

Diego Micheletti

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

5,139
citations

394421

19
h-index

580821

25
g-index

25
all docs

25
docs citations

25
times ranked

5396
citing authors

#	ARTICLE	IF	CITATIONS
1	On the Origin and Propagation of the COVID-19 Outbreak in the Italian Province of Trento, a Tourist Region of Northern Italy. <i>Viruses</i> , 2022, 14, 580.	3.3	1
2	Insights into the effect of human civilization on <i>Malus</i> evolution and domestication. <i>Plant Biotechnology Journal</i> , 2021, 19, 2206-2220.	8.3	23
3	Candidate gene mapping identifies genomic variations in the fire blight susceptibility genes HIPM and DIPM across the <i>Malus</i> germplasm. <i>Scientific Reports</i> , 2020, 10, 16317.	3.3	10
4	PhytoTypeDB: a database of plant protein inter-cultivar variability and function. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	1
5	Towards map-based cloning of FB_Mfu10: identification of a receptor-like kinase candidate gene underlying the <i>Malus fusca</i> fire blight resistance locus on linkage group 10. <i>Molecular Breeding</i> , 2018, 38, 106.	2.1	28
6	Genomic signatures of different adaptations to environmental stimuli between wild and cultivated <i>Vitis vinifera</i> L. <i>Horticulture Research</i> , 2018, 5, 34.	6.3	42
7	Genetic diversity, population structure, and linkage disequilibrium of elite and local apple accessions from Belgium using the IRSC array. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	31
8	High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. <i>Nature Genetics</i> , 2017, 49, 1099-1106.	21.4	693
9	Integrated QTL detection for key breeding traits in multiple peach progenies. <i>BMC Genomics</i> , 2017, 18, 404.	2.8	75
10	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
11	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.	6.3	68
12	Development and validation of the Axiom [®] Apple480K SNP genotyping array. <i>Plant Journal</i> , 2016, 86, 62-74.	5.7	156
13	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
14	ASSIST: an automatic SNP scoring tool for in- and outbreeding species. <i>Bioinformatics</i> , 2015, 31, 3873-3874.	4.1	45
15	Methods for the Design, Implementation, and Analysis of Illumina Infinium [®] SNP Assays in Plants. <i>Methods in Molecular Biology</i> , 2015, 1245, 281-298.	0.9	7
16	One-step reconstruction of multi-generation pedigree networks in apple (<i>Malus domestica</i> Borkh.) and the parentage of Golden Delicious. <i>Molecular Breeding</i> , 2014, 34, 511-524.	2.1	21
17	Recombination Rates and Genomic Shuffling in Human and Chimpanzee—A New Twist in the Chromosomal Speciation Theory. <i>Molecular Biology and Evolution</i> , 2013, 30, 853-864.	8.9	73
18	An Ancient Duplication of Apple MYB Transcription Factors Is Responsible for Novel Red Fruit-Flesh Phenotypes. <i>Plant Physiology</i> , 2012, 161, 225-239.	4.8	272

#	ARTICLE	IF	CITATIONS
19	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
20	High temperature reduces apple fruit colour via modulation of the anthocyanin regulatory complex. Plant, Cell and Environment, 2011, 34, 1176-1190.	5.7	330
21	Genetic diversity of the genus Malus and implications for linkage mapping with SNPs. Tree Genetics and Genomes, 2011, 7, 857-868.	1.6	51
22	On the evolutionary history of the domesticated apple. Nature Genetics, 2011, 43, 1044-1045.	21.4	11
23	The genome of the domesticated apple (<i>Malus domestica</i> Borkh.). Nature Genetics, 2010, 42, 833-839.	21.4	1,891
24	A SNP transferability survey within the genus Vitis. BMC Plant Biology, 2008, 8, 128.	3.6	40
25	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. PLoS ONE, 2007, 2, e1326.	2.5	945