

Juan Caballero Perez

List of Publications by Year in descending order

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papers

2,873
citations

394421

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docs citations

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5721
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Metatranscriptome Analysis of the Reef-Building Holobiont <i>Millepora complanata</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	2
2	Deep microbial community profiling along the fermentation process of pulque, a biocultural resource of Mexico. <i>Microbiological Research</i> , 2020, 241, 126593.	5.3	23
3	Multi-organ transcriptomic landscape of <i>Ambystoma velasci</i> metamorphosis. <i>Developmental Biology</i> , 2020, 466, 22-35.	2.0	6
4	Analysis of tRNACys processing under salt stress in <i>Bacillus subtilis</i> spore outgrowth using RNA sequencing data. <i>F1000Research</i> , 2020, 9, 501.	1.6	0
5	Comparative Analysis of the Soluble Proteome and the Cytolytic Activity of Unbleached and Bleached <i>Millepora complanata</i> (‘‘Fire Coral’’) from the Mexican Caribbean. <i>Marine Drugs</i> , 2019, 17, 393.	4.6	7
6	Emergent Protective Organogenesis in Date Palms: A Morpho-Devo-Dynamic Adaptive Strategy during Early Development. <i>Plant Cell</i> , 2019, 31, 1751-1766.	6.6	24
7	Evaluation of the presence of <i>Paenibacillus</i> larvae in commercial bee pollen using PCR amplification of the gene for tRNACys. <i>Brazilian Journal of Microbiology</i> , 2019, 50, 471-480.	2.0	8
8	Impact of El Niño-Southern Oscillation 2015-2016 on the soluble proteomic profile and cytolytic activity of <i>Millepora alcicornis</i> (‘‘fire coral’’) from the Mexican Caribbean. <i>PeerJ</i> , 2019, 7, e6593.	2.0	13
9	pMEX01, a 70 kb plasmid isolated from <i>Escherichia coli</i> that confers resistance to multiple β -lactam antibiotics. <i>Brazilian Journal of Microbiology</i> , 2018, 49, 569-574.	2.0	2
10	Transcriptome profiling of transgenic tobacco (<i>Nicotiana tabacum</i> cv. xanthi nc) expressing <i>CchGLP</i> gene from <i>Capsicum chinense</i> Jacq. reveals gene expression associated with stress tolerance. <i>Journal of Horticultural Science and Biotechnology</i> , 2018, 93, 595-604.	1.9	3
11	Transcriptional landscapes of Axolotl (<i>Ambystoma mexicanum</i>). <i>Developmental Biology</i> , 2018, 433, 227-239.	2.0	31
12	First Report of Cowpea mild mottle virus Infecting Cultivated and Wild Phaseolus in the Central-Western Region of Mexico. <i>Plant Disease</i> , 2018, 102, 1047-1047.	1.4	2
13	Transcriptional profiling of the CAM plant <i>Agave salmiana</i> reveals conservation of a genetic program for regeneration. <i>Developmental Biology</i> , 2018, 442, 28-39.	2.0	17
14	Identification by MALDI-TOF Mass Spectrometry of Mercury-resistant Bacteria Associated with the Rhizosphere of an Apple Orchard. <i>Geomicrobiology Journal</i> , 2017, 34, 176-182.	2.0	7
15	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	28.9	973
16	MicroRNAs Sequencing for Understanding the Genetic Regulation of Plant Genomes. , 2016, , .		3
17	Identification of Organ-Enriched Protein Biomarkers of Acute Liver Injury by Targeted Quantitative Proteomics of Blood in Acetaminophen- and Carbon-Tetrachloride-Treated Mouse Models and Acetaminophen Overdose Patients. <i>Journal of Proteome Research</i> , 2016, 15, 3724-3740.	3.7	28
18	miRNAs analysis during prickly pear development. <i>Acta Horticulturae</i> , 2016, , 99-104.	0.2	0

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19	Identification of novel drought-tolerant-associated SNPs in common bean (<i>Phaseolus vulgaris</i>). <i>Frontiers in Plant Science</i> , 2015, 6, 546.	3.6	51
20	Ancient Origin and Recent Innovations of RNA Polymerase IV and V. <i>Molecular Biology and Evolution</i> , 2015, 32, 1788-1799.	8.9	77
21	Multiple Lineages of Ancient CR1 Retroposons Shaped the Early Genome Evolution of Amniotes. <i>Genome Biology and Evolution</i> , 2015, 7, 205-217.	2.5	62
22	miRNA expression during prickly pear cactus fruit development. <i>Planta</i> , 2015, 241, 435-448.	3.2	23
23	Isolation of a conjugative F-like plasmid from a multidrug-resistant <i>Escherichia coli</i> strain CM6 using tandem shock wave-mediated transformation. <i>Journal of Microbiological Methods</i> , 2015, 114, 1-8.	1.6	4
24	Cooked common beans (<i>Phaseolus vulgaris</i> L.) modulate renal genes in streptozotocin-induced diabetic rats. <i>Journal of Nutritional Biochemistry</i> , 2015, 26, 761-768.	4.2	24
25	Accurate and Robust Prediction of Genetic Relationship from Whole-Genome Sequences. <i>PLoS ONE</i> , 2014, 9, e85437.	2.5	19
26	Relationship Estimation from Whole-Genome Sequence Data. <i>PLoS Genetics</i> , 2014, 10, e1004144.	3.5	67
27	Realistic artificial DNA sequences as negative controls for computational genomics. <i>Nucleic Acids Research</i> , 2014, 42, e99-e99.	14.5	26
28	Draft Genome Sequence of the Mercury-Resistant Bacterium <i>Acinetobacter idrijaensis</i> Strain MII, Isolated from a Mine-Impacted Area, Idrija, Slovenia. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
29	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	12.6	300
30	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. <i>Genome Biology</i> , 2014, 15, R53.	9.6	101
31	Cell type-specific genes show striking and distinct patterns of spatial expression in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3095-3100.	7.1	61
32	Optimal Scaling of Digital Transcriptomes. <i>PLoS ONE</i> , 2013, 8, e77885.	2.5	44
33	Functional analysis of the <i>Arabidopsis</i> PLDZ2 promoter reveals an evolutionarily conserved low-Pi-responsive transcriptional enhancer element. <i>Journal of Experimental Botany</i> , 2012, 63, 2189-2202.	4.8	36
34	A Bistable Circuit Involving SCARECROW-RETINOBLASTOMA Integrates Cues to Inform Asymmetric Stem Cell Division. <i>Cell</i> , 2012, 150, 1002-1015.	28.9	273
35	Kaviar: an accessible system for testing SNV novelty. <i>Bioinformatics</i> , 2011, 27, 3216-3217.	4.1	187
36	Enhancing gene detection with computer generated intergenic regions. , 2009, , .		0

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37	The genome of <i>Bacillus coahuilensis</i> reveals adaptations essential for survival in the relic of an ancient marine environment. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5803-5808.	7.1	94
38	Transcript profiling of Zea mays roots reveals gene responses to phosphate deficiency at the plant- and species-specific levels. Journal of Experimental Botany, 2008, 59, 2479-2497.	4.8	130
39	A Family of MicroRNAs Present in Plants and Animals. Plant Cell, 2007, 18, 3355-3369.	6.6	138