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List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

1,367
citations

516215

16
h-index

377514

34
g-index

48
all docs

48
docs citations

48
times ranked

1623
citing authors

#	ARTICLE	IF	CITATIONS
1	OneMap: software for genetic mapping in outcrossing species. <i>Hereditas</i> , 2007, 144, 78-79.	0.5	326
2	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	3.3	106
3	Studying the genetic basis of drought tolerance in sorghum by managed stress trials and adjustments for phenological and plant height differences. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1389-1402.	1.8	98
4	GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. <i>BMC Genomics</i> , 2017, 18, 72.	1.2	91
5	Functional integrated genetic linkage map based on EST-markers for a sugarcane (<i>Saccharum</i> spp.) commercial cross. <i>Molecular Breeding</i> , 2007, 20, 189-208.	1.0	79
6	A mixed model QTL analysis for sugarcane multiple-harvest-location trial data. <i>Theoretical and Applied Genetics</i> , 2012, 124, 835-849.	1.8	73
7	The Biotechnology Roadmap for Sugarcane Improvement. <i>Tropical Plant Biology</i> , 2010, 3, 75-87.	1.0	62
8	A fully automated pipeline for quantitative genotype calling from next generation sequencing data in autopolyploids. <i>BMC Bioinformatics</i> , 2018, 19, 398.	1.2	62
9	An Integrated Molecular Map of Yellow Passion Fruit Based on Simultaneous Maximum-likelihood Estimation of Linkage and Linkage Phases. <i>Journal of the American Society for Horticultural Science</i> , 2008, 133, 35-41.	0.5	44
10	Evaluation of algorithms used to order markers on genetic maps. <i>Heredity</i> , 2009, 103, 494-502.	1.2	41
11	ConPADE: Genome Assembly Ploidy Estimation from Next-Generation Sequencing Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004229.	1.5	41
12	Genomic resources for energy cane breeding in the post genomics era. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1404-1414.	1.9	38
13	A model for quantitative trait loci mapping, linkage phase, and segregation pattern estimation for a full-sib progeny. <i>Tree Genetics and Genomes</i> , 2014, 10, 791-801.	0.6	34
14	Evidence for Strong Kinship Influence on the Extent of Linkage Disequilibrium in Cultivated Common Beans. <i>Genes</i> , 2019, 10, 5.	1.0	32
15	Genomic prediction applied to high-biomass sorghum for bioenergy production. <i>Molecular Breeding</i> , 2018, 38, 49.	1.0	28
16	Time-series expression profiling of sugarcane leaves infected with <i>Puccinia kuehnii</i> reveals an ineffective defense system leading to susceptibility. <i>Plant Cell Reports</i> , 2020, 39, 873-889.	2.8	25
17	Linkage Disequilibrium and Population Structure in Wild and Cultivated Populations of Rubber Tree (<i>Hevea brasiliensis</i>). <i>Frontiers in Plant Science</i> , 2018, 9, 815.	1.7	20
18	Multi-trait multi-environment quantitative trait loci mapping for a sugarcane commercial cross provides insights on the inheritance of important traits. <i>Molecular Breeding</i> , 2015, 35, 175.	1.0	19

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19	The Wild Sugarcane and Sorghum Kinomes: Insights Into Expansion, Diversification, and Expression Patterns. <i>Frontiers in Plant Science</i> , 2021, 12, 668623.	1.7	18
20	Boosting predictive ability of tropical maize hybrids via genotype×environment interaction under multivariate GBLUP models. <i>Crop Science</i> , 2020, 60, 3049-3065.	0.8	15
21	Improvements in the sequencing and assembly of plant genomes. <i>GigaByte</i> , 0, 2021, 1-10.	0.0	15
22	Genomic prediction with allele dosage information in highly polyploid species. <i>Theoretical and Applied Genetics</i> , 2022, 135, 723-739.	1.8	13
23	Genomic prediction applied to multiple traits and environments in second season maize hybrids. <i>Heredity</i> , 2020, 125, 60-72.	1.2	12
24	Long-term comparison between index selection and optimal independent culling in plant breeding programs with genomic prediction. <i>PLoS ONE</i> , 2021, 16, e0235554.	1.1	11
25	Differential expression in leaves of <i>Saccharum</i> genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. <i>BMC Genomics</i> , 2020, 21, 673.	1.2	10
26	Means, motive and opportunity for biological invasions: Genetic introgression in a fungal pathogen. <i>Molecular Ecology</i> , 2023, 32, 2428-2442.	2.0	10
27	Limited allele-specific gene expression in highly polyploid sugarcane. <i>Genome Research</i> , 2022, 32, 297-308.	2.4	8
28	Molecular markers for conservation genetic resources of four <i>Passiflora</i> species. <i>Scientia Horticulturae</i> , 2016, 212, 251-261.	1.7	5
29	Restriction site associated <i><sc>DNA</sc></i> (<i><sc>RAD</sc></i>) for de novo sequencing and marker discovery in sugarcane borer, <i><i>Diatraea saccharalis</i></i> Fab. (Lepidoptera: Crambidae). <i>Molecular Ecology Resources</i> , 2017, 17, 454-465.	2.2	5
30	Single nucleotide polymorphism calling and imputation strategies for cost-effective genotyping in a tropical maize breeding program. <i>Crop Science</i> , 2020, 60, 3066-3082.	0.8	4
31	A Missense Mutation in the MYBPH Gene Is Associated With Abdominal Fat Traits in Meat-Type Chickens. <i>Frontiers in Genetics</i> , 2021, 12, 698163.	1.1	4
32	Precision of distances and ordering of microsatellite markers in consensus linkage maps of chromosomes 1, 3 and 4 from two reciprocal chicken populations using bootstrap sampling. <i>Genetics and Molecular Research</i> , 2010, 9, 1357-1376.	0.3	4
33	Comparaçãodos algoritmos delineaçãorápida em cadeia e seriã, para a construçãode mapas genéticos. <i>Pesquisa Agropecuaria Brasileira</i> , 2008, 43, 505-512.	0.9	1
34	Transcriptome changes in the developing sugarcane culm associated with high yield and early-season high sugar content. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1619-1636.	1.8	1
35	Temporal Gene Expression in Apical Culms Shows Early Changes in Cell Wall Biosynthesis Genes in Sugarcane. <i>Frontiers in Plant Science</i> , 2021, 12, 736797.	1.7	1
36	Allele expression biases in mixed-ploid sugarcane accessions. <i>Scientific Reports</i> , 2022, 12, .	1.6	1

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37	Differential Gene Expression Among Genotypes of the Genus <i>Saccharum</i> Contrasting in Biomass Production. <i>Proceedings (mdpi)</i> , 2019, 36, .	0.2	0
38	Modern Approaches for Transcriptome Analyses in Plants. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1346, 11-50.	0.8	0