

Roberto Lozano

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7544784/publications.pdf>

Version: 2024-02-01

20
papers

3,107
citations

516215

16
h-index

752256

20
g-index

31
all docs

31
docs citations

31
times ranked

4231
citing authors

#	ARTICLE	IF	CITATIONS
1	The patterns of deleterious mutations during the domestication of soybean. <i>Nature Communications</i> , 2021, 12, 97.	5.8	49
2	Machine learning-enabled phenotyping for GWAS and TWAS of WUE traits in 869 field-grown sorghum accessions. <i>Plant Physiology</i> , 2021, 187, 1481-1500.	2.3	44
3	Phenotyping stomatal closure by thermal imaging for GWAS and TWAS of water use efficiency-related genes. <i>Plant Physiology</i> , 2021, 187, 2544-2562.	2.3	23
4	RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	11
5	Comparative evolutionary genetics of deleterious load in sorghum and maize. <i>Nature Plants</i> , 2021, 7, 17-24.	4.7	52
6	Novel Bayesian Networks for Genomic Prediction of Developmental Traits in Biomass Sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 769-781.	0.8	25
7	Genomic prediction and quantitative trait locus discovery in a cassava training population constructed from multiple breeding stages. <i>Crop Science</i> , 2020, 60, 896-913.	0.8	9
8	A sorghum practical haplotype graph facilitates genome-wide imputation and cost-effective genomic prediction. <i>Plant Genome</i> , 2020, 13, e20009.	1.6	54
9	Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. <i>Genetics</i> , 2019, 213, 1237-1253.	1.2	27
10	Genome wide association study of 5 agronomic traits in olive (<i>Olea europaea</i> L.). <i>Scientific Reports</i> , 2019, 9, 18764.	1.6	18
11	Deleterious Mutation Burden and Its Association with Complex Traits in Sorghum (<i>Sorghum</i>) Tj ETQq1 1 0.784314 rgBT /Qyerlock 10	1.2	91
12	Genome-wide association mapping and genomic prediction for CBSD resistance in <i>Manihot esculenta</i> . <i>Scientific Reports</i> , 2018, 8, 1549.	1.6	66
13	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. <i>Population Genomics</i> , 2018, , 361-425.	0.2	6
14	Training Population Optimization for Prediction of Cassava Brown Streak Disease Resistance in West African Clones. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3903-3913.	0.8	23
15	Prospects for Genomic Selection in Cassava Breeding. <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0015.	1.6	101
16	Genome-Wide Association and Prediction Reveals Genetic Architecture of Cassava Mosaic Disease Resistance and Prospects for Rapid Genetic Improvement. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0118.	1.6	120
17	Identification and distribution of the NBS-LRR gene family in the Cassava genome. <i>BMC Genomics</i> , 2015, 16, 360.	1.2	130
18	Construction of Reference Chromosome-Scale Pseudomolecules for Potato: Integrating the Potato Genome with Genetic and Physical Maps. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2031-2047.	0.8	244

#	ARTICLE	IF	CITATIONS
19	Genome-Wide Identification and Mapping of NBS-Encoding Resistance Genes in Solanum tuberosum Group Phureja. PLoS ONE, 2012, 7, e34775.	1.1	107
20	Genome sequence and analysis of the tuber crop potato. Nature, 2011, 475, 189-195.	13.7	1,912