Juan Caballero Perez

List of Publications by Year
in descending order

39 papers	**2,873** citations	394421 **19** h-index	345221 **36** g-index
46 all docs	**46** docs citations	**46** times ranked	**5721** citing authors

#	Article	IF	Citations
1	Insights into Land Plant Evolution Garnered from the Marchantia polymorpha Genome. Cell, 2017, 171, 287-304.e15.	28.9	973
2	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	12.6	300
3	A Bistable Circuit Involving SCARECROW-RETINOBLASTOMA Integrates Cues to Inform Asymmetric Stem Cell Division. Cell, 2012, 150, 1002-1015.	28.9	273
4	Kaviar: an accessible system for testing SNV novelty. Bioinformatics, 2011, 27, 3216-3217.	4.1	187
5	A Family of MicroRNAs Present in Plants and Animals. Plant Cell, 2007, 18, 3355-3369.	6.6	138
6	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
7	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	9.6	101
8	The genome of *Bacillus coahuilensis* 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
9	Ancient Origin and Recent Innovations of RNA Polymerase IV and V. Molecular Biology and Evolution, 2015, 32, 1788-1799.	8.9	77
10	Relationship Estimation from Whole-Genome Sequence Data. PLoS Genetics, 2014, 10, e1004144.	3.5	67
11	Multiple Lineages of Ancient CR1 Retroposons Shaped the Early Genome Evolution of Amniotes. Genome Biology and Evolution, 2015, 7, 205-217.	2.5	62
12	Cell type-specific genes show striking and distinct patterns of spatial expression in the mouse brain. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3095-3100.	7.1	61
13	Identification of novel drought-tolerant-associated SNPs in common bean (Phaseolus vulgaris). Frontiers in Plant Science, 2015, 6, 546.	3.6	51
14	Optimal Scaling of Digital Transcriptomes. PLoS ONE, 2013, 8, e77885.	2.5	44
15	Functional analysis of the Arabidopsis PLDZ2 promoter reveals an evolutionarily conserved low-Pi-responsive transcriptional enhancer element. Journal of Experimental Botany, 2012, 63, 2189-2202.	4.8	36
16	Transcriptional landscapes of Axolotl (Ambystoma mexicanum). Developmental Biology, 2018, 433, 227-239.	2.0	31
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. Journal of Proteome Research, 2016, 15, 3724-3740.	3.7	28
18	Realistic artificial DNA sequences as negative controls for computational genomics. Nucleic Acids Research, 2014, 42, e99-e99.	14.5	26

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19	Cooked common beans (Phaseolus vulgaris L.) modulate renal genes in streptozotocin-induced diabetic rats. Journal of Nutritional Biochemistry, 2015, 26, 761-768.	4.2	24
20	Emergent Protective Organogenesis in Date Palms: A Morpho-Devo-Dynamic Adaptive Strategy during Early Development. Plant Cell, 2019, 31, 1751-1766.	6.6	24
21	miRNA expression during prickly pear cactus fruit development. Planta, 2015, 241, 435-448.	3.2	23
22	Deep microbial community profiling along the fermentation process of pulque, a biocultural resource of Mexico. Microbiological Research, 2020, 241, 126593.	5.3	23
23	Accurate and Robust Prediction of Genetic Relationship from Whole-Genome Sequences. PLoS ONE, 2014, 9, e85437.	2.5	19
24	Transcriptional profiling of the CAM plant Agave salmiana reveals conservation of a genetic program for regeneration. Developmental Biology, 2018, 442, 28-39.	2.0	17
25	Impact of El NiÃ±o-Southern Oscillation 2015-2016 on the soluble proteomic profile and cytolytic activity of Millepora alcicornis (â€œfire coralâ€) from the Mexican Caribbean. PeerJ, 2019, 7, e6593.	2.0	13
26	Evaluation of the presence of Paenibacillus larvae in commercial bee pollen using PCR amplification of the gene for tRNACys. Brazilian Journal of Microbiology, 2019, 50, 471-480.	2.0	8
27	Identification by MALDI-TOF Mass Spectrometry of Mercury-resistant Bacteria Associated with the Rhizosphere of an Apple Orchard. Geomicrobiology Journal, 2017, 34, 176-182.	2.0	7
28	Comparative Analysis of the Soluble Proteome and the Cytolytic Activity of Unbleached and Bleached Millepora complanata (â€œFire Coralâ€) from the Mexican Caribbean. Marine Drugs, 2019, 17, 393.	4.6	7
29	Multi-organ transcriptomic landscape of Ambystoma velasci metamorphosis. Developmental Biology, 2020, 466, 22-35.	2.0	6
30	Isolation of a conjugative F-like plasmid from a multidrug-resistant Escherichia coli strain CM6 using tandem shock wave-mediated transformation. Journal of Microbiological Methods, 2015, 114, 1-8.	1.6	4
31	Draft Genome Sequence of the Mercury-Resistant Bacterium Acinetobacter idrijaensis Strain MII, Isolated from a Mine-Impacted Area, Idrija, Slovenia. Genome Announcements, 2014, 2, .	0.8	3
32	MicroRNAs Sequencing for Understanding the Genetic Regulation of Plant Genomes. , 2016, , .		3
33	Transcriptome profiling of transgenic tobacco (*Nicotiana tabacum* cv. xanthi nc) expressing *CchGLP* gene from *Capsicum chinense* Jacq. reveals gene expression associated with stress tolerance. Journal of Horticultural Science and Biotechnology, 2018, 93, 595-604.	1.9	3
34	pMEX01, a 70 kb plasmid isolated from Escherichia coli that confers resistance to multiple Î²-lactam antibiotics. Brazilian Journal of Microbiology, 2018, 49, 569-574.	2.0	2
35	First Report of Cowpea mild mottle virus Infecting Cultivated and Wild Phaseolus in the Central-Western Region of Mexico. Plant Disease, 2018, 102, 1047-1047.	1.4	2
36	Comprehensive Metatranscriptome Analysis of the Reef-Building Holobiont Millepora complanata. Frontiers in Marine Science, 2021, 8, .	2.5	2

#	Article	IF	Citations
37	Enhancing gene detection with computer generated intergenic regions. , 2009, , .		0
38	miRNAs analysis during prickly pear development. Acta Horticulturae, 2016, , 99-104.	0.2	0
39	Analysis of tRNACys processing under salt stress in Bacillus subtilis spore outgrowth using RNA sequencing data. F1000Research, 2020, 9, 501.	1.6	0