

Juan Burgueño

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

6,968
citations

117453

34
h-index

76769

74
g-index

79
all docs

79
docs citations

79
times ranked

4963
citing authors

#	ARTICLE	IF	CITATIONS
1	Maximizing efficiency of genomic selection in CIMMYT's tropical maize breeding program. <i>Theoretical and Applied Genetics</i> , 2021, 134, 279-294.	1.8	36
2	Effects of conservation agriculture on physicochemical soil health in 20 maize-based trials in different agro-ecological regions across Mexico. <i>Land Degradation and Development</i> , 2021, 32, 2242-2256.	1.8	15
3	Scalable Sparse Testing Genomic Selection Strategy for Early Yield Testing Stage. <i>Frontiers in Plant Science</i> , 2021, 12, 658978.	1.7	15
4	Application of Genomic Selection at the Early Stage of Breeding Pipeline in Tropical Maize. <i>Frontiers in Plant Science</i> , 2021, 12, 685488.	1.7	18
5	Disaggregating the Value of Conservation Agriculture to Inform Smallholder Transition to Sustainable Farming: A Mexican Case Study. <i>Agronomy</i> , 2021, 11, 1214.	1.3	14
6	Effect of Flowering Time-Related Genes on Biomass, Harvest Index, and Grain Yield in CIMMYT Elite Spring Bread Wheat. <i>Biology</i> , 2021, 10, 855.	1.3	12
7	Genome-enabled prediction for sparse testing in multi-environment wheat trials. <i>Plant Genome</i> , 2021, 14, e20151.	1.6	15
8	Introgression of Maize Diversity for Drought Tolerance: Subtropical Maize Landraces as Source of New Positive Variants. <i>Frontiers in Plant Science</i> , 2021, 12, 691211.	1.7	11
9	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.	5.8	129
10	Genomic Prediction Enhanced Sparse Testing for Multi-environment Trials. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2725-2739.	0.8	68
11	META-R: A software to analyze data from multi-environment plant breeding trials. <i>Crop Journal</i> , 2020, 8, 745-756.	2.3	164
12	An Evaluation of Kernel Zinc in Hybrids of Elite Quality Protein Maize (QPM) and Non-QPM Inbred Lines Adapted to the Tropics Based on a Mating Design. <i>Agronomy</i> , 2020, 10, 695.	1.3	11
13	Hybrid Breeding for MLN Resistance: Heterosis, Combining Ability, and Hybrid Prediction. <i>Plants</i> , 2020, 9, 468.	1.6	10
14	GWAS to Identify Genetic Loci for Resistance to Yellow Rust in Wheat Pre-Breeding Lines Derived From Diverse Exotic Crosses. <i>Frontiers in Plant Science</i> , 2019, 10, 1390.	1.7	55
15	Effect of F1 and F2 generations on genetic variability and working steps of doubled haploid production in maize. <i>PLoS ONE</i> , 2019, 14, e0224631.	1.1	11
16	Factor analysis to investigate genotype and genotype×environment interaction effects on pro-vitamin A content and yield in maize synthetics. <i>Euphytica</i> , 2019, 215, 1.	0.6	12
17	isqg: A Binary Framework for in Silico Quantitative Genetics. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2425-2428.	0.8	1
18	Maize responsiveness to <i>Azospirillum brasilense</i> : Insights into genetic control, heterosis and genomic prediction. <i>PLoS ONE</i> , 2019, 14, e0217571.	1.1	19

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19	Identification of donors for low-nitrogen stress with maize lethal necrosis (MLN) tolerance for maize breeding in sub-Saharan Africa. <i>Euphytica</i> , 2019, 215, 80.	0.6	24
20	Modeling Genotype \times Environment Interaction Using a Factor Analytic Model of On-Farm Wheat Trials in the Yaqui Valley of Mexico. <i>Agronomy Journal</i> , 2019, 111, 2647-2657.	0.9	7
21	Deep Kernel for Genomic and Near Infrared Predictions in Multi-environment Breeding Trials. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2913-2924.	0.8	61
22	Multivariate Bayesian Analysis of On-Farm Trials with Multiple Trait and Multiple Environment Data. <i>Agronomy Journal</i> , 2019, 111, 2658-2669.	0.9	17
23	Genomic-Enabled Prediction Kernel Models with Random Intercepts for Multi-environment Trials. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1347-1365.	0.8	32
24	Genotype by tillage interaction and performance progress for bread and durum wheat genotypes on irrigated raised beds. <i>Field Crops Research</i> , 2018, 216, 42-52.	2.3	19
25	SASHAYDIALL: A SAS Program for Hayman's Diallel Analysis. <i>Crop Science</i> , 2018, 58, 1605-1615.	0.8	12
26	Bayesian functional regression as an alternative statistical analysis of high-throughput phenotyping data of modern agriculture. <i>Plant Methods</i> , 2018, 14, 46.	1.9	11
27	BCGE: A New Package for Genomic-Enabled Prediction Incorporating Genotype \times Environment Interaction Models. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3039-3047.	0.8	47
28	A Bayesian Decision Theory Approach for Genomic Selection. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3019-3037.	0.8	4
29	Chapter 13: Augmented Designs-Experimental Designs in Which All Treatments are not Replicated. <i>ACSESS Publications</i> , 2018, , .	0.2	2
30	A study of allelic diversity underlying flowering-time adaptation in maize landraces. <i>Nature Genetics</i> , 2017, 49, 476-480.	9.4	254
31	Genomic-Enabled Prediction in Maize Using Kernel Models with Genotype \times Environment Interaction. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1995-2014.	0.8	92
32	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2315-2326.	0.8	92
33	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. <i>Trends in Plant Science</i> , 2017, 22, 961-975.	4.3	1,004
34	Single-Step Genomic and Pedigree Genotype \times Environment Interaction Models for Predicting Wheat Lines in International Environments. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0089.	1.6	66
35	Predicting grain yield using canopy hyperspectral reflectance in wheat breeding data. <i>Plant Methods</i> , 2017, 13, 4.	1.9	107
36	Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations. <i>Frontiers in Plant Science</i> , 2017, 8, 1916.	1.7	145

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37	Genomic Bayesian functional regression models with interactions for predicting wheat grain yield using hyper-spectral image data. <i>Plant Methods</i> , 2017, 13, 62.	1.9	38
38	Use of Hyperspectral Image Data Outperforms Vegetation Indices in Prediction of Maize Yield. <i>Crop Science</i> , 2017, 57, 2517-2524.	0.8	66
39	Bayesian Genomic Prediction with Genotype \times Environment Interaction Kernel Models. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 41-53.	0.8	126
40	Gains in Maize Genetic Improvement in Eastern and Southern Africa: II. CIMMYT Open-Pollinated Variety Breeding Pipeline. <i>Crop Science</i> , 2017, 57, 180-191.	0.8	63
41	Interrelations among Early Vigor, Flowering Time, Physiological Maturity, and Grain Yield in Tropical Maize (<i>Zea mays</i> L.) under Multiple Abiotic Stresses. <i>Crop Science</i> , 2017, 57, 229-242.	0.8	13
42	Extending the Marker \times Environment Interaction Model for Genomic-Enabled Prediction and Genome-Wide Association Analysis in Durum Wheat. <i>Crop Science</i> , 2016, 56, 2193-2209.	0.8	101
43	Genomic Prediction of Genotype \times Environment Interaction Kernel Regression Models. <i>Plant Genome</i> , 2016, 9, plantgenome2016.03.0024.	1.6	118
44	The Development of Quality Control Genotyping Approaches: A Case Study Using Elite Maize Lines. <i>PLoS ONE</i> , 2016, 11, e0157236.	1.1	67
45	Identification of Tropical Maize Germplasm with Tolerance to Drought, Nitrogen Deficiency, and Combined Heat and Drought Stresses. <i>Crop Science</i> , 2016, 56, 3031-3045.	0.8	26
46	A Hierarchical Bayesian Estimation Model for Multienvironment Plant Breeding Trials in Successive Years. <i>Crop Science</i> , 2016, 56, 2260-2276.	0.8	16
47	Genomic Prediction of Gene Bank Wheat Landraces. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1819-1834.	0.8	159
48	Genomic Bayesian Prediction Model for Count Data with Genotype \times Environment Interaction. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1165-1177.	0.8	26
49	Evaluation and Interpretation of Interactions. <i>Agronomy Journal</i> , 2015, 107, 736-747.	0.9	23
50	Genomic-Enabled Prediction of Ordinal Data with Bayesian Logistic Ordinal Regression. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2113-2126.	0.8	22
51	Holistic Risk Index: A Case Study of Cattle Producers in the Protected Area of Farrapos Estuaries—Uruguay. <i>Agroecology and Sustainable Food Systems</i> , 2015, 39, 209-223.	1.0	4
52	Genomic-enabled prediction with classification algorithms. <i>Heredity</i> , 2014, 112, 616-626.	1.2	52
53	Genomic prediction in CIMMYT maize and wheat breeding programs. <i>Heredity</i> , 2014, 112, 48-60.	1.2	357
54	A DNA Microarray-Based Assay to Detect Dual Infection with Two Dengue Virus Serotypes. <i>Sensors</i> , 2014, 14, 7580-7601.	2.1	13

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55	A reaction norm model for genomic selection using high-dimensional genomic and environmental data. <i>Theoretical and Applied Genetics</i> , 2014, 127, 595-607.	1.8	439
56	Enhancing laccase production by a newly-isolated strain of <i>Pycnoporus sanguineus</i> with high potential for dye decolouration. <i>RSC Advances</i> , 2014, 4, 34096.	1.7	16
57	Effectiveness of selection at CIMMYT's main maize breeding sites in Mexico for performance at sites in Africa and vice versa. <i>Plant Breeding</i> , 2013, 132, 299-304.	1.0	5
58	Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1903-1926.	0.8	235
59	Genomic Prediction of Breeding Values when Modeling Genotype \times Environment Interaction using Pedigree and Dense Molecular Markers. <i>Crop Science</i> , 2012, 52, 707-719.	0.8	478
60	<i>In Vivo</i> Expression of <i>Helicobacter pylori</i> Virulence Genes in Patients with Gastritis, Ulcer, and Gastric Cancer. <i>Infection and Immunity</i> , 2012, 80, 594-601.	1.0	25
61	Genomic Prediction of Genetic Values for Resistance to Wheat Rusts. <i>Plant Genome</i> , 2012, 5, .	1.6	94
62	Molecular and cytogenetic characterization of a collection of bahiagrass (<i>Paspalum notatum</i> Flügge) native to Uruguay. <i>Genetic Resources and Crop Evolution</i> , 2012, 59, 1823-1832.	0.8	16
63	Prediction Assessment of Linear Mixed Models for Multienvironment Trials. <i>Crop Science</i> , 2011, 51, 944-954.	0.8	84
64	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. <i>Genetics</i> , 2010, 186, 713-724.	1.2	664
65	Biplot Analysis of Genotype \times Environment Interaction: Proceed with Caution. <i>Crop Science</i> , 2009, 49, 1564-1576.	0.8	232
66	Classification of Peruvian highland maize races using plant traits. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 151-162.	0.8	62
67	Using Factor Analytic Models for Joining Environments and Genotypes without Crossover Genotype \times Environment Interaction. <i>Crop Science</i> , 2008, 48, 1291-1305.	0.8	86
68	Association Analysis of Historical Bread Wheat Germplasm Using Additive Genetic Covariance of Relatives and Population Structure. <i>Genetics</i> , 2007, 177, 1889-1913.	1.2	426
69	Modeling Additive \times Environment and Additive \times Additive \times Environment Using Genetic Covariances of Relatives of Wheat Genotypes. <i>Crop Science</i> , 2007, 47, 311-320.	0.8	55
70	Modeling Genotype \times Environment Interaction Using Additive Genetic Covariances of Relatives for Predicting Breeding Values of Wheat Genotypes. <i>Crop Science</i> , 2006, 46, 1722-1733.	0.8	113
71	Using linear-bilinear models for studying gene expression \times treatment interaction in microarray experiments. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2005, 10, 337-353.	0.7	5
72	Spatial Analysis of cDNA Microarray Experiments. <i>Crop Science</i> , 2005, 45, 748-757.	0.8	4

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73	SENSORY AND INSTRUMENTAL EVALUATION OF STRAWBERRY YOGURT COLOR. Journal of Sensory Studies, 2001, 16, 11-22.	0.8	10
74	Augmented Designs-Experimental Designs in Which All Treatments are not Replicated. Assa, Cssa and Sssa, 0, , 345-369.	0.6	3
75	Spatial Analysis of Field Experiments. Assa, Cssa and Sssa, 0, , 319-344.	0.6	13