

Cassia da Silva Linge

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

606
citations

759233

12
h-index

839539

18
g-index

21
all docs

21
docs citations

21
times ranked

546
citing authors

#	ARTICLE	IF	CITATIONS
1	Feasibility of genomic prediction for brown rot (<i>Monilinia</i> spp.) resistance in peach. <i>Fruit Research</i> , 2022, 2, 1-12.	2.0	4
2	Multi-Locus Genome-Wide Association Studies Reveal Fruit Quality Hotspots in Peach Genome. <i>Frontiers in Plant Science</i> , 2021, 12, 644799.	3.6	18
3	Genome-Wide Association Study of Brown Rot (<i>Monilinia</i> spp.) Tolerance in Peach. <i>Frontiers in Plant Science</i> , 2021, 12, 635914.	3.6	17
4	Mapping and characterization QTLs for phenological traits in seven pedigree-connected peach families. <i>BMC Genomics</i> , 2021, 22, 187.	2.8	13
5	Identification and characterization of QTLs for fruit quality traits in peach through a multi-family approach. <i>BMC Genomics</i> , 2020, 21, 522.	2.8	25
6	RosBREED: bridging the chasm between discovery and application to enable DNA-informed breeding in rosaceous crops. <i>Horticulture Research</i> , 2020, 7, 177.	6.3	34
7	Mapping QTLs for phytochemical compounds and fruit quality in peach. <i>Molecular Breeding</i> , 2020, 40, 1.	2.1	15
8	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.	2.5	67
9	High-density multi-population consensus genetic linkage map for peach. <i>PLoS ONE</i> , 2018, 13, e0207724.	2.5	19
10	Linkage and association mapping for the slow softening (SWS) trait in peach (<i>P. persica</i> L. Batsch) fruit. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	1.6	9
11	Deletion of the miR172 target site in a <i>TOE</i> gene is a strong candidate variant for dominant double-flower trait in Rosaceae. <i>Plant Journal</i> , 2018, 96, 358-371.	5.7	43
12	Genome-enabled predictions for fruit weight and quality from repeated records in European peach progenies. <i>BMC Genomics</i> , 2017, 18, 432.	2.8	44
13	Exploring and exploiting phenotypic and genetic diversity in peach: identification of major genes and QTLs by GWAS. <i>Acta Horticulturae</i> , 2017, , 419-424.	0.2	1
14	Agro-morphological diversity in yam genotypes from Recncavo of Bahia, Brazil. <i>African Journal of Agricultural Research Vol Pp</i> , 2017, 12, 2070-2077.	0.5	2
15	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
16	GENETIC VARIABILITY AND POPULATION STRUCTURE OF PEACH ACCESSIONS FROM MAS.PES GERmplasm BANK. <i>Acta Horticulturae</i> , 2015, , 233-239.	0.2	0
17	Whole-Genome Analysis of Diversity and SNP-Major Gene Association in Peach Germplasm. <i>PLoS ONE</i> , 2015, 10, e0136803.	2.5	98
18	Genetic dissection of fruit weight and size in an F2 peach (<i>Prunus persica</i> (L.) Batsch) progeny. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	48

#	ARTICLE	IF	CITATIONS
19	Fine mapping and identification of a candidate gene for a major locus controlling maturity date in peach. BMC Plant Biology, 2013, 13, 166.	3.6	113