

# Eric Van de Weg

## List of Publications by Year in descending order

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136  
papers

7,837  
citations

47409

49  
h-index

64407

83  
g-index

143  
all docs

143  
docs citations

143  
times ranked

5042  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	9.4	693
2	Development and characterisation of 140 new microsatellites in apple ( <i>Malus x domestica</i> Borkh.). <i>Molecular Breeding</i> , 2002, 10, 217-241.	1.0	451
3	Microsatellite markers spanning the apple ( <i>Malus x domestica</i> Borkh.) genome. <i>Tree Genetics and Genomes</i> , 2006, 2, 202-224.	0.6	300
4	Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple. <i>PLoS ONE</i> , 2012, 7, e31745.	1.1	249
5	Development and Validation of a 20K Single Nucleotide Polymorphism (SNP) Whole Genome Genotyping Array for Apple ( <i>Malus x domestica</i> Borkh.). <i>PLoS ONE</i> , 2014, 9, e110377.	1.1	200
6	Development and preliminary evaluation of a 90K Axiom® SNP array for the allo-octoploid cultivated strawberry <i>Fragaria x ananassa</i> . <i>BMC Genomics</i> , 2015, 16, 155.	1.2	179
7	Silencing the major apple allergen Mal d 1 by using the RNA interference approach. <i>Journal of Allergy and Clinical Immunology</i> , 2005, 115, 364-369.	1.5	160
8	Quantitative Trait Loci (QTL) Analysis Reveals Both Broad-Spectrum and Isolate-Specific QTL for Scab Resistance in an Apple Progeny Challenged with Eight Isolates of <i>Venturia inaequalis</i> . <i>Phytopathology</i> , 2004, 94, 370-379.	1.1	159
9	Role of the genes Md-ACO1 and Md-ACS1 in ethylene production and shelf life of apple ( <i>Malus</i> ) Tj ETQq1 1 0.784314 rgBT / Overlock 0.6 158	0.6	158
10	Development and validation of the Axiom® Apple480K SNP genotyping array. <i>Plant Journal</i> , 2016, 86, 62-74.	2.8	156
11	QTL dynamics for fruit firmness and softening around an ethylene-dependent polygalacturonase gene in apple ( <i>Malus domestica</i> Borkh.). <i>Journal of Experimental Botany</i> , 2010, 61, 3029-3039.	2.4	146
12	Development of simple sequence repeat (SSR) markers from a genome survey of Chinese bayberry ( <i>Myrica rubra</i> ). <i>BMC Genomics</i> , 2012, 13, 201.	1.2	133
13	In vivo assessment with prick-to-prick testing and double-blind, placebo-controlled food challenge of allergenicity of apple cultivars. <i>Journal of Allergy and Clinical Immunology</i> , 2005, 116, 1080-1086.	1.5	130
14	Accuracy and responses of genomic selection on key traits in apple breeding. <i>Horticulture Research</i> , 2015, 2, 15060.	2.9	130
15	Bayesian QTL analyses using pedigreed families of an outcrossing species, with application to fruit firmness in apple. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1073-1090.	1.8	129
16	Localisation and distribution of the major allergens in apple fruits. <i>Plant Science</i> , 2005, 169, 387-394.	1.7	111
17	Identification of a major QTL together with several minor additive or epistatic QTLs for resistance to fire blight in apple in two related progenies. <i>Theoretical and Applied Genetics</i> , 2005, 111, 128-135.	1.8	110
18	Bayesian analysis of complex traits in pedigreed plant populations. <i>Euphytica</i> , 2008, 161, 85-96.	0.6	107

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19	Resistance gene analogues identified through the NBS-profiling method map close to major genes and QTL for disease resistance in apple. <i>Theoretical and Applied Genetics</i> , 2005, 110, 660-668.	1.8	103
20	Genomic cloning and linkage mapping of the Mal d 1 (PR-10) gene family in apple ( <i>Malus domestica</i> ). <i>Theoretical and Applied Genetics</i> , 2005, 111, 171-183.	1.8	103
21	An integrated approach for increasing breeding efficiency in apple and peach in Europe. <i>Horticulture Research</i> , 2018, 5, 11.	2.9	98
22	The Vh8 locus of a new gene-for-gene interaction between <i>Venturia inaequalis</i> and the wild apple <i>Malus sieversii</i> is closely linked to the Vh2 locus in <i>Malus pumila</i> R12740-7A. <i>New Phytologist</i> , 2005, 166, 1035-1049.	3.5	92
23	Detecting QTLs and putative candidate genes involved in budbreak and flowering time in an apple multiparental population. <i>Journal of Experimental Botany</i> , 2016, 67, 2875-2888.	2.4	91
24	Genetic dissection of partial resistance to race 6 of <i>Venturia inaequalis</i> in apple. <i>Genome</i> , 2003, 46, 224-234.	0.9	87
25	The Vh2 and Vh4 scab resistance genes in two differential hosts derived from Russian apple R12740-7A map to the same linkage group of apple. <i>Molecular Breeding</i> , 2005, 15, 103-116.	1.0	85
26	Map position and functional allelic diversity of Md-Exp7, a new putative expansin gene associated with fruit softening in apple ( <i>Malus domestica</i> Borkh.) and pear ( <i>Pyrus communis</i> ). <i>Tree Genetics and Genomes</i> , 2008, 4, 575-586.	0.6	83
27	Apple whole genome sequences: recent advances and new prospects. <i>Horticulture Research</i> , 2019, 6, 59.	2.9	77
28	Genomic rearrangements and signatures of breeding in the allo-octoploid strawberry as revealed through an allele dose based SSR linkage map. <i>BMC Plant Biology</i> , 2014, 14, 55.	1.6	75
29	Integrated QTL detection for key breeding traits in multiple peach progenies. <i>BMC Genomics</i> , 2017, 18, 404.	1.2	75
30	Genetic analysis of metabolites in apple fruits indicates an mQTL hotspot for phenolic compounds on linkage group 16. <i>Journal of Experimental Botany</i> , 2012, 63, 2895-2908.	2.4	74
31	Fruit size QTL identification and the prediction of parental QTL genotypes and breeding values in multiple pedigreed populations of sweet cherry. <i>Molecular Breeding</i> , 2013, 32, 875-887.	1.0	74
32	Genotyping of pedigreed apple breeding material with a genome-covering set of SSRs: trueness-to-type of cultivars and their parentages. <i>Molecular Breeding</i> , 2011, 28, 535-547.	1.0	72
33	Using RNA-Seq to assemble a rose transcriptome with more than 13,000 full-length expressed genes and to develop the WagRhSNP 68k Axiom SNP array for rose ( <i>Rosa</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 249.	1.7	72
34	GENETIC LINKAGE MAPS OF JAPANESE AND EUROPEAN PEARS ALIGNED TO THE APPLE CONSENSUS MAP. <i>Acta Horticulturae</i> , 2004, , 51-56.	0.1	71
35	Estimation of genetic parameters and prediction of breeding values for apple fruit-quality traits using pedigreed plant material in Europe. <i>Tree Genetics and Genomes</i> , 2009, 5, 659-672.	0.6	71
36	A high-density, multi-parental SNP genetic map on apple validates a new mapping approach for outcrossing species. <i>Horticulture Research</i> , 2016, 3, 16057.	2.9	68

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37	ROSBREED: ENABLING MARKER-ASSISTED BREEDING IN ROSACEAE. <i>Acta Horticulturae</i> , 2010, , 389-394.	0.1	67
38	High-quality, genome-wide SNP genotypic data for pedigreed germplasm of the diploid outbreeding species apple, peach, and sweet cherry through a common workflow. <i>PLoS ONE</i> , 2019, 14, e0210928.	1.1	67
39	QTL mapping of pomological traits in peach and related species breeding germplasm. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	64
40	Identification of RAPD markers linked to a <i>Phytophthora fragariae</i> resistance gene (Rpf1) in the cultivated strawberry. <i>Theoretical and Applied Genetics</i> , 1997, 94, 1097-1101.	1.8	62
41	Genomic characterization of putative allergen genes in peach/almond and their synteny with apple. <i>BMC Genomics</i> , 2008, 9, 543.	1.2	61
42	The red bayberry genome and genetic basis of sex determination. <i>Plant Biotechnology Journal</i> , 2019, 17, 397-409.	4.1	61
43	Pedimap: Software for the Visualization of Genetic and Phenotypic Data in Pedigrees. <i>Journal of Heredity</i> , 2012, 103, 903-907.	1.0	60
44	Pedigree-Based Analysis in a Multiparental Population of Octoploid Strawberry Reveals QTL Alleles Conferring Resistance to <i>Phytophthora cactorum</i> . <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1707-1719.	0.8	58
45	Linkage map positions and allelic diversity of two Malus (non-specific lipid transfer protein) genes in the cultivated apple ( <i>Malus domestica</i> ). <i>Theoretical and Applied Genetics</i> , 2005, 110, 479-491.	1.8	56
46	A strategy for developing representative germplasm sets for systematic QTL validation, demonstrated for apple, peach, and sweet cherry. <i>Tree Genetics and Genomes</i> , 2014, 10, 1679-1694.	0.6	55
47	Elucidation of the "Honeycrisp"™ pedigree through haplotype analysis with a multi-family integrated SNP linkage map and a large apple ( <i>Malus domestica</i> ) pedigree-connected SNP data set. <i>Horticulture Research</i> , 2017, 4, 17003.	2.9	54
48	Development of SCAR Markers Linked to a <i>Phytophthora fragariae</i> Resistance Gene and Their Assessment in European and North American Strawberry Genotypes. <i>Journal of the American Society for Horticultural Science</i> , 2000, 125, 330-339.	0.5	53
49	Development and test of 21 multiplex PCRs composed of SSRs spanning most of the apple genome. <i>Tree Genetics and Genomes</i> , 2009, 5, 211-223.	0.6	52
50	Genetic Diversity and Identity of Chinese Loquat Cultivars/Accessions ( <i>Eriobotrya japonica</i> ) Using Apple SSR Markers. <i>Plant Molecular Biology Reporter</i> , 2011, 29, 197-208.	1.0	52
51	Genetic mapping in <i>Lilium</i> : mapping of major genes and quantitative trait loci for several ornamental traits and disease resistances. <i>Plant Breeding</i> , 2011, 130, 372-382.	1.0	51
52	Epistatic fire blight resistance QTL alleles in the apple cultivar "Enterprise"™ and selection X-6398 discovered and characterized through pedigree-informed analysis. <i>Molecular Breeding</i> , 2018, 38, 1.	1.0	51
53	Deciphering the genetic control of fruit texture in apple by multiple family-based analysis and genome-wide association. <i>Journal of Experimental Botany</i> , 2017, 68, 1451-1466.	2.4	50
54	Two large-effect QTLs, Ma and Ma3, determine genetic potential for acidity in apple fruit: breeding insights from a multi-family study. <i>Tree Genetics and Genomes</i> , 2019, 15, 1.	0.6	50

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55	Genomic characterization and linkage mapping of the apple allergen genes Mal d 2 (thaumatin-like) Tj ETQq1 1 0.784314 rgBT/Overl	1.8	49
56	FaRXf1: a locus conferring resistance to angular leaf spot caused by <i>Xanthomonas fragariae</i> in octoploid strawberry. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1191-1201.	1.8	49
57	Measurement of Lipid Transfer Protein in 88 Apple Cultivars. <i>International Archives of Allergy and Immunology</i> , 2008, 146, 19-26.	0.9	47
58	QTL mapping and breeding value estimation through pedigree-based analysis of fruit size and weight in four diverse peach breeding programs. <i>Tree Genetics and Genomes</i> , 2016, 12, 1.	0.6	46
59	Assessment of allelic diversity in intron-containing Mal d 1 genes and their association to apple allergenicity. <i>BMC Plant Biology</i> , 2008, 8, 116.	1.6	45
60	ASSIST: an automatic SNP scoring tool for in- and outbreeding species. <i>Bioinformatics</i> , 2015, 31, 3873-3874.	1.8	45
61	PediHaplotyper: software for consistent assignment of marker haplotypes in pedigrees. <i>Molecular Breeding</i> , 2016, 36, 119.	1.0	44
62	Development and evaluation of the Axiom <sup>®</sup> IStraw35 384HT array for the allo-octoploid cultivated strawberry <i>Fragaria</i> <i>—</i> <i>ananassa</i> . <i>Acta Horticulturae</i> , 2017, , 75-82.	0.1	44
63	Identification and mapping of the novel apple scab resistance gene Vd3. <i>Tree Genetics and Genomes</i> , 2009, 5, 475-482.	0.6	43
64	High-density SNP-based genetic maps for the parents of an outcrossed and a selfed tetraploid garden rose cross, inferred from admixed progeny using the 68k rose SNP array. <i>Horticulture Research</i> , 2016, 3, 16052.	2.9	42
65	A gene-for-gene model to explain interactions between cultivars of strawberry and races of <i>Phytophthora fragariae</i> var. <i>fragariae</i> . <i>Theoretical and Applied Genetics</i> , 1997, 94, 445-451.	1.8	41
66	Diversity arrays technology (DART) markers in apple for genetic linkage maps. <i>Molecular Breeding</i> , 2012, 29, 645-660.	1.0	41
67	Linked vs. unlinked markers: multilocus microsatellite haplotype-sharing as a tool to estimate gene flow and introgression. <i>Molecular Ecology</i> , 2006, 16, 243-256.	2.0	40
68	Allergenicity Assessment of Apple Cultivars: Hurdles in Quantifying Labile Fruit Allergens. <i>International Archives of Allergy and Immunology</i> , 2006, 141, 230-240.	0.9	39
69	A qRT-PCR assay for the expression of all Mal d 1 isoallergen genes. <i>BMC Plant Biology</i> , 2013, 13, 51.	1.6	39
70	First successful reduction of clinical allergenicity of food by genetic modification: <i>Mal d 1</i> -silenced apples cause fewer allergy symptoms than the wild-type cultivar. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015, 70, 1406-1412.	2.7	37
71	Identification of low allergenic apple cultivars using skin prick tests and oral food challenges. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2011, 66, 491-498.	2.7	36
72	Erosion of quantitative host resistance in the apple <i>—</i> <i>Venturia inaequalis</i> pathosystem. <i>Infection, Genetics and Evolution</i> , 2014, 27, 481-489.	1.0	36

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73	Genetic linkage of QTLs for late blight resistance and foliage maturity type in six related potato progenies. <i>Euphytica</i> , 2005, 143, 189-199.	0.6	35
74	RosBREED: bridging the chasm between discovery and application to enable DNA-informed breeding in rosaceous crops. <i>Horticulture Research</i> , 2020, 7, 177.	2.9	34
75	Construction of an integrated consensus map of the apple genome based on four mapping populations. <i>Tree Genetics and Genomes</i> , 2008, 4, 727-743.	0.6	32
76	Microsatellite allele dose and configuration establishment (MADCE): an integrated approach for genetic studies in allopolyploids. <i>BMC Plant Biology</i> , 2012, 12, 25.	1.6	32
77	Genetic diversity of male and female Chinese bayberry ( <i>Myrica rubra</i> ) populations and identification of sex-associated markers. <i>BMC Genomics</i> , 2015, 16, 394.	1.2	31
78	Comparison of marker-based pairwise relatedness estimators on a pedigreed plant population. <i>Theoretical and Applied Genetics</i> , 2008, 117, 843-855.	1.8	30
79	Genetic structure of a QTL hotspot on chromosome 2 in sweet cherry indicates positive selection for favorable haplotypes. <i>Molecular Breeding</i> , 2017, 37, 1.	1.0	30
80	PEDIGREE GENOTYPING: A NEW PEDIGREE-BASED APPROACH OF QTL IDENTIFICATION AND ALLELE MINING. <i>Acta Horticulturae</i> , 2004, , 45-50.	0.1	29
81	A PROPOSAL FOR THE NOMENCLATURE OF <i>VENTURIA INAEQUALIS</i> RACES. <i>Acta Horticulturae</i> , 2009, , 739-746.	0.1	29
82	â€˜Schmidt's Antonovkaâ€™™ is identical to â€˜Common Antonovkaâ€™™, an apple cultivar widely used in Russia in breeding for biotic and abiotic stresses. <i>Tree Genetics and Genomes</i> , 2014, 10, 261-271.	0.6	29
83	Two QTL characterized for soft scald and soggy breakdown in apple ( <i>Malus Ã— domestica</i> ) through pedigree-based analysis of a large population of interconnected families. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	26
84	AN OVERVIEW OF THE POSITION AND ROBUSTNESS OF SCAB RESISTANCE QTLs AND MAJOR GENES BY ALIGNING GENETIC MAPS OF FIVE APPLE PROGENIES. <i>Acta Horticulturae</i> , 2004, , 135-140.	0.1	25
85	Identification and characterization of QTLs for fruit quality traits in peach through a multi-family approach. <i>BMC Genomics</i> , 2020, 21, 522.	1.2	25
86	SCREENING OF APPLE CULTIVARS FOR RESISTANCE TO EUROPEAN CANKER, <i>NEONECTRIA DITISSIMA</i> . <i>Acta Horticulturae</i> , 2013, , 529-536.	0.1	24
87	Resistance to <i>Phytophthora fragariae</i> var. <i>fragariae</i> in strawberry: the <i>Rpf2</i> gene. <i>Theoretical and Applied Genetics</i> , 1997, 94, 1092-1096.	1.8	23
88	The <i>V f</i> gene for scab resistance in apple is linked to sub-lethal genes. <i>Euphytica</i> , 2006, 151, 123-132.	0.6	22
89	Screening for resistance to <i>Nectria galligena</i> Bres. in cut shoots of apple. <i>Euphytica</i> , 1989, 42, 233-240.	0.6	21
90	A new versatile database created for geneticists and breeders to link molecular and phenotypic data in perennial crops: the AppleBreed DataBase. <i>Bioinformatics</i> , 2007, 23, 882-891.	1.8	21

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91	Genomic organisation of the Mal d 1 gene cluster on linkage group 16 in apple. <i>Molecular Breeding</i> , 2012, 29, 759-778.	1.0	19
92	REVIEW OF FRUIT GENETICS AND BREEDING PROGRAMMES AND A NEW EUROPEAN INITIATIVE TO INCREASE FRUIT BREEDING EFFICIENCY. <i>Acta Horticulturae</i> , 2012, , 95-102.	0.1	18
93	Where to prick the apple for skin testing?. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2013, 68, 1196-1198.	2.7	18
94	LARGE-SCALE STANDARDIZED PHENOTYPING OF APPLE IN ROSBREED. <i>Acta Horticulturae</i> , 2012, , 233-238.	0.1	17
95	Fine mapping of the gene Rvi18 (V25) for broad-spectrum resistance to apple scab, and development of a linked SSR marker suitable for marker-assisted breeding. <i>Molecular Breeding</i> , 2014, 34, 2021-2032.	1.0	16
96	Predicting Flowering Behavior and Exploring Its Genetic Determinism in an Apple Multi-family Population Based on Statistical Indices and Simplified Phenotyping. <i>Frontiers in Plant Science</i> , 2017, 8, 858.	1.7	16
97	Detection of QTL for apple fruit acidity and sweetness using sensorial evaluation in multiple pedigreed full-sib families. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	0.6	15
98	Integration of Infinium and Axiom SNP array data in the outcrossing species <i>Malus × domestica</i> and causes for seemingly incompatible calls. <i>BMC Genomics</i> , 2021, 22, 246.	1.2	15
99	The role of Schmidt <i>Antonovka</i> ™ in apple scab resistance breeding. <i>Tree Genetics and Genomes</i> , 2012, 8, 627-642.	0.6	14
100	Additional Indications for the Low Allergenic Properties of the Apple Cultivars Santana and Elise. <i>Plant Foods for Human Nutrition</i> , 2013, 68, 391-395.	1.4	14
101	The use of shared haplotype length information for pedigree reconstruction in asexually propagated outbreeding crops, demonstrated for apple and sweet cherry. <i>Horticulture Research</i> , 2021, 8, 202.	2.9	14
102	Mapping and characterization QTLs for phenological traits in seven pedigree-connected peach families. <i>BMC Genomics</i> , 2021, 22, 187.	1.2	13
103	DELINEATION OF A SCAB RESISTANCE GENE CLUSTER ON LINKAGE GROUP 2 OF APPLE. <i>Acta Horticulturae</i> , 2004, , 57-62.	0.1	13
104	A FIRST PEDIGREE-BASED ANALYSIS (PBA) APPROACH FOR THE DISSECTION OF DISEASE RESISTANCE TRAITS IN GRAPEVINE HYBRIDS. <i>Acta Horticulturae</i> , 2015, , 113-121.	0.1	11
105	Frequency of a natural truncated allele of MdMLO19 in the germplasm of <i>Malus domestica</i> . <i>Molecular Breeding</i> , 2017, 37, 7.	1.0	11
106	Public Availability of a Genotyped Segregating Population May Foster Marker Assisted Breeding (MAB) and Quantitative Trait Loci (QTL) Discovery: An Example Using Strawberry. <i>Frontiers in Plant Science</i> , 2016, 7, 619.	1.7	10
107	Approaches for evaluation of resistance to European canker ( <i>Neonectria ditissima</i> ) in apple. <i>Acta Horticulturae</i> , 2016, , 75-82.	0.1	10
108	Methods for the Quantification of Resistance of Apple Genotypes to European Fruit Tree Canker Caused by <i>Neonectria ditissima</i> . <i>Plant Disease</i> , 2017, 101, 2012-2019.	0.7	10



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109	Inheritance of resistance to <i>Phytophthora fragariae</i> Hickman in strawberry. <i>Euphytica</i> , 1989, 42, 25-30.	0.6	9
110	Note on an inoculation method to infect young apple seedlings with <i>Nectria galligena</i> Bres.. <i>Euphytica</i> , 1987, 36, 853-854.	0.6	8
111	A quantitative classification method for assessing resistance to <i>Phytophthora fragariae</i> var. <i>fragariae</i> in strawberry. <i>Euphytica</i> , 1996, 91, 119-125.	0.6	8
112	HIGH THROUGHPUT MARKER DEVELOPMENT AND APPLICATION IN HORTICULTURAL CROPS. <i>Acta Horticulturae</i> , 2012, , 547-551.	0.1	8
113	Exploiting expressed sequence tag databases for mapping markers associated with fruit development and fruit quality in apple. <i>Molecular Breeding</i> , 2012, 29, 699-715.	1.0	7
114	DEVELOPMENT OF THE WAGRHSNP AXIOM SNP ARRAY BASED ON SEQUENCES FROM TETRAPLOID CUT ROSES AND GARDEN ROSES. <i>Acta Horticulturae</i> , 2015, , 177-184.	0.1	7
115	Where are we now as we merge genomics into plant breeding and what are our limitations? Experiences from RosBREED. <i>Acta Horticulturae</i> , 2016, , 1-6.	0.1	7
116	Elucidating the genetic background of the early-flowering transgenic genetic stock T1190 with a high-density SNP array. <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	7
117	FUNCTIONAL MARKERS AS GENETIC APPROACH TO STUDY ETHYLENE PRODUCTION AND FRUIT SOFTENING IN APPLE ( <i>MALUS X DOMESTICA</i> BORKH.). <i>Acta Horticulturae</i> , 2005, , 389-394.	0.1	6
118	Detection of ploidy and chromosomal aberrations in commercial oil palm using high-throughput SNP markers. <i>Planta</i> , 2021, 253, 63.	1.6	6
119	Advanced genebank management of genetic resources of European wild apple, <i>Malus sylvestris</i> , using genome-wide SNP array data. <i>Tree Genetics and Genomes</i> , 2021, 17, 1.	0.6	6
120	PEDIGREE GENOTYPING: A NEW PEDIGREE-BASED APPROACH OF QTL IDENTIFICATION AND ALLELE MINING BY EXPLOITING BREEDING MATERIAL. <i>Acta Horticulturae</i> , 2006, , 483-488.	0.1	4
121	Production of hypoallergenic plant foods by selection, breeding and genetic modification. , 2006, , 97-107.		4
122	DEVELOPMENT OF A SET OF APPLE SSRs MARKERS SPANNING THE APPLE GENOME, GENOTYPING OF HIDRAS PLANT MATERIAL AND VALIDATION OF GENOTYPIC DATA. <i>Acta Horticulturae</i> , 2009, , 603-608.	0.1	3
123	Searching for interacting QTL in related populations of an outbreeding species. <i>Euphytica</i> , 2009, 166, 131-144.	0.6	3
124	USING GENERAL AND SPECIFIC COMBINING ABILITY TO FURTHER ADVANCE STRAWBERRY ( <i>FRAGARIA</i> SP.) BREEDING. <i>Acta Horticulturae</i> , 2014, , 193-200.	0.1	3
125	Heritability of flower size and heat stress in diploid roses. <i>Acta Horticulturae</i> , 2019, , 51-56.	0.1	3
126	ALLERGEN EXPRESSION IN CONTROL AND TRANSGENIC APPLE PLANTS. <i>Acta Horticulturae</i> , 2012, , 135-142.	0.1	3



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127	A new method to reconstruct the direction of parent-offspring duo relationships using SNP array data and its demonstration on ancient and modern cultivars in the outcrossing species <i>malus A-domestica</i> . Horticulture Research, 2022, , .	2.9	3
128	Where To Prick The Apple For Skin Testing?. Journal of Allergy and Clinical Immunology, 2009, 123, S29-S29.	1.5	2
129	IDENTIFICATION OF BREEDING SIGNATURES IN GRAPEVINE HYBRIDS, DONORS OF RESISTANCES AGAINST DOWNY AND POWDERY MILDEW. Acta Horticulturae, 2015, , 145-148.	0.1	1
130	Genomics tools available for unravelling mechanisms underlying agronomical traits in strawberry with more to come. Acta Horticulturae, 2017, , 13-24.	0.1	1
131	Comprehensive analysis of candidate genes involved in ethylene production and perception during apple ripening: phenotypic dissection and functional profiling. , 2007, , 423-429.		1
132	QTL ANALYSIS OF THE GENETIC ARCHITECTURE DETERMINING RESISTANCE TO FIRE BLIGHT IN AN APPLE PROGENY. Acta Horticulturae, 2004, , 141-146.	0.1	1
133	AN ASSESSMENT OF THE DURABILITY AND SUSCEPTIBILITY OF SCAB RESISTANCE IN APPLE CULTIVARS. Acta Horticulturae, 2004, , 221-224.	0.1	1
134	A JOINT LAIMBURG - FEM MOLECULAR MARKERS PROJECT FOR APPLE FRUIT QUALITY TRAITS USING THE PEDIGREE BASED ANALYSIS STRATEGY. Acta Horticulturae, 2015, , 91-94.	0.1	0
135	MOLECULAR MAPPING AND CONSTRUCTION OF SCAR MARKERS OF THE STRAWBERRY RPF1 RESISTANCE GENE TO PHYTOPHTHORA FRAGARIAE AND THEIR USE IN BREEDING PROGRAMMES. Acta Horticulturae, 1997, , 845-852.	0.1	0
136	GENES FOR AND MOLECULAR MARKERS LINKED WITH RESISTANCE TO PHYTOPHTHORA FRAGARIAE IN STRAWBERRY. Acta Horticulturae, 1997, , 839-844.	0.1	0