Juan BurgueÃ±o

List of Publications by Year in descending order

75 papers	6,968 citations	117625 34 h-index	76900 74 g-index
79 all docs	79 docs citations	79 times ranked	4963 citing authors

#	Article	IF	Citations
1	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975.	8.8	1,004
2	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. Genetics, 2010, 186, 713-724.	2.9	664
3	Genomic Prediction of Breeding Values when Modeling Genotype Ã— Environment Interaction using Pedigree and Dense Molecular Markers. Crop Science, 2012, 52, 707-719.	1.8	478
4	A reaction norm model for genomic selection using high-dimensional genomic and environmental data. Theoretical and Applied Genetics, 2014, 127, 595-607.	3.6	439
5	Association Analysis of Historical Bread Wheat Germplasm Using Additive Genetic Covariance of Relatives and Population Structure. Genetics, 2007, 177, 1889-1913.	2.9	426
6	Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity, 2014, 112, 48-60.	2.6	357
7	A study of allelic diversity underlying flowering-time adaptation in maize landraces. Nature Genetics, 2017, 49, 476-480.	21.4	254
8	Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 1903-1926.	1.8	235
9	Biplot Analysis of Genotype Ã— Environment Interaction: Proceed with Caution. Crop Science, 2009, 49, 1564-1576.	1.8	232
10	META-R: A software to analyze data from multi-environment plant breeding trials. Crop Journal, 2020, 8, 745-756.	5.2	164
11	Genomic Prediction of Gene Bank Wheat Landraces. G3: Genes, Genomes, Genetics, 2016, 6, 1819-1834.	1.8	159
12	Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations. Frontiers in Plant Science, 2017, 8, 1916.	3.6	145
13	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. Nature Communications, 2020, 11, 4572.	12.8	129
14	Bayesian Genomic Prediction with Genotype Ã— Environment Interaction Kernel Models. G3: Genes, Genomes, Genetics, 2017, 7, 41-53.	1.8	126
15	Genomic Prediction of Genotype Ã— Environment Interaction Kernel Regression Models. Plant Genome, 2016, 9, plantgenome2016.03.0024.	2.8	118
16	Modeling Genotype Ã— Environment Interaction Using Additive Genetic Covariances of Relatives for Predicting Breeding Values of Wheat Genotypes. Crop Science, 2006, 46, 1722-1733.	1.8	113
17	Predicting grain yield using canopy hyperspectral reflectance in wheat breeding data. Plant Methods, 2017, 13, 4.	4.3	107
18	Extending the Marker Ã— Environment Interaction Model for Genomicâ€Enabled Prediction and Genomeâ€Wide Association Analysis in Durum Wheat. Crop Science, 2016, 56, 2193-2209.	1.8	101

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19	Genomic Prediction of Genetic Values for Resistance to Wheat Rusts. Plant Genome, 2012, 5, .	2.8	94
20	Genomic-Enabled Prediction in Maize Using Kernel Models with Genotype Ã— Environment Interaction. G3: Genes, Genomes, Genetics, 2017, 7, 1995-2014.	1.8	92
21	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. G3: Genes, Genomes, Genetics, 2017, 7, 2315-2326.	1.8	92
22	Using Factor Analytic Models for Joining Environments and Genotypes without Crossover Genotype Ã— Environment Interaction. Crop Science, 2008, 48, 1291-1305.	1.8	86
23	Prediction Assessment of Linear Mixed Models for Multienvironment Trials. Crop Science, 2011, 51, 944-954.	1.8	84
24	Genomic Prediction Enhanced Sparse Testing for Multi-environment Trials. G3: Genes, Genomes, Genetics, 2020, 10, 2725-2739.	1.8	68
25	The Development of Quality Control Genotyping Approaches: A Case Study Using Elite Maize Lines. PLoS ONE, 2016, 11, e0157236.	2.5	67
26	Singleâ€Step Genomic and Pedigree Genotype Ã— Environment Interaction Models for Predicting Wheat Lines in International Environments. Plant Genome, 2017, 10, plantgenome2016.09.0089.	2.8	66
27	Use of Hyperspectral Image Data Outperforms Vegetation Indices in Prediction of Maize Yield. Crop Science, 2017, 57, 2517-2524.	1.8	66
28	Gains in Maize Genetic Improvement in Eastern and Southern Africa: II. CIMMYT Openâ€Pollinated Variety Breeding Pipeline. Crop Science, 2017, 57, 180-191.	1.8	63
29	Classification of Peruvian highland maize races using plant traits. Genetic Resources and Crop Evolution, 2008, 55, 151-162.	1.6	62
30	Deep Kernel for Genomic and Near Infrared Predictions in Multi-environment Breeding Trials. G3: Genes, Genomes, Genetics, 2019, 9, 2913-2924.	1.8	61
31	Modeling Additive Ã— Environment and Additive Ã— Additive Ã— Environment Using Genetic Covariances of Relatives of Wheat Genotypes. Crop Science, 2007, 47, 311-320.	1.8	55
32	GWAS to Identify Genetic Loci for Resistance to Yellow Rust in Wheat Pre-Breeding Lines Derived From Diverse Exotic Crosses. Frontiers in Plant Science, 2019, 10, 1390.	3.6	55
33	Genomic-enabled prediction with classification algorithms. Heredity, 2014, 112, 616-626.	2.6	52
34	BGGE: A New Package for Genomic-Enabled Prediction Incorporating Genotype Ã— Environment Interaction Models. G3: Genes, Genomes, Genetics, 2018, 8, 3039-3047.	1.8	47
35	Genomic Bayesian functional regression models with interactions for predicting wheat grain yield using hyper-spectral image data. Plant Methods, 2017, 13, 62.	4.3	38
36	Maximizing efficiency of genomic selection in CIMMYTâ€™s tropical maize breeding program. Theoretical and Applied Genetics, 2021, 134, 279-294.	3.6	36

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37	Genomic-Enabled Prediction Kernel Models with Random Intercepts for Multi-environment Trials. G3: Genes, Genomes, Genetics, 2018, 8, 1347-1365.	1.8	32
38	Identification of Tropical Maize Germplasm with Tolerance to Drought, Nitrogen Deficiency, and Combined Heat and Drought Stresses. Crop Science, 2016, 56, 3031-3045.	1.8	26
39	Genomic Bayesian Prediction Model for Count Data with Genotype Ã— Environment Interaction. G3: Genes, Genomes, Genetics, 2016, 6, 1165-1177.	1.8	26
40	In Vivo Expression of Helicobacter pylori Virulence Genes in Patients with Gastritis, Ulcer, and Gastric Cancer. Infection and Immunity, 2012, 80, 594-601.	2.2	25
41	Identification of donors for low-nitrogen stress with maize lethal necrosis (MLN) tolerance for maize breeding in sub-Saharan Africa. Euphytica, 2019, 215, 80.	1.2	24
42	Evaluation and Interpretation of Interactions. Agronomy Journal, 2015, 107, 736-747.	1.8	23
43	Genomic-Enabled Prediction of Ordinal Data with Bayesian Logistic Ordinal Regression. G3: Genes, Genomes, Genetics, 2015, 5, 2113-2126.	1.8	22
44	Genotype by tillage interaction and performance progress for bread and durum wheat genotypes on irrigated raised beds. Field Crops Research, 2018, 216, 42-52.	5.1	19
45	Maize responsiveness to Azospirillum brasilense: Insights into genetic control, heterosis and genomic prediction. PLoS ONE, 2019, 14, e0217571.	2.5	19
46	Application of Genomic Selection at the Early Stage of Breeding Pipeline in Tropical Maize. Frontiers in Plant Science, 2021, 12, 685488.	3.6	18
47	Multivariate Bayesian Analysis of Onâ€Farm Trials with Multipleâ€Trait and Multipleâ€Environment Data. Agronomy Journal, 2019, 111, 2658-2669.	1.8	17
48	Molecular and cytogenetic characterization of a collection of bahiagrass (Paspalum notatum FlÃ¼gge) native to Uruguay. Genetic Resources and Crop Evolution, 2012, 59, 1823-1832.	1.6	16
49	Enhancing laccase production by a newly-isolated strain of Pycnoporus sanguineus with high potential for dye decolouration. RSC Advances, 2014, 4, 34096.	3.6	16
50	A Hierarchical Bayesian Estimation Model for Multienvironment Plant Breeding Trials in Successive Years. Crop Science, 2016, 56, 2260-2276.	1.8	16
51	Effects of conservation agriculture on physicochemical soil health in 20 maizeâ€based trials in different agroâ€ecological regions across Mexico. Land Degradation and Development, 2021, 32, 2242-2256.	3.9	15
52	Scalable Sparse Testing Genomic Selection Strategy for Early Yield Testing Stage. Frontiers in Plant Science, 2021, 12, 658978.	3.6	15
53	Genomeâ€enabled prediction for sparse testing in multiâ€environmental wheat trials. Plant Genome, 2021, 14, e20151.	2.8	15
54	Disaggregating the Value of Conservation Agriculture to Inform Smallholder Transition to Sustainable Farming: A Mexican Case Study. Agronomy, 2021, 11, 1214.	3.0	14

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55	A DNA Microarray-Based Assay to Detect Dual Infection with Two Dengue Virus Serotypes. Sensors, 2014, 14, 7580-7601.	3.8	13
56	Interrelations among Early Vigor, Flowering Time, Physiological Maturity, and Grain Yield in Tropical Maize (Zea mays L.) under Multiple Abiotic Stresses. Crop Science, 2017, 57, 229-242.	1.8	13
57	Spatial Analysis of Field Experiments. Assa, Cssa and Sssa, 0, , 319-344.	0.6	13
58	SASHAYDIALL: A SAS Program for Hayman's Diallel Analysis. Crop Science, 2018, 58, 1605-1615.	1.8	12
59	Factor analysis to investigate genotype and genotypeâ€‰Ã—â€‰environment interaction effects on pro-vitamin A content and yield in maize synthetics. Euphytica, 2019, 215, 1.	1.2	12
60	Effect of Flowering Time-Related Genes on Biomass, Harvest Index, and Grain Yield in CIMMYT Elite Spring Bread Wheat. Biology, 2021, 10, 855.	2.8	12
61	Bayesian functional regression as an alternative statistical analysis of high-throughput phenotyping data of modern agriculture. Plant Methods, 2018, 14, 46.	4.3	11
62	Effect of F1 and F2 generations on genetic variability and working steps of doubled haploid production in maize. PLoS ONE, 2019, 14, e0224631.	2.5	11
63	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. Agronomy, 2020, 10, 695.	3.0	11
64	Introgression of Maize Diversity for Drought Tolerance: Subtropical Maize Landraces as Source of New Positive Variants. Frontiers in Plant Science, 2021, 12, 691211.	3.6	11
65	SENSORY AND INSTRUMENTAL EVALUATION OF STRAWBERRY YOGURT COLOR. Journal of Sensory Studies, 2001, 16, 11-22.	1.6	10
66	Hybrid Breeding for MLN Resistance: Heterosis, Combining Ability, and Hybrid Prediction. Plants, 2020, 9, 468.	3.5	10
67	Modeling Genotype Ã— Environment Interaction Using a Factor Analytic Model of Onâ€Farm Wheat Trials in the Yaqui Valley of Mexico. Agronomy Journal, 2019, 111, 2647-2657.	1.8	7
68	Using linear-bilinear models for studying gene expression Ã— treatment interaction in microarray experiments. Journal of Agricultural, Biological, and Environmental Statistics, 2005, 10, 337-353.	1.4	5
69	Effectiveness of selection at <scp>CIMMYT</scp>'s main maize breeding sites in Mexico for performance at sites in Africa and vice versa. Plant Breeding, 2013, 132, 299-304.	1.9	5
70	Spatial Analysis of cDNA Microarray Experiments. Crop Science, 2005, 45, 748-757.	1.8	4
71	Holistic Risk Index: A Case Study of Cattle Producers in the Protected Area of Farrapos Estuariesâ€"Uruguay. Agroecology and Sustainable Food Systems, 2015, 39, 209-223.	1.9	4
72	A Bayesian Decision Theory Approach for Genomic Selection. G3: Genes, Genomes, Genetics, 2018, 8, 3019-3037.	1.8	4

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73	Augmented Designs-Experimental Designs in Which All Treatments are not Replicated. Assa, Cssa and Sssa, 0, , 345-369.	0.6	3
74	Chapter 13: Augmented Designs-Experimental Designs in Which All Treatments are not Replicated. ACSESS Publications, 2018, , .	0.2	2
75	isqg: A Binary Framework for in Silico Quantitative Genetics. G3: Genes, Genomes, Genetics, 2019, 9, 2425-2428.	1.8	1