Herman P Silva

List of Publications by Year in Descending Order

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

67	5,088	27	71
papers	citations	h-index	g-index
71	5,775 ext. citations	5.7	4.67
ext. papers		avg, IF	L-index

#	Paper	IF	Citations
67	An Upgraded, Highly Saturated Linkage Map of Japanese Plum (Lindl.), and Identification of a New Major Locus Controlling the Flavan-3-ol Composition in Fruits <i>Frontiers in Plant Science</i> , 2022 , 13, 8057	4 ⁶ 1 ²	
66	PressureNolume curve traits of chia (Salvia hispanica L.): an assessment of water-stress tolerance under field conditions. <i>Irrigation Science</i> , 2021 , 39, 789	3.1	О
65	Improved physiological performance in grapevine (Vitis vinifera L.) cv. Cabernet Sauvignon facing recurrent drought stress. <i>Australian Journal of Grape and Wine Research</i> , 2021 , 27, 258-268	2.4	2
64	Genome-Wide Analysis of Somatic Embryogenesis-Related Transcription Factors in Cultivated Strawberry (Fragaria Lananassa) and Evolutionary Relationships among Rosaceae Species. <i>Agronomy</i> , 2021 , 11, 356	3.6	1
63	Identification of a conserved set of cytokinin-responsive genes expressed in the fruits of Prunus persica. <i>Plant Growth Regulation</i> , 2020 , 92, 65-80	3.2	О
62	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, 137	9²:1392	<u>3</u>
61	Biogeography, phylogenetic relationships and morphological analyses of the South American genus Mutisia L.f. (Asteraceae) shows early connections of two disjunct biodiversity hotspots. <i>Organisms Diversity and Evolution</i> , 2020 , 20, 639-656	1.7	2
60	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	О
59	Present and future of marker-assisted breeding in sweet and sour cherry. Acta Horticulturae, 2019, 1-14	0.3	3
58	RNA-seq Analysis of Salt-Stressed Non Salt-Stressed Transcriptomes of Landrace R49. <i>Genes</i> , 2019 , 10,	4.2	10
57	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
56	Discovery of mutations in Chenopodium quinoa 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
55	Nitrogen physiology of contrasting genotypes of Chenopodium quinoa Willd. (Amaranthaceae). <i>Scientific Reports</i> , 2018 , 8, 17524	4.9	14
54	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
53	Regeneration of highland papaya () from anther culture. <i>Applications in Plant Sciences</i> , 2018 , 6, e01182	2.3	5
52	Effect of sowing date and water availability on growth of plants of chia (Salvia hispanica L) established in Chile. <i>PLoS ONE</i> , 2018 , 13, e0203116	3.7	6
51	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

(2013-2017)

50	Genetic, cytological and molecular characterization of chia (Salvia hispanica L.) provenances. <i>Biochemical Systematics and Ecology</i> , 2017 , 73, 16-21	1.4	3	
49	Characterization of the high-affinity phosphate transporter PHT1;4 gene promoter of Arabidopsis thaliana in transgenic wheat. <i>Biologia Plantarum</i> , 2017 , 61, 453-462	2.1	3	
48	RNA-seq analysis of the head-kidney transcriptome response to handling-stress in the red cusk-eel (Genypterus chilensis). <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2017 , 24, 111-117	2	2	
47	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	
46	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	
45	Climatic zoning of chia (Salvia hispanica L.) in Chile using a species distribution model. <i>Spanish Journal of Agricultural Research</i> , 2017 , 15, e0302	1.1	3	
44	De novo transcriptome assembly of 'Angeleno' and 'Lamoon' Japanese plum cultivars (Prunus salicina). <i>Genomics Data</i> , 2016 , 9, 35-6		7	
43	Genetic structure based on ESTBSR: 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	
42	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	
41	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	
40	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	
39	Characterization of the acetohydroxyacid synthase multigene family in the tetraploide plant Chenopodium quinoa. <i>Electronic Journal of Biotechnology</i> , 2015 , 18, 393-398	3.1	8	
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	Genetic and morphological characterization of the endangered Austral papaya Vasconcellea chilensis (Planch. ex A. DC.) Solms. <i>Genetic Resources and Crop Evolution</i> , 2014 , 61, 1423-1432	2	4	
36	Sequencing and de novo assembly of the red cusk-eel (Genypterus chilensis) transcriptome. <i>Marine Genomics</i> , 2014 , 18 Pt B, 105-7	1.9	9	
35	IDENTIFICATION OF SSRS WITH POLYMORPHISMS BETWEEN DIFFERENT PRUNUS AVIUM CULTIVARS. <i>Acta Horticulturae</i> , 2014 , 39-45	0.3		
34	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	
33	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	

32	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013 , 45, 487-94	36.3	777
31	Comparative genomics analysis in Prunoideae to identify biologically relevant polymorphisms. <i>Plant Biotechnology Journal</i> , 2013 , 11, 883-93	11.6	13
30	Profiling carbohydrate composition, biohydrogen capacity, and disease resistance in potato. <i>Electronic Journal of Biotechnology</i> , 2013 , 16,	3.1	2
29	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
28	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
27	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
26	A molecular marker approach using intron flanking EST-PCR to map candidate genes in peach (Prunus persica). <i>Electronic Journal of Biotechnology</i> , 2012 , 15,	3.1	1
25	Functional Genomics 2012 , 292-322		2
24	The genome of woodland strawberry (Fragaria vesca). <i>Nature Genetics</i> , 2011 , 43, 109-16	36.3	881
23	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
22	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
21	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
20	Identification of woolliness response genes in peach fruit after post-harvest treatments. <i>Journal of Experimental Botany</i> , 2008 , 59, 1973-86	7	66
19	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
18	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
17	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
16	Seasonal variation in the development of chilling injury in DHenry Deaches. <i>Scientia Horticulturae</i> , 2006 , 110, 79-83	4.1	28
15	Arabidopsis thaliana: a model host plant to study plant-pathogen interaction using Chilean field isolates of Botrytis cinerea. <i>Biological Research</i> , 2006 , 39, 221-8	7.6	11

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14	The Ca2+ pump inhibitor, thapsigargin, inhibits root gravitropism in Arabidopsis thaliana. <i>Biological Research</i> , 2006 , 39, 289-96	7.6	12
13	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
12	A rapid and efficient method for purifying high quality total RNA from peaches (Prunus persica) for functional genomics analyses. <i>Biological Research</i> , 2005 , 38, 83-8	7.6	155
11	Transport of UDP-galactose in plants. Identification and functional characterization of AtUTr1, an Arabidopsis thaliana UDP-galactos/UDP-glucose transporter. <i>Journal of Biological Chemistry</i> , 2002 , 277, 32923-9	5.4	72
10	Salicylic Acid- And Nitric Oxide-Mediated Signal Transduction In Disease Resistance 2001 , 201-207		
9	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
8	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
7	Characterization of a new Arabidopsis mutant exhibiting enhanced disease resistance. <i>Molecular Plant-Microbe Interactions</i> , 1999 , 12, 1053-63	3.6	43
6	Engineering disease and pest resistance in plants. <i>Trends in Microbiology</i> , 1998 , 6, 54-61	12.4	64
5	Protein dephosphorylation mediates salicylic acid-induced expression of PR-1 genes in tobacco. <i>Plant Journal</i> , 1997 , 11, 747-757	6.9	76
4	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
3	The Salicylic Acid Signal for Activation of Plant Defenses is Mediated by Active Oxygen Species Current Plant Science and Biotechnology in Agriculture, 1994, 349-354		
2	Active oxygen species in the induction of plant systemic acquired resistance by salicylic acid. <i>Science</i> , 1993 , 262, 1883-6	33.3	984
1	Characterization of palo podrido, a natural process of delignification in wood. <i>Applied and Environmental Microbiology</i> , 1990 , 56, 65-74	4.8	46