

Prisca ViehÄ¶ver

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

605
citations

933447

10
h-index

794594

19
g-index

22
all docs

22
docs citations

22
times ranked

904
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete pan-plastome sequences enable high resolution phylogenetic classification of sugar beet and closely related crop wild relatives. <i>BMC Genomics</i> , 2022, 23, 113.	2.8	10
2	Transcriptomic analysis of temporal shifts in berry development between two grapevine cultivars of the Pinot family reveals potential genes controlling ripening time. <i>BMC Plant Biology</i> , 2021, 21, 327.	3.6	8
3	Characterization of the Brassica napus Flavonol Synthase Gene Family Reveals Bifunctional Flavonol Synthases. <i>Frontiers in Plant Science</i> , 2021, 12, 733762.	3.6	24
4	RNA-Seq Time Series of Vitis vinifera Bud Development Reveals Correlation of Expression Patterns with the Local Temperature Profile. <i>Plants</i> , 2020, 9, 1548.	3.5	7
5	Genome Sequencing of <i>Musa acuminata</i> Dwarf Cavendish Reveals a Duplication of a Large Segment of Chromosome 2. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 37-42.	1.8	10
6	Genome Sequences of Both Organelles of the Grapevine Rootstock Cultivar 'Bârnâ€™™. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
7	High Contiguity de novo Genome Sequence Assembly of Trifoliolate Yam (<i>Dioscorea dumetorum</i>) Using Long Read Sequencing. <i>Genes</i> , 2020, 11, 274.	2.4	54
8	A Partially Phase-Separated Genome Sequence Assembly of the Vitis Rootstock 'Bârnâ€™™ (<i>Vitis riparia</i> L.) Tj ETQq0 0 0 rgBT /Over Science, 2020, 11, 156.	3.6	6
9	Selective egg cell polyspermy bypasses the triploid block. <i>ELife</i> , 2020, 9, .	6.0	24
10	Characterization of genes and alleles involved in the control of flowering time in grapevine. <i>PLoS ONE</i> , 2019, 14, e0214703.	2.5	9
11	Twenty-Five Years of Propagation in Suspension Cell Culture Results in Substantial Alterations of the Arabidopsis Thaliana Genome. <i>Genes</i> , 2019, 10, 671.	2.4	15
12	Repeat Composition of CenH3-chromatin and H3K9me2-marked heterochromatin in Sugar Beet (Beta) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.6	32
13	Rapid gene identification in sugar beet using deep sequencing of DNA from phenotypic pools selected from breeding panels. <i>BMC Genomics</i> , 2016, 17, 236.	2.8	26
14	Natural variation in flavonol accumulation in Arabidopsis is determined by the flavonol glucosyltransferase BGLU6. <i>Journal of Experimental Botany</i> , 2016, 67, 1505-1517.	4.8	67
15	A De Novo Genome Sequence Assembly of the Arabidopsis thaliana Accession Niederzenz-1 Displays Presence/Absence Variation and Strong Synteny. <i>PLoS ONE</i> , 2016, 11, e0164321.	2.5	63
16	Exploiting single-molecule transcript sequencing for eukaryotic gene prediction. <i>Genome Biology</i> , 2015, 16, 184.	8.8	148
17	The Structural Features of Thousands of T-DNA Insertion Sites Are Consistent with a Double-Strand Break Repair-Based Insertion Mechanism. <i>Molecular Plant</i> , 2015, 8, 1651-1664.	8.3	80
18	Draft Genome Sequence of Pseudomonas aeruginosa Strain WS394, a Multidrug-Resistant and Highly Cytotoxic Wound Isolate from Chronic Ulcus Cruris. <i>Genome Announcements</i> , 2014, 2, .	0.8	1

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19	Reliable In Silico Identification of Sequence Polymorphisms and Their Application for Extending the Genetic Map of Sugar Beet (<i>Beta vulgaris</i>). PLoS ONE, 2014, 9, e110113.	2.5	18