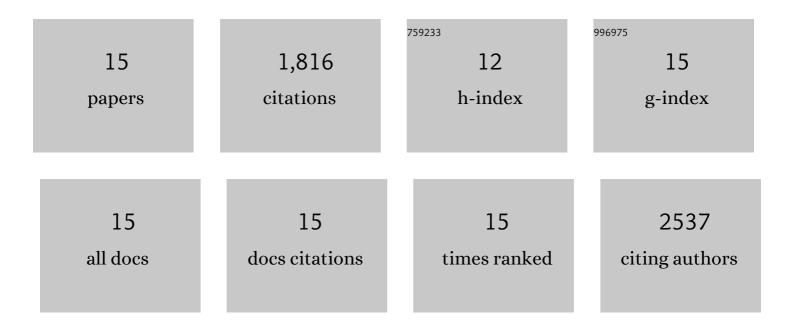
## **Raul Pirona**

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3265715/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Towards a Cardoon (Cynara cardunculus var. altilis)-Based Biorefinery: A Case Study of Improved Cell Cultures via Genetic Modulation of the Phenylpropanoid Pathway. International Journal of Molecular Sciences, 2021, 22, 11978.	4.1	4
2	Uniparental and transgressive expression of α-zeins in maize endosperm of o2 hybrid lines. PLoS ONE, 2018, 13, e0206993.	2.5	5
3	QTL mapping and candidate genes for resistance to Fusarium ear rot and fumonisin contamination in maize. BMC Plant Biology, 2017, 17, 20.	3.6	93
4	Genetic dissection of fruit weight and size in an F2 peach (Prunus persica (L.) Batsch) progeny. Molecular Breeding, 2015, 35, 1.	2.1	48
5	Epigenetic Variation, Inheritance, and Parent-of-Origin Effects of Cytosine Methylation in Maize ( <i>Zea mays</i> ). Genetics, 2014, 196, 653-666.	2.9	18
6	QTL mapping for brown rot (Monilinia fructigena) resistance in an intraspecific peach (Prunus persica) Tj ETQqO 0	0 rgBT /0 1.6	verlock 10 T
7	Expression profiling of genes involved in the formation of aroma in two peach genotypes. Plant Biology, 2013, 15, 443-451.	3.8	33
8	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
9	Genetic dissection of aroma volatile compounds from the essential oil of peach fruit: QTL analysis and identification of candidate genes using dense SNP maps. Tree Genetics and Genomes, 2013, 9, 189-204.	1.6	105

10	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	21.4	1,031
11	A CATALOG OF MOLECULAR DIVERSITY OF PRUNUS GERMPLASM GATHERED FROM ALIGNING NGS READS TO THE PEACH REFERENCE SEQUENCE: BIOINFORMATIC APPROACHES AND CHALLENGES. Acta Horticulturae, 2013, , 169-176.	0.2	4
12	The Zea mays mutants opaque-2 and opaque-7 disclose extensive changes in endosperm metabolism as revealed by protein, amino acid, and transcriptome-wide analyses. BMC Genomics, 2011, 12, 41.	2.8	37
13	Maize Histone Deacetylase hda101 Is Involved in Plant Development, Gene Transcription, and Sequence-Specific Modulation of Histone Modification of Genes and Repeats. Plant Cell, 2007, 19, 1145-1162.	6.6	68
14	The ectopic expression of the rice Osmyb4 gene in Arabidopsis increases tolerance to abiotic, environmental and biotic stresses. Physiological and Molecular Plant Pathology, 2006, 69, 26-42.	2.5	94
15	Extensive Maternal DNA Hypomethylation in the Endosperm of Zea mays. Plant Cell, 2004, 16, 510-522.	6.6	99