Juliana Benevenuto

List of Publications by Year
in descending order

16	618	932766 10	940134 16
papers	citations	h-index	g-index

19	19	19	720
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Using Population and Comparative Genomics to Understand the Genetic Basis of Effector-Driven Fungal Pathogen Evolution. Frontiers in Plant Science, 2017, 8, 119.	1.7	135
2	Complete Genome Sequence of Sporisorium scitamineum and Biotrophic Interaction Transcriptome with Sugarcane. PLoS ONE, 2015, 10, e0129318.	1.1	93
3	Genomeâ€wide association of volatiles reveals candidate loci for blueberry flavor. New Phytologist, 2020, 226, 1725-1737.	3.5	84
4	How can a high-quality genome assembly help plant breeders?. GigaScience, 2019, 8, .	3.3	67
5	Insights Into the Genetic Basis of Blueberry Fruit-Related Traits Using Diploid and Polyploid Models in a GWAS Context. Frontiers in Ecology and Evolution, 2018, 6, .	1.1	60
6	Molecular and Genetic Bases of Fruit Firmness Variation in Blueberryâ€”A Review. Agronomy, 2018, 8, 174.	1.3	35
7	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. Frontiers in Microbiology, 2018, 9, 660.	1.5	33
8	Impact of dominance effects on autotetraploid genomic prediction. Crop Science, 2020, 60, 656-665.	0.8	28
9	Genomic Selection in an Outcrossing Autotetraploid Fruit Crop: Lessons From Blueberry Breeding. Frontiers in Plant Science, 2021, 12, 676326.	1.7	26
10	High-Resolution Linkage Map and QTL Analyses of Fruit Firmness in Autotetraploid Blueberry. Frontiers in Plant Science, 2020, 11, 562171.	1.7	19
11	Genomic prediction for canopy height and dry matter yield in alfalfa using family bulks. Plant Genome, 2022, 15, .	1.6	10
12	Conservation study of an endangered stingless bee (Melipona capixabaâ€”Hymenoptera: Apidae) with restricted distribution in Brazil. Journal of Insect Conservation, 2014, 18, 317-326.	0.8	6
13	Molecular variability and genetic relationship among Brazilian strains of the sugarcane smut fungus. FEMS Microbiology Letters, 2016, 363, fnw277.	0.7	6
14	Cost-effective detection of genome-wide signatures for 2,4-D herbicide resistance adaptation in red clover. Scientific Reports, 2019, 9, 20037.	1.6	6
15	Complete Chromosome-Scale Genome Sequence Resource forSporisorium panici-leucophaei, the Causal Agent of Sourgrass Smut Disease. Molecular Plant-Microbe Interactions, 2021, 34, 448-452.	1.4	3
16	Progress in understanding fungal diseases affecting sugarcane: smut. Burleigh Dodds Series in Agricultural Science, 2018, , 221-243.	0.1	2