

# Elisabeth Dirlewanger

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

2,530  
citations

236833

25  
h-index

330025

37  
g-index

52  
all docs

52  
docs citations

52  
times ranked

2058  
citing authors

#	ARTICLE	IF	CITATIONS
1	New insights into flowering date in <i>Prunus</i> : fine mapping of a major QTL in sweet cherry. Horticulture Research, 2022, 9, .	2.9	8
2	Fine tuning of hormonal signaling is linked to dormancy status in sweet cherry flower buds. Tree Physiology, 2021, 41, 544-561.	1.4	20
3	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.). Horticulture Research, 2021, 8, 136.	2.9	16
4	Comparison of structure analyses and core collections for the management of walnut genetic resources. Tree Genetics and Genomes, 2020, 16, 1.	0.6	10
5	3D characterization of walnut morphological traits using X-ray computed tomography. Plant Methods, 2020, 16, 115.	1.9	15
6	Association and linkage mapping to unravel genetic architecture of phenological traits and lateral bearing in Persian walnut ( <i>Juglans regia</i> L.). BMC Genomics, 2020, 21, 203.	1.2	37
7	ChIP-seq and RNA-seq for complex and low-abundance tree buds reveal chromatin and expression co-dynamics during sweet cherry bud dormancy. Tree Genetics and Genomes, 2020, 16, 1.	0.6	20
8	Genome-Wide Association Study Reveals Candidate Genes Involved in Fruit Trait Variation in Persian Walnut ( <i>Juglans regia</i> L.). Frontiers in Plant Science, 2020, 11, 607213.	1.7	12
9	The walnut genetic resources of INRA: chronological phenotypic data and ontology. BMC Research Notes, 2019, 12, 662.	0.6	3
10	A fruit firmness QTL identified on linkage group 4 in sweet cherry ( <i>Prunus avium</i> L.) is associated with domesticated and bred germplasm. Scientific Reports, 2019, 9, 5008.	1.6	29
11	<i>Prunus</i> genetics and applications after de novo genome sequencing: achievements and prospects. Horticulture Research, 2019, 6, 58.	2.9	121
12	From bud formation to flowering: transcriptomic state defines the cherry developmental phases of sweet cherry bud dormancy. BMC Genomics, 2019, 20, 974.	1.2	54
13	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.	1.3	47
14	Walnut: past and future of genetic improvement. Tree Genetics and Genomes, 2018, 14, 1.	0.6	147
15	Analysis of genetic diversity and structure in a worldwide walnut ( <i>Juglans regia</i> L.) germplasm using SSR markers. PLoS ONE, 2018, 13, e0208021.	1.1	86
16	Bud Dormancy in Perennial Fruit Tree Species: A Pivotal Role for Oxidative Cues. Frontiers in Plant Science, 2018, 9, 657.	1.7	133
17	Integrated QTL detection for key breeding traits in multiple peach progenies. BMC Genomics, 2017, 18, 404.	1.2	75
18	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). Tree Genetics and Genomes, 2016, 12, 1.	0.6	28

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19	Genetic diversity, linkage disequilibrium, population structure and construction of a core collection of <i>Prunus avium</i> L. landraces and bred cultivars. <i>BMC Plant Biology</i> , 2016, 16, 49.	1.6	111
20	Mapping of Candidate Genes Involved in Bud Dormancy and Flowering Time in Sweet Cherry ( <i>Prunus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.1	81
21	New Insights into Fruit Firmness and Weight Control in Sweet Cherry. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 783-796.	1.0	39
22	Genetic determinism of phenological traits highly affected by climate change in <i>Prunus avium</i> : flowering date dissected into chilling and heat requirements. <i>New Phytologist</i> , 2014, 202, 703-715.	3.5	104
23	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
24	Construction and Comparative Analyses of Highly Dense Linkage Maps of Two Sweet Cherry Intra-Specific Progenies of Commercial Cultivars. <i>PLoS ONE</i> , 2013, 8, e54743.	1.1	64
25	Genetic analysis of iron chlorosis tolerance in <i>Prunus</i> rootstocks. <i>Tree Genetics and Genomes</i> , 2012, 8, 943-955.	0.6	9
26	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
27	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.	0.6	28
28	Molecular Linkage Maps. , 2012, , 76-104.		1
29	Map-based Cloning of Single Gene Traits and Quantitative Traits. , 2012, , 212-243.		1
30	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
31	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. <i>Plant Physiology</i> , 2011, 156, 779-792.	2.3	99
32	Characterization of the <i>RMja</i> 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.	0.6	43
33	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.	0.6	23
34	Phenotypic and fine genetic characterization of the D locus controlling fruit acidity in peach. <i>BMC Plant Biology</i> , 2009, 9, 59.	1.6	53
35	Genomics Tools Across Rosaceae Species. , 2009, , 539-561.		7
36	Sweet and Sour Cherries: Linkage Maps, QTL Detection and Marker Assisted Selection. , 2009, , 291-313.		14

#	ARTICLE	IF	CITATIONS
37	Plum. , 2007, , 119-135.		10
38	Mapping With a Few Plants: Using Selective Mapping for Microsatellite Saturation of the Prunus Reference Map. Genetics, 2005, 171, 1305-1309.	1.2	180
39	Marker-assisted selection for the wide-spectrum resistance to root-knot nematodes conferred by the Ma gene from Myrobalan plum (Prunus cerasifera) in interspecific Prunus material. Molecular Breeding, 2004, 13, 113-124.	1.0	44
40	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.	3.3	473
41	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.	2.6	113