

VerÃ³nica Cambiazo

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

1,695
citations

279798

23
h-index

289244

40
g-index

48
all docs

48
docs citations

48
times ranked

2117
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.4	215
2	Structure and co-occurrence patterns in microbial communities under acute environmental stress reveal ecological factors fostering resilience. <i>Scientific Reports</i> , 2018, 8, 5875.	3.3	123
3	Proteomic analysis of peach fruit mesocarp softening and chilling injury using difference gel electrophoresis (DIGE). <i>BMC Genomics</i> , 2010, 11, 43.	2.8	107
4	Transcriptional response of Atlantic salmon families to <i>Piscirickettsia salmonis</i> infection highlights the relevance of the iron-deprivation defence system. <i>BMC Genomics</i> , 2015, 16, 495.	2.8	94
5	Metallothionein is crucial for safe intracellular copper storage and cell survival at normal and supra-physiological exposure levels. <i>Biochemical Journal</i> , 2004, 378, 617-624.	3.7	92
6	Identification of woolliness response genes in peach fruit after post-harvest treatments. <i>Journal of Experimental Botany</i> , 2008, 59, 1973-1986.	4.8	78
7	Copper exposure modifies the content and distribution of trace metals in mammalian cultured cells. <i>BioMetals</i> , 2003, 16, 169-174.	4.1	75
8	Gene expression profiling analysis of copper homeostasis in <i>Arabidopsis thaliana</i> . <i>Biochemical and Biophysical Research Communications</i> , 2010, 393, 248-252.	2.1	72
9	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.	2.8	63
10	The bioleaching potential of a bacterial consortium. <i>Bioresource Technology</i> , 2016, 218, 659-666.	9.6	63
11	Complete genome sequence of <i>Piscirickettsia salmonis</i> LF-89 (ATCC VR-1361) a major pathogen of farmed salmonid fish. <i>Journal of Biotechnology</i> , 2015, 212, 30-31.	3.8	54
12	Interplay between copper and zinc homeostasis through the transcriptional regulator Zur in <i>Enterococcus faecalis</i> . <i>Metallomics</i> , 2015, 7, 1137-1145.	2.4	35
13	Soil Bacterial Communities From the Chilean Andean Highlands: Taxonomic Composition and Culturability. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 10.	4.1	34
14	Regulatory network for cell shape changes during <i>Drosophila</i> ventral furrow formation. <i>Journal of Theoretical Biology</i> , 2006, 239, 49-62.	1.7	33
15	Genomic-Based Restriction Enzyme Selection for Specific Detection of <i>Piscirickettsia salmonis</i> by 16S rDNA PCR-RFLP. <i>Frontiers in Microbiology</i> , 2016, 7, 643.	3.5	33
16	The Role of Fur in the Transcriptional and Iron Homeostatic Response of <i>Enterococcus faecalis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1580.	3.5	32
17	Bacterial communities associated to Chilean altiplanic native plants from the Andean grasslands soils. <i>Scientific Reports</i> , 2019, 9, 1042.	3.3	32
18	DMAP α 85: A β -Like Protein from <i>Drosophila melanogaster</i> Larvae. <i>Journal of Neurochemistry</i> , 1995, 64, 1288-1297.	3.9	31

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19	Transcriptomic response of <i>Enterococcus faecalis</i> to iron excess. <i>BioMetals</i> , 2012, 25, 737-747.	4.1	31
20	Seasonal variation in the development of chilling injury in 'Henry' peaches. <i>Scientia Horticulturae</i> , 2006, 110, 79-83.	3.6	30
21	Effects of postharvest treatments on gene expression in <i>Prunus persica</i> fruit: Normal and altered ripening. <i>Postharvest Biology and Technology</i> , 2013, 75, 125-134.	6.0	30
22	Microbiome analysis and bacterial isolation from Leja Lake soil in Atacama Desert. <i>Extremophiles</i> , 2018, 22, 665-673.	2.3	30
23	Transcriptomic Changes of <i>Piscirickettsia salmonis</i> During Intracellular Growth in a Salmon Macrophage-Like Cell Line. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 426.	3.9	27
24	Genome-wide transcriptome analysis of the adaptive response of <i>Enterococcus faecalis</i> to copper exposure. <i>BioMetals</i> , 2010, 23, 1105-1112.	4.1	24
25	Cop-like operon: Structure and organization in species of the Lactobacillale order. <i>Biological Research</i> , 2006, 39, 87-93.	3.4	23
26	<i>Piscirickettsia salmonis</i> Cryptic Plasmids: Source of Mobile DNA and Virulence Factors. <i>Pathogens</i> , 2019, 8, 269.	2.8	23
27	Genome wide identification of <i>Acidithiobacillus ferrooxidans</i> (ATCC 23270) transcription factors and comparative analysis of ArsR and MerR metal regulators. <i>BioMetals</i> , 2012, 25, 75-93.	4.1	21
28	Genome-scale metabolic models of <i>Microbacterium</i> species isolated from a high altitude desert environment. <i>Scientific Reports</i> , 2020, 10, 5560.	3.3	19
29	The β -isoform of heat shock protein hsp-90 is structurally related with human microtubule-interacting protein Mip-90. <i>FEBS Letters</i> , 1999, 457, 343-347.	2.8	17
30	Analysis of <i>Piscirickettsia salmonis</i> Metabolism Using Genome-Scale Reconstruction, Modeling, and Testing. <i>Frontiers in Microbiology</i> , 2017, 8, 2462.	3.5	17
31	Global Proteomic Profiling of <i>Piscirickettsia salmonis</i> and Salmon Macrophage-Like Cells during Intracellular Infection. <i>Microorganisms</i> , 2020, 8, 1845.	3.6	17
32	Overexpression of amyloid precursor protein increases copper content in HEK293 cells. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 740-744.	2.1	15
33	Genes encoding novel secreted and transmembrane proteins are temporally and spatially regulated during <i>Drosophila melanogaster</i> embryogenesis. <i>BMC Biology</i> , 2009, 7, 61.	3.8	12
34	Identification of genes expressed during <i>Drosophila melanogaster</i> gastrulation by using subtractive hybridization. <i>Gene</i> , 2005, 345, 213-224.	2.2	10
35	Microtubule binding of the <i>Drosophila</i> DMAP-85 protein is regulated by phosphorylation in vitro. <i>FEBS Letters</i> , 2000, 483, 37-42.	2.8	9
36	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.	2.6	9

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37	Complete genome sequence of <i>Microbacterium</i> sp. CGR1, bacterium tolerant to wide abiotic conditions isolated from the Atacama Desert. <i>Journal of Biotechnology</i> , 2015, 216, 149-150.	3.8	8
38	PCR-RFLP Detection and Genogroup Identification of <i>Piscirickettsia salmonis</i> in Field Samples. <i>Pathogens</i> , 2020, 9, 358.	2.8	8
39	Comparative gene expression analysis of Dtg, a novel target gene of Dpp signaling pathway in the early <i>Drosophila melanogaster</i> embryo. <i>Gene</i> , 2014, 535, 210-217.	2.2	7
40	Tubulin domains for the interaction of microtubule associated protein DMAP-85 from <i>Drosophila melanogaster</i> . <i>Molecular and Cellular Biochemistry</i> , 1996, 158, 149-59.	3.1	6
41	Gene expression profiling in wild-type and metallothionein mutant fibroblast cell lines. <i>Biological Research</i> , 2006, 39, 125-42.	3.4	6
42	Physiological copper exposure in Jurkat cells induces changes in the expression of genes encoding cholesterol biosynthesis proteins. <i>BioMetals</i> , 2013, 26, 1033-1040.	4.1	6
43	Target genes of Dpp/BMP signaling pathway revealed by transcriptome profiling in the early <i>D. melanogaster</i> embryo. <i>Gene</i> , 2016, 591, 191-200.	2.2	6
44	Spatial and temporal distribution of Patched-related protein in the <i>Drosophila</i> embryo. <i>Gene Expression Patterns</i> , 2015, 19, 120-128.	0.8	5
45	The dorsoventral patterning of <i>Musca domestica</i> embryos: insights into BMP/Dpp evolution from the base of the lower cyclorraphan flies. <i>EvoDevo</i> , 2018, 9, 13.	3.2	5
46	Molecular characterization of a novel patched-related protein in <i>Apis mellifera</i> and <i>Drosophila melanogaster</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2008, 68, 156-170.	1.5	4
47	Nutrient Scarcity in a New Defined Medium Reveals Metabolic Resistance to Antibiotics in the Fish Pathogen <i>Piscirickettsia salmonis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 734239.	3.5	4
48	Expression pattern of DMAP-85 during <i>Drosophila</i> embryonic development. <i>Mechanisms of Development</i> , 2001, 108, 197-201.	1.7	0