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List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

3,155
citations

236925

25
h-index

182427

51
g-index

58
all docs

58
docs citations

58
times ranked

3396
citing authors

#	ARTICLE	IF	CITATIONS
1	A chemical genetic roadmap to improved tomato flavor. <i>Science</i> , 2017, 355, 391-394.	12.6	561
2	Accuracy of Genomic Selection Methods in a Standard Data Set of Loblolly Pine (<i>Pinus taeda</i> L.). <i>Genetics</i> , 2012, 190, 1503-1510.	2.9	363
3	Genomic selection for growth and wood quality in <i>Eucalyptus</i> : capturing the missing heritability and accelerating breeding for complex traits in forest trees. <i>New Phytologist</i> , 2012, 194, 116-128.	7.3	301
4	Accelerating the domestication of trees using genomic selection: accuracy of prediction models across ages and environments. <i>New Phytologist</i> , 2012, 193, 617-624.	7.3	231
5	AGHmatrix: R Package to Construct Relationship Matrices for Autotetraploid and Diploid Species: A Blueberry Example. <i>Plant Genome</i> , 2016, 9, plantgenome2016.01.0009.	2.8	158
6	Unraveling Additive from Nonadditive Effects Using Genomic Relationship Matrices. <i>Genetics</i> , 2014, 198, 1759-1768.	2.9	156
7	Genome-wide association study reveals putative regulators of bioenergy traits in <i>Populus deltoides</i> . <i>New Phytologist</i> , 2017, 213, 799-811.	7.3	89
8	Genomic Relationship Matrix for Correcting Pedigree Errors in Breeding Populations: Impact on Genetic Parameters and Genomic Selection Accuracy. <i>Crop Science</i> , 2014, 54, 1115-1123.	1.8	77
9	Genomic prediction in contrast to a genome-wide association study in explaining heritable variation of complex growth traits in breeding populations of <i>Eucalyptus</i> . <i>BMC Genomics</i> , 2017, 18, 524.	2.8	76
10	The contribution of dominance to phenotype prediction in a pine breeding and simulated population. <i>Heredity</i> , 2016, 117, 33-41.	2.6	72
11	Ultraconserved Elements Sequencing as a Low-Cost Source of Complete Mitochondrial Genomes and Microsatellite Markers in Non-Model Amniotes. <i>PLoS ONE</i> , 2015, 10, e0138446.	2.5	66
12	Metabolomic selection for enhanced fruit flavor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	66
13	Insights Into the Genetic Basis of Blueberry Fruit-Related Traits Using Diploid and Polyploid Models in a GWAS Context. <i>Frontiers in Ecology and Evolution</i> , 2018, 6, .	2.2	60
14	Genomic Prediction of Autotetraploids; Influence of Relationship Matrices, Allele Dosage, and Continuous Genotyping Calls in Phenotype Prediction. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1189-1198.	1.8	60
15	Association genetics of oleoresin flow in loblolly pine: discovering genes and predicting phenotype for improved resistance to bark beetles and bioenergy potential. <i>New Phytologist</i> , 2013, 199, 89-100.	7.3	58
16	Population genomics of the eastern cottonwood (<i>Populus deltoides</i>). <i>Ecology and Evolution</i> , 2017, 7, 9426-9440.	1.9	55
17	Strawberry sweetness and consumer preference are enhanced by specific volatile compounds. <i>Horticulture Research</i> , 2021, 8, 66.	6.3	55
18	Increased Proportion of Variance Explained and Prediction Accuracy of Survival of Breast Cancer Patients with Use of Whole-Genome Multiomic Profiles. <i>Genetics</i> , 2016, 203, 1425-1438.	2.9	49

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19	Discovering candidate genes that regulate resin canal number in <i>Pinus taeda</i> stems by integrating genetic analysis across environments, ages, and populations. <i>New Phytologist</i> , 2015, 205, 627-641.	7.3	45
20	Natural Allelic Variations in Highly Polyploidy <i>Saccharum</i> Complex. <i>Frontiers in Plant Science</i> , 2016, 7, 804.	3.6	40
21	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. <i>Nature Communications</i> , 2021, 12, 1227.	12.8	37
22	Genomics-based diversity analysis of <i>Vanilla</i> species using a <i>Vanilla planifolia</i> draft genome and Genotyping-By-Sequencing. <i>Scientific Reports</i> , 2019, 9, 3416.	3.3	36
23	Mtodo alternativo para anlise de agrupamento. <i>Pesquisa Agropecuaria Brasileira</i> , 2007, 42, 1421-1428.	0.9	35
24	A high-density exome capture genotype-by-sequencing panel for forestry breeding in <i>Pinus radiata</i> . <i>PLoS ONE</i> , 2019, 14, e0222640.	2.5	30
25	Breeding Alfalfa (<i>Medicago sativa</i> L.) Adapted to Subtropical Agroecosystems. <i>Agronomy</i> , 2020, 10, 742.	3.0	30
26	Genomic Prediction of Additive and Non-additive Effects Using Genetic Markers and Pedigrees. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2739-2748.	1.8	24
27	Understanding the Complexity of Cold Tolerance in White Clover using Temperature Gradient Locations and a GWAS Approach. <i>Plant Genome</i> , 2018, 11, 170096.	2.8	23
28	Mapping Fusiform Rust Resistance Genes within a Complex Mating Design of Loblolly Pine. <i>Forests</i> , 2014, 5, 347-362.	2.1	22
29	Population structure and genetic diversity of coffee progenies derived from <i>Catua</i> and <i>Hbrido de Timor</i> revealed by genome-wide SNP marker. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	1.6	22
30	Exome Resequencing Reveals Evolutionary History, Genomic Diversity, and Targets of Selection in the Conifers <i>Pinus taeda</i> and <i>Pinus elliottii</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 508-520.	2.5	19
31	Accelerating forest tree breeding by integrating genomic selection and greenhouse phenotyping. <i>Plant Genome</i> , 2020, 13, e20048.	2.8	19
32	The effect of bienniality on genomic prediction of yield in arabica coffee. <i>Euphytica</i> , 2020, 216, 1.	1.2	19
33	Ganhos genticos preditos por diferentes mtodos de seleo em prognies de <i>Eucalyptus urophylla</i> . <i>Pesquisa Agropecuaria Brasileira</i> , 2009, 44, 1653-1659.	0.9	18
34	Xylem systems genetics analysis reveals a key regulator of lignin biosynthesis in <i>Populus deltoides</i> . <i>Genome Research</i> , 2020, 30, 1131-1143.	5.5	18
35	Genotyping-By-Sequencing diversity analysis of international <i>Vanilla</i> collections uncovers hidden diversity and enables plant improvement. <i>Plant Science</i> , 2021, 311, 111019.	3.6	17
36	Improvement of predictive ability in maize hybrids by including dominance effects and markerenvironment models. <i>Crop Science</i> , 2020, 60, 666-677.	1.8	14

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37	Genomic selection prediction models comparing sequence capture and SNP array genotyping methods. <i>Molecular Breeding</i> , 2018, 38, 1.	2.1	13
38	Genomic prediction applied to multiple traits and environments in second season maize hybrids. <i>Heredity</i> , 2020, 125, 60-72.	2.6	12
39	Competitive Growth Assay of Mutagenized <i>Chlamydomonas reinhardtii</i> Compatible With the International Space Station Veggie Plant Growth Chamber. <i>Frontiers in Plant Science</i> , 2020, 11, 631.	3.6	12
40	Plant Domestication: Reconstructing the Route to Modern Tomatoes. <i>Current Biology</i> , 2020, 30, R359-R361.	3.9	10
41	Genomic prediction for canopy height and dry matter yield in alfalfa using family bulks. <i>Plant Genome</i> , 2022, 15, .	2.8	10
42	Characterizing the Physical Properties and Cell Compatibility of Phytoglycogen Extracted from Different Sweet Corn Varieties. <i>Molecules</i> , 2020, 25, 637.	3.8	9
43	Genetic Perturbation of the Starch Biosynthesis in Maize Endosperm Reveals Sugar-Responsive Gene Networks. <i>Frontiers in Plant Science</i> , 2021, 12, 800326.	3.6	8
44	Genomic prediction in family bulks using different traits and cross-validations in pine. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	7
45	Limited transpiration rate and plant conductance in a diverse sweet corn population. <i>Crop Science</i> , 2022, 62, 374-381.	1.8	7
46	Cost-effective detection of genome-wide signatures for 2,4-D herbicide resistance adaptation in red clover. <i>Scientific Reports</i> , 2019, 9, 20037.	3.3	6
47	The Genetic Regulation of Alternative Splicing in <i>Populus deltoides</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 590.	3.6	5
48	Tombamento de mudas de espécies florestais causado por <i>Sclerotium rolfsii</i> Sacc. <i>Revista Arvore</i> , 2007, 31, 629-634.	0.5	5
49	Comparison of water flow capacity in leaves among sweet corn genotypes as basis for plant transpiration rate sensitivity to vapor pressure deficit. <i>Crop Science</i> , 0, , .	1.8	3
50	Genotyping-by-sequencing of passion fruit (<i>Passiflora</i> spp.) generates genomic resources for breeding and systematics. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 2769-2786.	1.6	3
51	Mega-environment analysis of maize breeding data from Brazil. <i>Scientia Agricola</i> , 2022, 79, .	1.2	2
52	Maize Genome Assembly with PacBio Reads. <i>Bio-protocol</i> , 2022, 12, .	0.4	0