Carla Cristina Da Silva

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9469236/publications.pdf

Version: 2024-02-01

18 papers 384 citations

840776 11 h-index 888059 17 g-index

24 all docs

24 docs citations

times ranked

24

334 citing authors

#	Article	IF	CITATIONS
1	De Novo Assembly and Transcriptome Analysis of the Rubber Tree (Hevea brasiliensis) and SNP Markers Development for Rubber Biosynthesis Pathways. PLoS ONE, 2014, 9, e102665.	2.5	113
2	Leaf-, panel- and latex-expressed sequenced tags from the rubber tree (Hevea brasiliensis) under cold-stressed and suboptimal growing conditions: the development of gene-targeted functional markers for stress response. Molecular Breeding, 2014, 34, 1035-1053.	2.1	32
3	High-Resolution Genetic Map and QTL Analysis of Growth-Related Traits of Hevea brasiliensis Cultivated Under Suboptimal Temperature and Humidity Conditions. Frontiers in Plant Science, 2018, 9, 1255.	3.6	27
4	Development of single nucleotide polymorphism markers in the large and complex rubber tree genome using next-generation sequence data. Molecular Breeding, 2016, 36, 1.	2.1	22
5	Genome-wide approaches for the identification of markers and genes associated with sugarcane yellow leaf virus resistance. Scientific Reports, 2021, 11, 15730.	3.3	21
6	Linkage Disequilibrium and Population Structure in Wild and Cultivated Populations of Rubber Tree (Hevea brasiliensis). Frontiers in Plant Science, 2018, 9, 815.	3.6	20
7	Deep expression analysis reveals distinct cold-response strategies in rubber tree (Hevea brasiliensis). BMC Genomics, 2019, 20, 455.	2.8	19
8	Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. Scientific Reports, 2019, 9, 19936.	3.3	19
9	QTL detection for growth and latex production in a full-sib rubber tree population cultivated under suboptimal climate conditions. BMC Plant Biology, 2018, 18, 223.	3.6	18
10	Altered expression of the caffeine synthase gene in a naturally caffeine-free mutant of Coffea arabica. Genetics and Molecular Biology, 2009, 32, 802-810.	1.3	17
11	Leaf transcriptome of two highly divergent genotypes of Urochloa humidicola (Poaceae), a tropical polyploid forage grass adapted to acidic soils and temporary flooding areas. BMC Genomics, 2016, 17, 910.	2.8	15
12	Unravelling Rubber Tree Growth by Integrating GWAS and Biological Network-Based Approaches. Frontiers in Plant Science, 2021, 12, 768589.	3.6	14
13	Assisted-selection of naturally caffeine-free coffee cultivarsâ€"characterization of SNPs from a methyltransferase gene. Molecular Breeding, 2017, 37, 1.	2.1	13
14	Coexpression and Transcriptome analyses identify active Apomixis-related genes in Paspalum notatum leaves. BMC Genomics, 2020, 21, 78.	2.8	12
15	Extremophiles as a Model of a Natural Ecosystem: Transcriptional Coordination of Genes Reveals Distinct Selective Responses of Plants Under Climate Change Scenarios. Frontiers in Plant Science, 2018, 9, 1376.	3.6	10
16	Secondary origin, hybridization and sexual reproduction in a diploid–tetraploid contact zone of the facultatively apomictic orchidZygopetalum mackayi. Plant Biology, 2020, 22, 939-948.	3.8	4
17	Construction and analysis of a leaf cDNA library from cold stressed rubber tree clones. BMC Proceedings, $2011, 5, .$	1.6	1
18	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. Frontiers in Plant Science, 2021, 12, 736797.	3.6	1