Maria M Pastina

List of Publications by Year
in descending order

40 papers	1,280 citations	393982 19 h-index	395343 33 g-index
43 all docs	43 docs citations	43 times ranked	1362 citing authors

#	Article	IF	Citations
1	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. Scientific Reports, 2013, 3, 3399.	1.6	129
2	Duplicate and Conquer: Multiple Homologs of *PHOSPHORUS-STARVATION TOLERANCE1* Enhance Phosphorus Acquisition and Sorghum Performance on Low-Phosphorus Soils Â Â Â. Plant Physiology, 2014, 166, 659-677.	2.3	117
3	Development of an integrated genetic map of a sugarcane (Saccharum spp.) commercial cross, based on a maximum-likelihood approach for estimation of linkage and linkage phases. Theoretical and Applied Genetics, 2006, 112, 298-314.	1.8	101
4	Functional integrated genetic linkage map based on EST-markers for a sugarcane (Saccharum spp.) commercial cross. Molecular Breeding, 2007, 20, 189-208.	1.0	79
5	A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. Theoretical and Applied Genetics, 2012, 124, 835-849.	1.8	73
6	Improving accuracies of genomic predictions for drought tolerance in maize by joint modeling of additive and dominance effects in multi-environment trials. Heredity, 2018, 121, 24-37.	1.2	68
7	A genome-wide association study identified loci for yield component traits in sugarcane (Saccharum) Tj ETQq1 1 0.784314 rgBT /Overlo	1.1	54
8	Tropical Bacillus Strains Inoculation Enhances Maize Root Surface Area, Dry Weight, Nutrient Uptake and Grain Yield. Journal of Plant Growth Regulation, 2021, 40, 867-877.	2.8	53
9	The genetic architecture of phosphorus efficiency in sorghum involves pleiotropic QTL for root morphology and grain yield under low phosphorus availability in the soil. BMC Plant Biology, 2019, 19, 87.	1.6	51
10	Analysis of genomic and functional RFLP derived markers associated with sucrose content, fiber and yield QTLs in a sugarcane (Saccharum spp.) commercial cross. Euphytica, 2010, 172, 313-327.	0.6	46
11	QTL mapping including codominant SNP markers with ploidy level information in a sugarcane progeny. Euphytica, 2016, 211, 1-16.	0.6	39
12	Evidence of Allopolyploidy in Urochloa humidicola Based on Cytological Analysis and Genetic Linkage Mapping. PLoS ONE, 2016, 11, e0153764.	1.1	39
13	Repeat variants for the SbMATE transporter protect sorghum roots from aluminum toxicity by transcriptional interplay in *cis* and *trans*. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 313-318.	3.3	38
14	Evaluation of the potential of lines and hybrids of biomass sorghum. Industrial Crops and Products, 2018, 125, 379-385.	2.5	36
15	Genotype-by-environment interaction and yield stability analysis of biomass sorghum hybrids using factor analytic models and environmental covariates. Field Crops Research, 2020, 257, 107929.	2.3	36
16	Genetic dissection of Al tolerance QTLs in the maize genome by high density SNP scan. BMC Genomics, 2014, 15, 153.	1.2	35
17	A model for quantitative trait loci mapping, linkage phase, and segregation pattern estimation for a full-sib progeny. Tree Genetics and Genomes, 2014, 10, 791-801.	0.6	34
18	Estimating Genotype Ã— Environment Interaction for and Genetic Correlations among Drought Tolerance Traits in Maize via Factor Analytic Multiplicative Mixed Models. Crop Science, 2018, 58, 72-83.	0.8	32

#	Article	IF	Citations
19	Genomic prediction applied to high-biomass sorghum for bioenergy production. Molecular Breeding, 2018, 38, 49.	1.0	28
20	Phenotypic and molecular characterization of sweet sorghum accessions for bioenergy production. PLoS ONE, 2017, 12, e0183504.	1.1	24
21	Novel strategies for genomic prediction of untested single-cross maize hybrids using unbalanced historical data. Theoretical and Applied Genetics, 2020, 133, 443-455.	1.8	22
22	Multi-trait multi-environment quantitative trait loci mapping for a sugarcane commercial cross provides insights on the inheritance of important traits. Molecular Breeding, 2015, 35, 175.	1.0	19
23	Boosting predictive ability of tropical maize hybrids via genotype‐by‐environment interaction under multivariate GBLUP models. Crop Science, 2020, 60, 3049-3065.	0.8	15
24	A multi-environment trials diallel analysis provides insights on the inheritance of fumonisin contamination resistance in tropical maize. Euphytica, 2016, 211, 277-285.	0.6	14
25	Genomic prediction applied to multiple traits and environments in second season maize hybrids. Heredity, 2020, 125, 60-72.	1.2	12
26	Quantitative Trait Loci and Resistance Gene Analogs Associated with Maize White Spot Resistance. Plant Disease, 2017, 101, 200-208.	0.7	9
27	High‐density SNP‐based genetic diversity and heterotic patterns of tropical maize breeding lines. Crop Science, 2020, 60, 779-787.	0.8	9
28	Association mapping and genomic selection for sorghum adaptation to tropical soils of Brazil in a sorghum multiparental random mating population. Theoretical and Applied Genetics, 2021, 134, 295-312.	1.8	9
29	Genetic diversity and heterotic grouping of sorghum lines using SNP markers. Scientia Agricola, 2021, 78, .	0.6	9
30	Genome-guided insights of tropical Bacillus strains efficient in maize growth promotion. FEMS Microbiology Ecology, 2020, 96, .	1.3	8
31	Leveraging probability concepts for cultivar recommendation in multi-environment trials. Theoretical and Applied Genetics, 2022, 135, 1385-1399.	1.8	8
32	The Sweet Passion Fruit (Passiflora alata) Crop: Genetic and Phenotypic Parameter Estimates and QTL Mapping for Fruit Traits. Tropical Plant Biology, 2017, 10, 18-29.	1.0	7
33	A first genetic map of Acca sellowiana based on ISSR, AFLP and SSR markers. Scientia Horticulturae, 2014, 169, 138-146.	1.7	6
34	Exploring genotype × environment interaction in sweet sorghum under tropical environments. Agronomy Journal, 2021, 113, 3005-3018.	0.9	6
35	Single nucleotide polymorphism calling and imputation strategies for cost‐effective genotyping in a tropical maize breeding program. Crop Science, 2020, 60, 3066-3082.	0.8	4
36	Universal tail sequence-SSR applied to molecular characterization of tropical maize hybrids. Scientia Agricola, 2017, 74, 163-168.	0.6	3

#	Article	IF	Citations
37	ZmMATE1 improves grain yield and yield stability in maize cultivated on acid soil. Crop Science, 2021, 61, 3497-3506.	0.8	3
38	QTL mapping for bioenergy traits in sweet sorghum recombinant inbred lines. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	3
39	Genomic Prediction of Complex Traits in an Allogamous Annual Crop: The Case of Maize Single-Cross Hybrids. Methods in Molecular Biology, 2022, 2467, 543-567.	0.4	0
40	Hitos tecnolÃ³gicos que cambiaron el rol de Brasil en la producciÃ³n de maÃz: 30 aÃ±os de crecimiento para convertirse en importante actor del escenario mundial, una revisiÃ³n. Avances En Ciencias E IngenierÃas, 2022, 14, .	0.1	0