Juan J Gutierrez-Gonzalez

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5647971/publications.pdf

Version: 2024-02-01

26 papers 4,495 citations

16 h-index 27 g-index

30 all docs 30 docs citations

30 times ranked

4935 citing authors

#	Article	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
2	The transcriptional landscape of polyploid wheat. Science, 2018, 361, .	12.6	768
3	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	27.8	513
4	Evaluation of Candidate Reference Genes for Normalization of Quantitative RT-PCR in Soybean Tissues under Various Abiotic Stress Conditions. PLoS ONE, 2012, 7, e46487.	2.5	115
5	Differential Expression of Isoflavone Biosynthetic Genes in Soybean During Water Deficits. Plant and Cell Physiology, 2010, 51, 936-948.	3.1	98
6	Genetic control of soybean seed isoflavone content: importance of statistical model and epistasis in complex traits. Theoretical and Applied Genetics, 2009, 119, 1069-1083.	3.6	67
7	Analysis and annotation of the hexaploid oat seed transcriptome. BMC Genomics, 2013, 14, 471.	2.8	62
8	Intricate environment-modulated genetic networks control isoflavone accumulation in soybean seeds. BMC Plant Biology, 2010, 10, 105.	3.6	60
9	Major locus and other novel additive and epistatic loci involved in modulation of isoflavone concentration in soybean seeds. Theoretical and Applied Genetics, 2011, 123, 1375-1385.	3.6	60
10	Overexpression of AtDREB1D transcription factor improves drought tolerance in soybean. Molecular Biology Reports, 2014, 41, 7995-8008.	2.3	56
11	Wildfire effects on diversity and composition in soil bacterial communities. Science of the Total Environment, 2020, 726, 138636.	8.0	52
12	Dense genotyping-by-sequencing linkage maps of two Synthetic W7984×Opata reference populations provide insights into wheat structural diversity. Scientific Reports, 2019, 9, 1793.	3.3	28
13	A developmental profile of tocol accumulation in oat seeds. Journal of Cereal Science, 2013, 57, 79-83.	3.7	24
14	MicroRNA Maturation and MicroRNA Target Gene Expression Regulation Are Severely Disrupted in Soybean dicer-like1 Double Mutants. G3: Genes, Genomes, Genetics, 2016, 6, 423-433.	1.8	23
15	Subgenomeâ€specific assembly of vitamin E biosynthesis genes and expression patterns during seed development provide insight into the evolution of oat genome. Plant Biotechnology Journal, 2016, 14, 2147-2157.	8.3	22
16	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. Plant Biotechnology Journal, 2020, 18, 1211-1222.	8.3	19
17	Genome Assembly of the Fungus Cochliobolus miyabeanus, and Transcriptome Analysis during Early Stages of Infection on American Wildrice (Zizania palustris L.). PLoS ONE, 2016, 11, e0154122.	2.5	17
18	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. Plant and Cell Physiology, 2021, 62, 8-27.	3.1	16

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19	Reference Genomeâ€Directed Resolution of Homologous and Homeologous Relationships within and between Different Oat Linkage Maps. Plant Genome, 2011, 4, .	2.8	15
20	De Novo Transcriptome Assembly in Polyploid Species. Methods in Molecular Biology, 2017, 1536, 209-221.	0.9	13
21	Potato improvement through genetic engineering. GM Crops and Food, 2021, 12, 479-496.	3.8	11
22	Alfalfa (<i>Medicago sativa</i> L.) <i>pho2</i> mutant plants hyperaccumulate phosphate. G3: Genes, Genomes, Genetics, 2022, , .	1.8	10
23	Multi-Species Transcriptome Assemblies of Cultivated and Wild Lentils (Lens sp.) Provide a First Glimpse at the Lentil Pangenome. Agronomy, 2022, 12, 1619.	3.0	6
24	Prokaryotic community diversity in the sediments of saline lagoons and its resistance to seasonal disturbances by water level cycles. Journal of Soils and Sediments, 2021, 21, 3169-3184.	3.0	5
25	Targeted Mutagenesis of Alfalfa. Compendium of Plant Genomes, 2021, , 271-283.	0.5	3
26	Bioinformatic-Based Approaches for Disease-Resistance Gene Discovery in Plants. Agronomy, 2021, 11, 2259.	3.0	3