

Elisabeth Dirlewanger

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

2,530
citations

236925

25
h-index

330143

37
g-index

52
all docs

52
docs citations

52
times ranked

2058
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Mapping With a Few Plants: Using Selective Mapping for Microsatellite Saturation of the Prunus Reference Map. Genetics, 2005, 171, 1305-1309.	2.9	180
3	Walnut: past and future of genetic improvement. Tree Genetics and Genomes, 2018, 14, 1.	1.6	147
4	Bud Dormancy in Perennial Fruit Tree Species: A Pivotal Role for Oxidative Cues. Frontiers in Plant Science, 2018, 9, 657.	3.6	133
5	Prunus genetics and applications after de novo genome sequencing: achievements and prospects. Horticulture Research, 2019, 6, 58.	6.3	121
6	Isolation and characterization of six peach cDNAs encoding key proteins in organic acid metabolism and solute accumulation: involvement in regulating peach fruit acidity. Physiologia Plantarum, 2002, 114, 259-270.	5.2	113
7	Genetic diversity, linkage disequilibrium, population structure and construction of a core collection of Prunus avium L. landraces and bred cultivars. BMC Plant Biology, 2016, 16, 49.	3.6	111
8	Genetic determinism of phenological traits highly affected by climate change in <i>Prunus avium</i> : flowering date dissected into chilling and heat requirements. New Phytologist, 2014, 202, 703-715.	7.3	104
9	The <i>Ma</i> Gene for Complete-Spectrum Resistance to <i>Meloidogyne</i> Species in <i>Prunus</i> Is a TNL with a Huge Repeated C-Terminal Post-LRR Region. Plant Physiology, 2011, 156, 779-792.	4.8	99
10	Analysis of genetic diversity and structure in a worldwide walnut (<i>Juglans regia</i> L.) germplasm using SSR markers. PLoS ONE, 2018, 13, e0208021.	2.5	86
11	Mapping of Candidate Genes Involved in Bud Dormancy and Flowering Time in Sweet Cherry (<i>Prunus</i>) Tj ETQq1 1 0,784314 rgBT /Ov	2.5	81
12	Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404.	2.8	75
13	Fruit size QTL identification and the prediction of parental QTL genotypes and breeding values in multiple pedigreed populations of sweet cherry. Molecular Breeding, 2013, 32, 875-887.	2.1	74
14	Construction and Comparative Analyses of Highly Dense Linkage Maps of Two Sweet Cherry Intra-Specific Progenies of Commercial Cultivars. PLoS ONE, 2013, 8, e54743.	2.5	64
15	From bud formation to flowering: transcriptomic state defines the cherry developmental phases of sweet cherry bud dormancy. BMC Genomics, 2019, 20, 974.	2.8	54
16	Phenotypic and fine genetic characterization of the D locus controlling fruit acidity in peach. BMC Plant Biology, 2009, 9, 59.	3.6	53
17	Saturating the Prunus (stone fruits) genome with candidate genes for fruit quality. Molecular Breeding, 2011, 28, 667-682.	2.1	53
18	Yield potential definition of the chilling requirement reveals likely underestimation of the risk of climate change on winter chill accumulation. International Journal of Biometeorology, 2019, 63, 183-192.	3.0	47

#	ARTICLE	IF	CITATIONS
19	Marker-assisted selection for the wide-spectrum resistance to root-knot nematodes conferred by the Ma gene from Myrobalan plum (<i>Prunus cerasifera</i>) in interspecific <i>Prunus</i> material. <i>Molecular Breeding</i> , 2004, 13, 113-124.	2.1	44
20	Characterization of the RMja gene for resistance to root-knot nematodes in almond: spectrum, location, and interest for <i>Prunus</i> breeding. <i>Tree Genetics and Genomes</i> , 2010, 6, 503-511.	1.6	43
21	New Insights into Fruit Firmness and Weight Control in Sweet Cherry. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 783-796.	1.8	39
22	Association and linkage mapping to unravel genetic architecture of phenological traits and lateral bearing in Persian walnut (<i>Juglans regia</i> L.). <i>BMC Genomics</i> , 2020, 21, 203.	2.8	37
23	A fruit firmness QTL identified on linkage group 4 in sweet cherry (<i>Prunus avium</i> L.) is associated with domesticated and bred germplasm. <i>Scientific Reports</i> , 2019, 9, 5008.	3.3	29
24	Rosaceae conserved orthologous sequences marker polymorphism in sweet cherry germplasm and construction of a SNP-based map. <i>Tree Genetics and Genomes</i> , 2012, 8, 237-247.	1.6	28
25	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
26	Development and mapping of peach candidate genes involved in fruit quality and their transferability and potential use in other Rosaceae species. <i>Tree Genetics and Genomes</i> , 2010, 6, 995-1012.	1.6	23
27	ChIP-seq and RNA-seq for complex and low-abundance tree buds reveal chromatin and expression co-dynamics during sweet cherry bud dormancy. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	20
28	Fine tuning of hormonal signaling is linked to dormancy status in sweet cherry flower buds. <i>Tree Physiology</i> , 2021, 41, 544-561.	3.1	20
29	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
30	Multi-year analyses on three populations reveal the first stable QTLs for tolerance to rain-induced fruit cracking in sweet cherry (<i>Prunus avium</i> L.). <i>Horticulture Research</i> , 2021, 8, 136.	6.3	16
31	3D characterization of walnut morphological traits using X-ray computed tomography. <i>Plant Methods</i> , 2020, 16, 115.	4.3	15
32	Sweet and Sour Cherries: Linkage Maps, QTL Detection and Marker Assisted Selection. , 2009, , 291-313.		14
33	Genome-Wide Association Study Reveals Candidate Genes Involved in Fruit Trait Variation in Persian Walnut (<i>Juglans regia</i> L.). <i>Frontiers in Plant Science</i> , 2020, 11, 607213.	3.6	12
34	Plum. , 2007, , 119-135.		10
35	Comparison of structure analyses and core collections for the management of walnut genetic resources. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	10
36	Genetic analysis of iron chlorosis tolerance in <i>Prunus</i> rootstocks. <i>Tree Genetics and Genomes</i> , 2012, 8, 943-955.	1.6	9

#	ARTICLE	IF	CITATIONS
37	New insights into flowering date in <i>Prunus</i> : fine mapping of a major QTL in sweet cherry. Horticulture Research, 2022, 9, .	6.3	8
38	Genomics Tools Across Rosaceae Species. , 2009, , 539-561.		7
39	The walnut genetic resources of INRA: chronological phenotypic data and ontology. BMC Research Notes, 2019, 12, 662.	1.4	3
40	Molecular Linkage Maps. , 2012, , 76-104.		1
41	Map-based Cloning of Single Gene Traits and Quantitative Traits. , 2012, , 212-243.		1