

Raul Pirona

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3265715/publications.pdf>

Version: 2024-02-01

15
papers

1,816
citations

759233

12
h-index

996975

15
g-index

15
all docs

15
docs citations

15
times ranked

2537
citing authors

#	ARTICLE	IF	CITATIONS
1	The high-quality draft genome of peach (<i>Prunus persica</i>) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,031
2	Fine mapping and identification of a candidate gene for a major locus controlling maturity date in peach. <i>BMC Plant Biology</i> , 2013, 13, 166.	3.6	113
3	Genetic dissection of aroma volatile compounds from the essential oil of peach fruit: QTL analysis and identification of candidate genes using dense SNP maps. <i>Tree Genetics and Genomes</i> , 2013, 9, 189-204.	1.6	105
4	Extensive Maternal DNA Hypomethylation in the Endosperm of <i>Zea mays</i> . <i>Plant Cell</i> , 2004, 16, 510-522.	6.6	99
5	The ectopic expression of the rice <i>Osmyb4</i> gene in <i>Arabidopsis</i> increases tolerance to abiotic, environmental and biotic stresses. <i>Physiological and Molecular Plant Pathology</i> , 2006, 69, 26-42.	2.5	94
6	QTL mapping and candidate genes for resistance to <i>Fusarium</i> ear rot and fumonisin contamination in maize. <i>BMC Plant Biology</i> , 2017, 17, 20.	3.6	93
7	Maize Histone Deacetylase <i>hda101</i> Is Involved in Plant Development, Gene Transcription, and Sequence-Specific Modulation of Histone Modification of Genes and Repeats. <i>Plant Cell</i> , 2007, 19, 1145-1162.	6.6	68
8	QTL mapping for brown rot (<i>Monilinia fructigena</i>) resistance in an intraspecific peach (<i>Prunus persica</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.6	64
9	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
10	The <i>Zea mays</i> mutants opaque-2 and opaque-7 disclose extensive changes in endosperm metabolism as revealed by protein, amino acid, and transcriptome-wide analyses. <i>BMC Genomics</i> , 2011, 12, 41.	2.8	37
11	Expression profiling of genes involved in the formation of aroma in two peach genotypes. <i>Plant Biology</i> , 2013, 15, 443-451.	3.8	33
12	Epigenetic Variation, Inheritance, and Parent-of-Origin Effects of Cytosine Methylation in Maize (<i>Zea mays</i>). <i>Genetics</i> , 2014, 196, 653-666.	2.9	18
13	Uniparental and transgressive expression of $\hat{1}\pm$ -zeins in maize endosperm of $\alpha 2$ hybrid lines. <i>PLoS ONE</i> , 2018, 13, e0206993.	2.5	5
14	A CATALOG OF MOLECULAR DIVERSITY OF PRUNUS GERMPLASM GATHERED FROM ALIGNING NGS READS TO THE PEACH REFERENCE SEQUENCE: BIOINFORMATIC APPROACHES AND CHALLENGES. <i>Acta Horticulturae</i> , 2013, , 169-176.	0.2	4
15	Towards a Cardoon (<i>Cynara cardunculus</i> var. <i>altilis</i>)-Based Biorefinery: A Case Study of Improved Cell Cultures via Genetic Modulation of the Phenylpropanoid Pathway. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11978.	4.1	4