

Herman P Silva

List of Publications by Citations

Source: <https://exaly.com/author-pdf/7663613/herman-p-silva-publications-by-citations.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

67
papers

5,088
citations

27
h-index

71
g-index

71
ext. papers

5,775
ext. citations

5.7
avg, IF

4.67
L-index

#	Paper	IF	Citations
67	Active oxygen species in the induction of plant systemic acquired resistance by salicylic acid. <i>Science</i> , 1993 , 262, 1883-6	33.3	984
66	The genome of woodland strawberry (<i>Fragaria vesca</i>). <i>Nature Genetics</i> , 2011 , 43, 109-16	36.3	881
65	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, 487-94	36.3	777
64	Nitric oxide and salicylic acid signaling in plant defense. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 8849-55	11.5	561
63	NPR1 differentially interacts with members of the TGA/OBF family of transcription factors that bind an element of the PR-1 gene required for induction by salicylic acid. <i>Molecular Plant-Microbe Interactions</i> , 2000 , 13, 191-202	3.6	355
62	A rapid and efficient method for purifying high quality total RNA from peaches (<i>Prunus persica</i>) for functional genomics analyses. <i>Biological Research</i> , 2005 , 38, 83-8	7.6	155
61	Induction, modification, and transduction of the salicylic acid signal in plant defense responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 4134-7	11.5	142
60	Proteomic analysis of peach fruit mesocarp softening and chilling injury using difference gel electrophoresis (DIGE). <i>BMC Genomics</i> , 2010 , 11, 43	4.5	97
59	Protein dephosphorylation mediates salicylic acid-induced expression of PR-1 genes in tobacco. <i>Plant Journal</i> , 1997 , 11, 747-757	6.9	76
58	Transport of UDP-galactose in plants. Identification and functional characterization of AtUTr1, an <i>Arabidopsis thaliana</i> UDP-galactos/UDP-glucose transporter. <i>Journal of Biological Chemistry</i> , 2002 , 277, 32923-9	5.4	72
57	Identification of woolliness response genes in peach fruit after post-harvest treatments. <i>Journal of Experimental Botany</i> , 2008 , 59, 1973-86	7	66
56	Engineering disease and pest resistance in plants. <i>Trends in Microbiology</i> , 1998 , 6, 54-61	12.4	64
55	Comparative EST transcript profiling of peach fruits under different post-harvest conditions reveals candidate genes associated with peach fruit quality. <i>BMC Genomics</i> , 2009 , 10, 423	4.5	56
54	Construction and comparative analyses of highly dense linkage maps of two sweet cherry intra-specific progenies of commercial cultivars. <i>PLoS ONE</i> , 2013 , 8, e54743	3.7	54
53	Isolation and comparative analysis of the wheat TaPT2 promoter: identification in silico of new putative regulatory motifs conserved between monocots and dicots. <i>Journal of Experimental Botany</i> , 2007 , 58, 2573-82	7	52
52	Characterization of palo podrido, a natural process of delignification in wood. <i>Applied and Environmental Microbiology</i> , 1990 , 56, 65-74	4.8	46
51	Cracking in sweet cherries: A comprehensive review from a physiological, molecular, and genomic perspective. <i>Chilean Journal of Agricultural Research</i> , 2013 , 73, 66-72	1.9	43

50	Characterization of a new Arabidopsis mutant exhibiting enhanced disease resistance. <i>Molecular Plant-Microbe Interactions</i> , 1999 , 12, 1053-63	3.6	43
49	AtUTr1, a UDP-glucose/UDP-galactose transporter from Arabidopsis thaliana, is located in the endoplasmic reticulum and up-regulated by the unfolded protein response. <i>Journal of Biological Chemistry</i> , 2006 , 281, 9145-51	5.4	41
48	Transcriptional Responses of Chilean Quinoa (Willd.) Under Water Deficit Conditions Uncovers ABA-Independent Expression Patterns. <i>Frontiers in Plant Science</i> , 2017 , 8, 216	6.2	38
47	Growth and yield of chia (Salvia hispanica L.) in the Mediterranean and desert climates of Chile. <i>Chilean Journal of Agricultural Research</i> , 2016 , 76, 255-264	1.9	35
46	Identification of volatile compounds associated with the aroma of white strawberries (Fragaria chiloensis). <i>Journal of the Science of Food and Agriculture</i> , 2014 , 94, 752-9	4.3	30
45	Breeding in peach, cherry and plum: from a tissue culture, genetic, transcriptomic and genomic perspective. <i>Biological Research</i> , 2013 , 46, 219-30	7.6	30
44	Isolation and functional characterization of cold-regulated promoters, by digitally identifying peach fruit cold-induced genes from a large EST dataset. <i>BMC Plant Biology</i> , 2009 , 9, 121	5.3	30
43	Characterization of cytokinin signaling and homeostasis gene families in two hardwood tree species: Populus trichocarpa and Prunus persica. <i>BMC Genomics</i> , 2013 , 14, 885	4.5	28
42	Seasonal variation in the development of chilling injury in Henry peaches. <i>Scientia Horticulturae</i> , 2006 , 110, 79-83	4.1	28
41	Salares versus coastal ecotypes of quinoa: Salinity responses in Chilean landraces from contrasting habitats. <i>Plant Physiology and Biochemistry</i> , 2016 , 101, 1-13	5.4	27
40	Phosphate deficiency regulates phosphoenolpyruvate carboxylase expression in proteoid root clusters of white lupin. <i>Journal of Experimental Botany</i> , 2005 , 56, 145-53	7	25
39	Association between the concentration of n-alkanes and tolerance to cracking in commercial varieties of sweet cherry fruits. <i>Scientia Horticulturae</i> , 2015 , 197, 57-65	4.1	23
38	mRNA-seq reveals skeletal muscle atrophy in response to handling stress in a marine teleost, the red cusk-eel (Genypterus chilensis). <i>BMC Genomics</i> , 2015 , 16, 1024	4.5	23
37	Comparing salt-induced responses at the transcript level in a salares and coastal-lowlands landrace of quinoa (Chenopodium quinoa Willd). <i>Environmental and Experimental Botany</i> , 2017 , 139, 127-142	5.9	18
36	Genetic structure based on EST-SSR: a putative tool for fruit color selection in Japanese plum (Prunus salicina L.) breeding programs. <i>Molecular Breeding</i> , 2016 , 36, 1	3.4	16
35	Transcriptomic analysis of the hepatic response to stress in the red cusk-eel (Genypterus chilensis): Insights into lipid metabolism, oxidative stress and liver steatosis. <i>PLoS ONE</i> , 2017 , 12, e0176447	3.7	14
34	Nitrogen physiology of contrasting genotypes of Chenopodium quinoa Willd. (Amaranthaceae). <i>Scientific Reports</i> , 2018 , 8, 17524	4.9	14
33	Construction of a highly saturated linkage map in Japanese plum (Prunus salicina L.) using GBS for SNP marker calling. <i>PLoS ONE</i> , 2018 , 13, e0208032	3.7	14

32	Comparative genomics analysis in Prunoideae to identify biologically relevant polymorphisms. <i>Plant Biotechnology Journal</i> , 2013 , 11, 883-93	11.6	13
31	The Ca ²⁺ pump inhibitor, thapsigargin, inhibits root gravitropism in <i>Arabidopsis thaliana</i> . <i>Biological Research</i> , 2006 , 39, 289-96	7.6	12
30	<i>Arabidopsis thaliana</i> : a model host plant to study plant-pathogen interaction using Chilean field isolates of <i>Botrytis cinerea</i> . <i>Biological Research</i> , 2006 , 39, 221-8	7.6	11
29	RNA-seq Analysis of Salt-Stressed Non Salt-Stressed Transcriptomes of Landrace R49. <i>Genes</i> , 2019 , 10,	4.2	10
28	Sequencing and de novo assembly of the red cusk-eel (<i>Genypterus chilensis</i>) transcriptome. <i>Marine Genomics</i> , 2014 , 18 Pt B, 105-7	1.9	9
27	Characterization of the acetohydroxyacid synthase multigene family in the tetraploide plant <i>Chenopodium quinoa</i> . <i>Electronic Journal of Biotechnology</i> , 2015 , 18, 393-398	3.1	8
26	JUICE: a data management system that facilitates the analysis of large volumes of information in an EST project workflow. <i>BMC Bioinformatics</i> , 2006 , 7, 513	3.6	8
25	De novo transcriptome assembly of 'Angeleno' and 'Lamoon' Japanese plum cultivars (<i>Prunus salicina</i>). <i>Genomics Data</i> , 2016 , 9, 35-6		7
24	Effect of sowing date and water availability on growth of plants of chia (<i>Salvia hispanica</i> L) established in Chile. <i>PLoS ONE</i> , 2018 , 13, e0203116	3.7	6
23	Evaluation of Morpho-Physiological Traits Adjustment of Under Long-Term Groundwater Depletion in the Hyper-Arid Atacama Desert. <i>Frontiers in Plant Science</i> , 2018 , 9, 453	6.2	5
22	Regeneration of highland papaya () from anther culture. <i>Applications in Plant Sciences</i> , 2018 , 6, e01182	2.3	5
21	Genetic and morphological characterization of the endangered Austral papaya <i>Vasconcellea chilensis</i> (Planch. ex A. DC.) Solms. <i>Genetic Resources and Crop Evolution</i> , 2014 , 61, 1423-1432	2	4
20	Discovery of mutations in <i>Chenopodium quinoa</i> Willd through EMS mutagenesis and mutation screening using pre-selection phenotypic data and next-generation sequencing. <i>Journal of Agricultural Science</i> , 2018 , 156, 1196-1204	1	4
19	Genetic, cytological and molecular characterization of chia (<i>Salvia hispanica</i> L.) provenances. <i>Biochemical Systematics and Ecology</i> , 2017 , 73, 16-21	1.4	3
18	Characterization of the high-affinity phosphate transporter PHT1;4 gene promoter of <i>Arabidopsis thaliana</i> in transgenic wheat. <i>Biologia Plantarum</i> , 2017 , 61, 453-462	2.1	3
17	Present and future of marker-assisted breeding in sweet and sour cherry. <i>Acta Horticulturae</i> , 2019 , 1-14	0.3	3
16	Climatic zoning of chia (<i>Salvia hispanica</i> L.) in Chile using a species distribution model. <i>Spanish Journal of Agricultural Research</i> , 2017 , 15, e0302	1.1	3
15	A de novo transcriptome analysis revealed that photomorphogenic genes are required for carotenoid synthesis in the dark-grown carrot taproot. <i>Molecular Genetics and Genomics</i> , 2020 , 295, 1379-1392 ³	1.1	3

14	RNA-seq analysis of the head-kidney transcriptome response to handling-stress in the red cusk-eel (<i>Genypterus chilensis</i>). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017 , 24, 111-117	2	2
13	Profiling carbohydrate composition, biohydrogen capacity, and disease resistance in potato. <i>Electronic Journal of Biotechnology</i> , 2013 , 16,	3.1	2
12	Functional Genomics 2012 , 292-322		2
11	Biogeography, phylogenetic relationships and morphological analyses of the South American genus <i>Mutisia</i> L.f. (Asteraceae) shows early connections of two disjunct biodiversity hotspots. <i>Organisms Diversity and Evolution</i> , 2020 , 20, 639-656	1.7	2
10	Improved physiological performance in grapevine (<i>Vitis vinifera</i> L.) cv. Cabernet Sauvignon facing recurrent drought stress. <i>Australian Journal of Grape and Wine Research</i> , 2021 , 27, 258-268	2.4	2
9	A molecular marker approach using intron flanking EST-PCR to map candidate genes in peach (<i>Prunus persica</i>). <i>Electronic Journal of Biotechnology</i> , 2012 , 15,	3.1	1
8	Genome-Wide Analysis of Somatic Embryogenesis-Related Transcription Factors in Cultivated Strawberry (<i>Fragaria × ananassa</i>) and Evolutionary Relationships among Rosaceae Species. <i>Agronomy</i> , 2021 , 11, 356	3.6	1
7	Transcriptome datasets from leaves and fruits of the sweet cherry cultivars 'Bing', 'Lapins' and 'Rainier'. <i>Data in Brief</i> , 2019 , 23, 103696	1.2	0
6	Identification of a conserved set of cytokinin-responsive genes expressed in the fruits of <i>Prunus persica</i> . <i>Plant Growth Regulation</i> , 2020 , 92, 65-80	3.2	0
5	Pressure-volume curve traits of chia (<i>Salvia hispanica</i> L.): an assessment of water-stress tolerance under field conditions. <i>Irrigation Science</i> , 2021 , 39, 789	3.1	0
4	IDENTIFICATION OF SSRS WITH POLYMORPHISMS BETWEEN DIFFERENT PRUNUS AVIUM CULTIVARS. <i>Acta Horticulturae</i> , 2014 , 39-45	0.3	
3	Salicylic Acid- And Nitric Oxide-Mediated Signal Transduction In Disease Resistance 2001 , 201-207		
2	The Salicylic Acid Signal for Activation of Plant Defenses is Mediated by Active Oxygen Species <i>Current Plant Science and Biotechnology in Agriculture</i> , 1994 , 349-354		
1	An Upgraded, Highly Saturated Linkage Map of Japanese Plum (<i>Lindl.</i>), and Identification of a New Major Locus Controlling the Flavan-3-ol Composition in Fruits.. <i>Frontiers in Plant Science</i> , 2022 , 13, 805744	6.2	