

Diego Micheletti

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2000706/publications.pdf>

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	The genome of the domesticated apple (<i>Malus Æ— domestica</i> Borkh.). <i>Nature Genetics</i> , 2010, 42, 833-839.	21.4	1,891
2	A High Quality Draft Consensus Sequence of the Genome of a Heterozygous Grapevine Variety. <i>PLoS ONE</i> , 2007, 2, e1326.	2.5	945
3	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
4	High temperature reduces apple fruit colour via modulation of the anthocyanin regulatory complex. <i>Plant, Cell and Environment</i> , 2011, 34, 1176-1190.	5.7	330
5	An Ancient Duplication of Apple MYB Transcription Factors Is Responsible for Novel Red Fruit-Flesh Phenotypes Æ Æ. <i>Plant Physiology</i> , 2012, 161, 225-239.	4.8	272
6	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.	2.5	199
7	Development and validation of the Axiom ^Æ Apple480K <sc>SNP</sc> genotyping array. <i>Plant Journal</i> , 2016, 86, 62-74.	5.7	156
8	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
9	Integrated QTL detection for key breeding traits in multiple peach progenies. <i>BMC Genomics</i> , 2017, 18, 404.	2.8	75
10	Recombination Rates and Genomic Shuffling in Human and ChimpanzeeÆ”A New Twist in the Chromosomal Speciation Theory. <i>Molecular Biology and Evolution</i> , 2013, 30, 853-864.	8.9	73
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	Genetic diversity of the genus <i>Malus</i> and implications for linkage mapping with SNPs. <i>Tree Genetics and Genomes</i> , 2011, 7, 857-868.	1.6	51
13	ASSIsT: an automatic SNP scoring tool for in- and outbreeding species. <i>Bioinformatics</i> , 2015, 31, 3873-3874.	4.1	45
14	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
15	A SNP transferability survey within the genus <i>Vitis</i> . <i>BMC Plant Biology</i> , 2008, 8, 128.	3.6	40
16	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
17	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
18	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

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19	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
20	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
21	On the evolutionary history of the domesticated apple. <i>Nature Genetics</i> , 2011, 43, 1044-1045.	21.4	11
22	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
23	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
24	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
25	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