2	180
98	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
99	Physical mapping of rDNA genes establishes the karyotype of almond. <i>Annals of Applied Biology</i> , 2004, 144, 219-222.	1.3	23
100	Phylogenetic relationships among <i>Cucumis</i> species based on the ribosomal internal transcribed spacer sequence and microsatellite markers. <i>Plant Systematics and Evolution</i> , 2004, 248, 191.	0.3	42
101	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.	1.8	159
102	Genetic linkage maps of two apricot cultivars (<i>Prunus armeniaca</i> L.) compared with the almond Texas A— peach Earlygold reference map for <i>Prunus</i> . <i>Theoretical and Applied Genetics</i> , 2004, 108, 1120-1130.	1.8	83
103	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.	1.8	25
104	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.	1.8	109
105	Single-nucleotide polymorphisms detected in expressed sequence tags of melon (<i>Cucumis</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 100	0.9	45
106	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.	3.3	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 <i>Prunus</i> genome. <i>Theoretical and Applied Genetics</i> , 2003, 106, 819-825.	1.8	199

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109	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.	1.8	113
110	The potential of <i>Prunus davidiana</i> for introgression into peach [<i>Prunus persica</i> (L.) Batsch] assessed by comparative mapping. <i>Theoretical and Applied Genetics</i> , 2003, 107, 227-238.	1.8	60
111	Identification of incompatibility genotypes in almond (<i>Prunus dulcis</i> Mill.) using specific primers based on the introns of the S-alleles. <i>Plant Breeding</i> , 2003, 122, 164-168.	1.0	57
112	Genetic variability in melon based on microsatellite variation. <i>Plant Breeding</i> , 2003, 122, 153-157.	1.0	92
113	Plant genome archaeology: evidence for conserved ancestral chromosome segments in dicotyledonous plant species. <i>Plant Biotechnology Journal</i> , 2003, 1, 91-99.	4.1	46
114	Using Amplified Fragment-length Polymorphisms (AFLPs) to Identify Peach Cultivars. <i>Journal of the American Society for Horticultural Science</i> , 2003, 128, 672-677.	0.5	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 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.	0.9	10
117	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.	1.8	492
118	Development and variability analysis of microsatellite markers in peach. <i>Plant Breeding</i> , 2002, 121, 87-92.	1.0	221
119	Cloning and mapping of resistance gene homologues in melon. <i>Plant Science</i> , 2001, 161, 165-172.	1.7	27
120	A reciprocal translocation between 'Garfi' almond and 'Nemared' peach. <i>Theoretical and Applied Genetics</i> , 2001, 102, 1169-1176.	1.8	76
121	Genetic mapping of a major gene delaying blooming time in almond. <i>Plant Breeding</i> , 2001, 120, 268-270.	1.0	88
122	Simple sequence repeats in <i>Cucumis</i> mapping and map merging. <i>Genome</i> , 2000, 43, 963-974.	0.9	50
123	Location of the self-incompatibility gene on the almond linkage map. <i>Plant Breeding</i> , 1998, 117, 69-72.	1.0	48
124	RFLP variability in apricot (<i>Prunus armeniaca</i> L.). <i>Plant Breeding</i> , 1998, 117, 153-158.	1.0	41
125	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.	1.8	202
126	Accumulation of specific mRNAs during almond fruit development. <i>Plant Science</i> , 1996, 113, 185-192.	1.7	9

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127	Molecular characterization of cDNAs corresponding to genes expressed during almond (<i>Prunus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	2.0	50
128	Mapping of a gene determining linolenic acid concentration in rapeseed with DNA-based markers. <i>Theoretical and Applied Genetics</i> , 1995, 90, 258-262.	1.8	60
129	A linkage map with RFLP and isozyme markers for almond. <i>Theoretical and Applied Genetics</i> , 1995, 91-91, 964-971.	1.8	103
130	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.	1.0	28
131	Identifying Olive Cultivars by Isozyme Analysis. <i>Journal of the American Society for Horticultural Science</i> , 1995, 120, 318-324.	0.5	80
132	The European <i>Prunus</i> mapping project Progress in the almond linkage map. <i>Euphytica</i> , 1994, 77, 97-100.	0.6	37
133	Inheritance and linkage relationships of ten isozyme genes in hazelnut. <i>Theoretical and Applied Genetics</i> , 1993, 86-86, 322-328.	1.8	10
134	A highly conserved β -tubulin sequence from <i>Prunus amygdalus</i> . <i>Plant Molecular Biology</i> , 1993, 22, 913-916.	2.0	10
135	The Extensin from <i>Prunus amygdalus</i> . <i>Plant Physiology</i> , 1992, 100, 1603-1604.	2.3	15
136	Identification of peach cultivars with pollen isozymes. <i>Scientia Horticulturae</i> , 1987, 31, 107-117.	1.7	33
137	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.	0.6	38
138	Outcrossing in celery (<i>Apium graveolens</i>). <i>Euphytica</i> , 1984, 33, 471-480.	0.6	6
139	Inheritance patterns and linkage relationships of eight genes of celery. <i>Journal of Heredity</i> , 1984, 75, 11-14.	1.0	26
140	On Estimating the Sib Proportion in Seed-Purity Determinations. <i>Biometrics</i> , 1983, 39, 563.	0.8	6
141	Inheritance and linkage relationships of isozyme loci in <i>Brassica oleracea</i> . <i>Journal of Heredity</i> , 1983, 74, 405-412.	1.0	88
142	Electrophoretic variation as a tool for determining seed purity and for breeding hybrid varieties of <i>Brassica oleracea</i> . <i>Euphytica</i> , 1982, 31, 417-428.	0.6	42
143	Construction of a collection of introgression lines of "Texas" almond DNA fragments in the "Earlygold" peach genetic background. <i>Horticulture Research</i> , 0, , .	2.9	1