

# Claudio Meneses

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

1,590  
citations

279798

23  
h-index

377865

34  
g-index

79  
all docs

79  
docs citations

79  
times ranked

1846  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Gut Microbiome of the Vector <i>Lutzomyia longipalpis</i> Is Essential for Survival of <i>Leishmania infantum</i> . <i>MBio</i> , 2017, 8, .	4.1	115
2	Identification of candidate genes associated with mealiness and maturity date in peach [ <i>Prunus persica</i> (L.) Batsch] using QTL analysis and deep sequencing. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	82
3	Monitoring the sensorial quality and aroma through an electronic nose in peaches during cold storage. <i>Journal of the Science of Food and Agriculture</i> , 2008, 88, 2073-2078.	3.5	62
4	Transcriptomic analysis of fruit stored under cold conditions using controlled atmosphere in <i>Prunus persica</i> cv. "Red Pearl". <i>Frontiers in Plant Science</i> , 2015, 6, 788.	3.6	50
5	Biochemical and physiological study of the firmness of table grape berries. <i>Postharvest Biology and Technology</i> , 2014, 93, 15-23.	6.0	46
6	Primary Metabolism in Avocado Fruit. <i>Frontiers in Plant Science</i> , 2019, 10, 795.	3.6	45
7	A codominant diagnostic marker for the slow ripening trait in peach. <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	44
8	Identification of Metabolite and Lipid Profiles in a Segregating Peach Population Associated with Mealiness in <i>Prunus persica</i> (L.) Batsch. <i>Metabolites</i> , 2020, 10, 154.	2.9	44
9	Expression QTL (eQTLs) Analyses Reveal Candidate Genes Associated With Fruit Flesh Softening Rate in Peach [ <i>Prunus persica</i> (L.) Batsch]. <i>Frontiers in Plant Science</i> , 2019, 10, 1581.	3.6	41
10	Non-destructive monitoring of flesh softening in the black-skinned Japanese plums "Angelena" and "Autumn beauty" on-tree and postharvest. <i>Postharvest Biology and Technology</i> , 2011, 61, 35-40.	6.0	40
11	New insights into the heterogeneous ripening in Hass avocado via LC-MS/MS proteomics. <i>Postharvest Biology and Technology</i> , 2017, 132, 51-61.	6.0	38
12	In-Depth Genomic and Phenotypic Characterization of the Antarctic Psychrotolerant Strain <i>Pseudomonas</i> sp. MPC6 Reveals Unique Metabolic Features, Plasticity, and Biotechnological Potential. <i>Frontiers in Microbiology</i> , 2019, 10, 1154.	3.5	36
13	Integration of proteomics and metabolomics data of early and middle season Hass avocados under heat treatment. <i>Food Chemistry</i> , 2019, 289, 512-521.	8.2	35
14	Quantitative determination of flesh mealiness in peach [ <i>Prunus persica</i> L. (Batch.)] through paper absorption of free juice. <i>Postharvest Biology and Technology</i> , 2009, 51, 118-121.	6.0	32
15	Identification and Evaluation of Long Noncoding RNAs in Response to Handling Stress in Red Cusk-Eel ( <i>Genypterus chilensis</i> ) via RNA-seq. <i>Marine Biotechnology</i> , 2020, 22, 94-108.	2.4	31
16	High-density genetic map and QTL analysis of soluble solid content, maturity date, and mealiness in peach using genotyping by sequencing. <i>Scientia Horticulturae</i> , 2019, 257, 108734.	3.6	30
17	mRNA-seq reveals skeletal muscle atrophy in response to handling stress in a marine teleost, the red cusk-eel ( <i>Genypterus chilensis</i> ). <i>BMC Genomics</i> , 2015, 16, 1024.	2.8	29
18	Copper-induced overexpression of genes encoding antioxidant system enzymes and metallothioneins involve the activation of CaMs, CDPKs and MEK1/2 in the marine alga <i>Ulva compressa</i> . <i>Aquatic Toxicology</i> , 2016, 177, 433-440.	4.0	29

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19	Using genomics to improve fruit quality. <i>Biological Research</i> , 2013, 46, 347-352.	3.4	28
20	The Endophytic Fungus <i>Chaetomium cupreum</i> Regulates Expression of Genes Involved in the Tolerance to Metals and Plant Growth Promotion in <i>Eucalyptus globulus</i> Roots. <i>Microorganisms</i> , 2019, 7, 490.	3.6	28
21	A <i>Prunus persica</i> genome-wide RNA-seq approach uncovers major differences in the transcriptome among chilling injury sensitive and non-sensitive varieties. <i>Physiologia Plantarum</i> , 2019, 166, 772-793.	5.2	28
22	A RAD-based linkage map of kiwifruit ( <i>Actinidia chinensis</i> Pl.) as a tool to improve the genome assembly and to scan the genomic region of the gender determinant for the marker-assisted breeding. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	27
23	Dormant but Active: Chilling Accumulation Modulates the Epigenome and Transcriptome of <i>Prunus avium</i> During Bud Dormancy. <i>Frontiers in Plant Science</i> , 2020, 11, 1115.	3.6	27
24	Effect of harvest maturity stage on the sensory quality of "Palsteyn" apricot ( <i>Prunus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 828-832.	1.9	26
25	SENSORY QUALITY PERFORMANCE OF TWO NECTARINE FLESH TYPOLOGIES EXPOSED TO DISTANT MARKET CONDITIONS. <i>Journal of Food Quality</i> , 2008, 31, 526-535.	2.6	25
26	Transcriptome analysis during ripening of table grape berry cv. Thompson Seedless. <i>PLoS ONE</i> , 2018, 13, e0190087.	2.5	23
27	Orchid Mycorrhizal Interactions on the Pacific Side of the Andes from Chile. A Review. <i>Journal of Soil Science and Plant Nutrition</i> , 2019, 19, 187-202.	3.4	23
28	Reference gene selection for quantitative real-time PCR in <i>Solanum lycopersicum</i> L. inoculated with the mycorrhizal fungus <i>Rhizophagus irregularis</i> . <i>Plant Physiology and Biochemistry</i> , 2016, 101, 124-131.	5.8	22
29	Preconditioning treatment maintains taste characteristic perception of ripe "September Sun" peach following cold storage. <i>International Journal of Food Science and Technology</i> , 2009, 44, 1011-1016.	2.7	20
30	WRKY7, -11 and -17 transcription factors are modulators of the bZIP28 branch of the unfolded protein response during PAMP-triggered immunity in <i>Arabidopsis thaliana</i> . <i>Plant Science</i> , 2018, 277, 242-250.	3.6	20
31	The transcription factor SlyA from <i>Salmonella Typhimurium</i> regulates genes in response to hydrogen peroxide and sodium hypochlorite. <i>Research in Microbiology</i> , 2018, 169, 263-278.	2.1	20
32	De novo assembly of <i>Persea americana</i> cv. "Hass" transcriptome during fruit development. <i>BMC Genomics</i> , 2019, 20, 108.	2.8	20
33	Variability in Genomic and Virulent Properties of <i>Porphyromonas gingivalis</i> Strains Isolated From Healthy and Severe Chronic Periodontitis Individuals. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 246.	3.9	19
34	Copper-induced increased expression of genes involved in photosynthesis, carotenoid synthesis and C assimilation in the marine alga <i>Ulva compressa</i> . <i>BMC Genomics</i> , 2018, 19, 829.	2.8	18
35	A first insight into the structure and function of rhizosphere microbiota in Antarctic plants using shotgun metagenomic. <i>Polar Biology</i> , 2019, 42, 1825-1835.	1.2	18
36	Identification of SNPs and InDels associated with berry size in table grapes integrating genetic and transcriptomic approaches. <i>BMC Plant Biology</i> , 2020, 20, 365.	3.6	18

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37	Can metabolites at harvest be used as physiological markers for modelling the softening behaviour of Chilean Hass avocados destined to local and distant markets?. <i>Postharvest Biology and Technology</i> , 2021, 174, 111457.	6.0	18
38	Comparative Study of Two Table Grape Varieties with Contrasting Texture during Cold Storage. <i>Molecules</i> , 2015, 20, 3667-3680.	3.8	17
39	The Transcription Factor ArcA Modulates Salmonella's Metabolism in Response to Neutrophil Hypochlorous Acid-Mediated Stress. <i>Frontiers in Microbiology</i> , 2019, 10, 2754.	3.5	17
40	Transcriptomic analysis of the hepatic response to stress in the red cusk-eel ( <i>Genypterus chilensis</i> ): Insights into lipid metabolism, oxidative stress and liver steatosis. <i>PLoS ONE</i> , 2017, 12, e0176447.	2.5	17
41	bZIP17 regulates the expression of genes related to seed storage and germination, reducing seed susceptibility to osmotic stress. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 6857-6868.	2.6	16
42	A catechol oxidase AcPPO from cherimoya ( <i>Annona cherimola</i> Mill.) is localized to the Golgi apparatus. <i>Plant Science</i> , 2018, 266, 46-54.	3.6	16
43	Early transcriptomic responses associated with the membrane-initiated action of cortisol in the skeletal muscle of rainbow trout ( <i>Oncorhynchus mykiss</i> ). <i>Physiological Genomics</i> , 2019, 51, 596-606.	2.3	15
44	Genetic diversity of wild species and cultivated varieties of alstroemeria estimated through morphological descriptors and RAPD markers. <i>Scientia Horticulturae</i> , 2006, 108, 86-90.	3.6	14
45	New steps in mucilage biosynthesis revealed by analysis of the transcriptome of the UDP-rhamnose/UDP-galactose transporter 2 mutant. <i>Journal of Experimental Botany</i> , 2019, 70, 5071-5088.	4.8	14
46	Identification of a novel long noncoding RNA that promotes osteoblast differentiation. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 7657-7666.	2.6	13
47	Floral scent evaluation of segregating lines of <i>Alstroemeria caryophyllaea</i> . <i>Scientia Horticulturae</i> , 2015, 185, 183-192.	3.6	12
48	Draft Whole Genome Sequence Analyses on <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> Hypersensitive Response Negative Strains Detected from Kiwifruit Bleeding Sap Samples. <i>Phytopathology</i> , 2018, 108, 552-560.	2.2	12
49	Cell wall and metabolite composition of berries of <i>Vitis vinifera</i> (L.) cv. Thompson Seedless with different firmness. <i>Food Chemistry</i> , 2018, 268, 492-497.	8.2	12
50	Contrasting grapevines grafted into naturalized rootstock suggest scion-driven transcriptomic changes in response to water deficit. <i>Scientia Horticulturae</i> , 2020, 262, 109031.	3.6	12
51	Identification of DNA Methylation and Transcriptomic Profiles Associated With Fruit Mealiness in <i>Prunus persica</i> (L.) Batsch. <i>Frontiers in Plant Science</i> , 2021, 12, 684130.	3.6	12
52	Ripe nectarines segregated through sensory quality evaluation and electronic nose assessment. <i>Fruits</i> , 2011, 66, 109-119.	0.4	11
53	Transcriptomic study of pedicels from GA3-treated table grape genotypes with different susceptibility to berry drop reveals responses elicited in cell wall yield, primary growth and phenylpropanoids synthesis. <i>BMC Plant Biology</i> , 2020, 20, 66.	3.6	10
54	RNA-seq analysis of compensatory growth in the skeletal muscle of fine flounder ( <i>Paralichthys</i> )	3.5	9

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55	PRESENT SITUATION OF PEACH BREEDING PROGRAMS: POST HARVEST AND FRUIT QUALITY ASSESSMENT. <i>Acta Horticulturae</i> , 2006, , 121-124.	0.2	8
56	Transcriptome and hormone analyses reveals differences in physiological age of "Hass" avocado fruit. <i>Postharvest Biology and Technology</i> , 2022, 185, 111806.	6.0	8
57	Phenolics contents and sensory characterisation of melting and non-melting peach. <i>Journal of Horticultural Science and Biotechnology</i> , 2011, 86, 255-260.	1.9	7
58	Draft Genome Sequence of the Phenol-Degrading Bacterium <i>Pseudomonas putida</i> H. <i>Genome Announcements</i> , 2015, 3, .	0.8	7
59	Evaluating the genetic structure of wild and commercial red cusk-eel ( <i>Genypterus chilensis</i> ) populations through the development of novel microsatellite markers from a reference transcriptome. <i>Molecular Biology Reports</i> , 2019, 46, 5875-5882.	2.3	7
60	A RAD-BASED LINKAGE MAP OF KIWIFRUIT ( <i>ACTINIDIA CHINENSIS</i> PL.) AND MAP POSITION OF GENETIC DETERMINANTS OF TRAITS OF INTEREST TO BREEDERS. <i>Acta Horticulturae</i> , 2015, , 191-198.	0.2	6
61	RNA-seq analysis of the head-kidney transcriptome response to handling-stress in the red cusk-eel ( <i>Genypterus blacodes</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq0 0 0 1.0 6	1.0	6
62	Development of a molecular marker for self-incompatible S4 haplotype in sweet cherry ( <i>Prunus avium</i> ) Tj ETQq0 0 0 1.9 6	1.9	6
63	Origin, genomic diversity and microevolution of the <i>Clostridium difficile</i> B1/NAP1/RT027/ST01 strain in Costa Rica, Chile, Honduras and Mexico. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
64	Metabolomic and biochemical analysis of mesocarp tissues from table grape berries with contrasting firmness reveals cell wall modifications associated to harvest and cold storage. <i>Food Chemistry</i> , 2022, 389, 133052.	8.2	6
65	PRELIMINARY STUDY ON EDIBLE FILM WITH A NATURAL PLANT EXTRACT TO IMPROVE QUALITY OF FRESH FRUITS FOR SUPPLY CHAINS. <i>Acta Horticulturae</i> , 2006, , 617-622.	0.2	5
66	Transcriptome Profiles of Contrasting Potato ( <i>Solanum tuberosum</i> L.) Genotypes Under Water Stress. <i>Agronomy</i> , 2019, 9, 848.	3.0	5
67	RNA-Seq-Based Analysis of Cortisol-Induced Differential Gene Expression Associated with <i>Piscirickettsia salmonis</i> Infection in Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Myotubes. <i>Animals</i> , 2021, 11, 2399.	2.3	5
68	Pre-Anthesis Cytokinin Applications Increase Table Grape Berry Firmness by Modulating Cell Wall Polysaccharides. <i>Plants</i> , 2021, 10, 2642.	3.5	5
69	De Novo Transcriptome Sequencing in Kiwifruit ( <i>Actinidia chinensis</i> var. <i>deliciosa</i> (A Chev) Liang et) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq0 0 0 3.0 4	3.0	4
70	Rapid sequence modification in the highly polymorphic region (HPR) of the hemagglutinin gene of the infectious salmon anaemia virus (ISAV) suggests intra-segmental template switching recombination. <i>Journal of Fish Diseases</i> , 2020, 43, 1483-1496.	1.9	3
71	Unravelling the Molecular Regulation Mechanisms of Slow Ripening Trait in <i>Prunus persica</i> . <i>Plants</i> , 2021, 10, 2380.	3.5	3
72	A draft genome of <i>Prunus avium</i> "Karina"™ as a tool for genomic studies. <i>Acta Horticulturae</i> , 2019, , 85-92.	0.2	2

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73	De novo Assembly and Analysis of Tissue-Specific Transcriptomes of the Edible Red Sea Urchin <i>Loxechinus albus</i> Using RNA-Seq. <i>Biology</i> , 2021, 10, 995.	2.8	2
74	Genome Sequence of <i>Clostridium paraputrificum</i> 373-A1 Isolated in Chile from a Patient Infected with <i>Clostridium difficile</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	1
75	Exploratory quantitative trait locus analysis for fruit-related traits in kiwifruit ( <i>Actinidia chinensis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.2	1
76	Proteomics analysis reveals new insights into surface pitting of sweet cherry cultivars displaying contrasting susceptibility. <i>Journal of Horticultural Science and Biotechnology</i> , 2022, 97, 615-625.	1.9	1
77	Genome sequence of two members of the chloroaromatic-degrading MT community: <i>Pseudomonas reinekei</i> MT1 and <i>Achromobacter xylosoxidans</i> MT3. <i>Journal of Biotechnology</i> , 2018, 275, 13-16.	3.8	0
78	Single-base resolution of the methylome in sweet cherry ( <i>Prunus avium</i> L.) during dormancy. <i>Acta Horticulturae</i> , 2019, , 401-406.	0.2	0
79	Modeling the softening behavior of Chilean Hass avocado to commercially segregate different batches destined for local and distant markets. <i>Acta Horticulturae</i> , 2021, , 571-576.	0.2	0