Paulino PÃ©rez-RodrÃguez

List of Publications by Year
in descending order

98	8,073	94381	56687
98	**8,073**	**37**	**83**
papers	citations	h-index	g-index

102	102	102	5874
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic prediction of the performance of hybrids and the combining abilities for line by tester trials in maize. Crop Journal, 2022, 10, 109-116.	2.3	7
2	The power of genomic estimated breeding values for selection when using a finite population size in genetic improvement of tetraploid potato. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	11
3	Genome-Wide Association Study for Resistance to Tan Spot in Synthetic Hexaploid Wheat. Plants, 2022, 11, 433.	1.6	8
4	Genome-Based Genotype Ã— Environment Prediction Enhances Potato (Solanum tuberosum L.) Improvement Using Pseudo-Diploid and Polysomic Tetraploid Modeling. Frontiers in Plant Science, 2022, 13, 785196.	1.7	19
5	Genome and EnvironmentÂBased Prediction Models and Methods of Complex Traits Incorporating Genotype Ã— Environment Interaction. Methods in Molecular Biology, 2022, 2467, 245-283.	0.4	13
6	Genetic diversity in reproductive traits of Braunvieh cattle determined with SNP markers. Veterinary Medicine and Science, 2022, 8, 1709-1720.	0.6	2
7	AnÃ¡lisis espacial bayesiano del Ãndice de Desarrollo Humano municipal, Oaxaca, 2010: una medida de eficiencia. EconomÃa, Sociedad Y Territorio, 2022, 22, 631-659.	0.1	0
8	A review of deep learning applications for genomic selection. BMC Genomics, 2021, 22, 19.	1.2	122
9	Allelic and genotypic frequencies for loci associated with meat quality in Mexican Braunvieh cattle. Tropical Animal Health and Production, 2021, 53, 307.	0.5	2
10	Target Population of Environments for Wheat Breeding in India: Definition, Prediction and Genetic Gains. Frontiers in Plant Science, 2021, 12, 638520.	1.7	26
11	Application of Genomic Selection at the Early Stage of Breeding Pipeline in Tropical Maize. Frontiers in Plant Science, 2021, 12, 685488.	1.7	18
12	lme4GS: An R-Package for Genomic Selection. Frontiers in Genetics, 2021, 12, 680569.	1.1	10
13	Multi-trait genomic-enabled prediction enhances accuracy in multi-year wheat breeding trials. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	13
14	Assessing combining abilities, genomic data, and genotypeÂÃ— environment interactions to predict hybrid grain sorghum performance. Plant Genome, 2021, 14, e20127.	1.6	12
15	Genomeâ€enabled prediction for sparse testing in multiâ€environmental wheat trials. Plant Genome, 2021, 14, e20151.	1.6	15
16	Multi-generation genomic prediction of maize yield using parametric and non-parametric sparse selection indices. Heredity, 2021, 127, 423-432.	1.2	4
17	A Comparison of the Adoption of Genomic Selection Across Different Breeding Institutions. Frontiers in Plant Science, 2021, 12, 728567.	1.7	4
18	Response to Early Generation Genomic Selection for Yield in Wheat. Frontiers in Plant Science, 2021, 12, 718611.	1.7	10

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19	Genetic Diversity and Population Structure for Resistance and Susceptibility to Mastitis in Braunvieh Cattle. Veterinary Sciences, 2021, 8, 329.	0.6	1
20	A data-driven simulation platform to predict cultivars' performances under uncertain weather conditions. Nature Communications, 2020, 11, 4876.	5.8	50
21	Approximate Genome-Based Kernel Models for Large Data Sets Including Main Effects and Interactions. Frontiers in Genetics, 2020, 11, 567757.	1.1	15
22	Genome-based prediction of Bayesian linear and non-linear regression models for ordinal data. Plant Genome, 2020, 13, e20021.	1.6	14
23	Genomic prediction across years in a maize doubled haploid breeding program to accelerate early-stage testcross testing. Theoretical and Applied Genetics, 2020, 133, 2869-2879.	1.8	26
24	Genomic Prediction with Genotype by Environment Interaction Analysis for Kernel Zinc Concentration in Tropical Maize Germplasm. G3: Genes, Genomes, Genetics, 2020, 10, 2629-2639.	0.8	21
25	Genomic prediction of sugar content and cane yield in sugar cane clones in different stages of selection in a breeding program, with and without pedigree information. Molecular Breeding, 2020, 40, 1.	1.0	35
26	Strategies for Effective Use of Genomic Information in Crop Breeding Programs Serving Africa and South Asia. Frontiers in Plant Science, 2020, 11, 353.	1.7	33
27	Bayesian regularized quantile regression: A robust alternative for genome-based prediction of skewed data. Crop Journal, 2020, 8, 713-722.	2.3	5
28	Patterns of Oviposition and Feeding in the Monophagous Fly Anastrepha spatulata (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 T 1178-1186.	0.7	1
29	Deep Kernel and Deep Learning for Genome-Based Prediction of Single Traits in Multienvironment Breeding Trials. Frontiers in Genetics, 2019, 10, 1168.	1.1	77
30	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. PLoS ONE, 2019, 14, e0222337.	1.1	1
31	SNP and Haplotype-Based Genomic Selection of Quantitative Traits in Eucalyptus globulus. Plants, 2019, 8, 331.	1.6	32
32	isqg: A Binary Framework for in Silico Quantitative Genetics. G3: Genes, Genomes, Genetics, 2019, 9, 2425-2428.	0.8	1
33	Maize responsiveness to Azospirillum brasilense: Insights into genetic control, heterosis and genomic prediction. PLoS ONE, 2019, 14, e0217571.	1.1	19
34	Beta-Diversity Modeling and Mapping with LiDAR and Multispectral Sensors in a Semi-Evergreen Tropical Forest. Forests, 2019, 10, 419.	0.9	6
35	An R Package for Bayesian Analysis of Multi-environment and Multi-trait Multi-environment Data for Genome-Based Prediction. G3: Genes, Genomes, Genetics, 2019, 9, 1355-1369.	0.8	39
36	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. G3: Genes, Genomes, Genetics, 2019, 9, 1231-1247.	0.8	96

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37	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.	0.9	7
38	Joint Use of Genome, Pedigree, and Their Interaction with Environment for Predicting the Performance of Wheat Lines in New Environments. G3: Genes, Genomes, Genetics, 2019, 9, 2925-2934.	0.8	13
39	Deep Kernel for Genomic and Near Infrared Predictions in Multi-environment Breeding Trials. G3: Genes, Genomes, Genetics, 2019, 9, 2913-2924.	0.8	61
40	Empirical Comparison of Tropical Maize Hybrids Selected Through Genomic and Phenotypic Selections. Frontiers in Plant Science, 2019, 10, 1502.	1.7	54
41	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. Nature Genetics, 2019, 51, 1530-1539.	9.4	216
42	Hybrid Wheat Prediction Using Genomic, Pedigree, and Environmental Covariables Interaction Models. Plant Genome, 2019, 12, 180051.	1.6	58
43	Multivariate Bayesian Analysis of Onâ€Farm Trials with Multipleâ€Trait and Multipleâ€Environment Data. Agronomy Journal, 2019, 111, 2658-2669.	0.9	17
44	Integrating genomic-enabled prediction and high-throughput phenotyping in breeding for climate-resilient bread wheat. Theoretical and Applied Genetics, 2019, 132, 177-194.	1.8	78
45	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
46	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
47	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
48	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
49	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
50	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
51	Genomic prediction of the general combining ability of maize lines (*Zea mays* L.) and the performance of their single crosses. Plant Breeding, 2018, 137, 379-387.	1.0	14
52	A Bayesian Genomic Regression Model with Skew Normal Random Errors. G3: Genes, Genomes, Genetics, 2018, 8, 1771-1785.	0.8	6
53	Prospects and Challenges of Applied Genomic Selectionâ€"A New Paradigm in Breeding for Grain Yield in Bread Wheat. Plant Genome, 2018, 11, 180017.	1.6	65
54	Artificial Neuronal Networks: A Bayesian Approach Using Parallel Computing. Revista Colombiana De Estadistica, 2018, 41, 173-189.	0.2	2

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55	When less can be better: How can we make genomic selection more cost-effective and accurate in barley?. Theoretical and Applied Genetics, 2018, 131, 1873-1890.	1.8	45
56	Applications of Machine Learning Methods to Genomic Selection in Breeding Wheat for Rust Resistance. Plant Genome, 2018, 11, 170104.	1.6	94
57	A Bayesian Decision Theory Approach for Genomic Selection. G3: Genes, Genomes, Genetics, 2018, 8, 3019-3037.	0.8	4
58	Genomic models with genotype‰Ã—‰environment interaction for predicting hybrid performance: an application in maize hybrids. Theoretical and Applied Genetics, 2017, 130, 1431-1440.	1.8	46
59	Genomic-Enabled Prediction in Maize Using Kernel Models with Genotype Ã— Environment Interaction. G3: Genes, Genomes, Genetics, 2017, 7, 1995-2014.	0.8	92
60	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. G3: Genes, Genomes, Genetics, 2017, 7, 2315-2326.	0.8	92
61	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975.	4.3	1,004
62	Single‐Step Genomic and Pedigree Genotype Ã— Environment Interaction Models for Predicting Wheat Lines in International Environments. Plant Genome, 2017, 10, plantgenome2016.09.0089.	1.6	66
63	Diacylglycerol Kinases Are Widespread in Higher Plants and Display Inducible Gene Expression in Response to Beneficial Elements, Metal, and Metalloid Ions. Frontiers in Plant Science, 2017, 08, 129.	1.7	25
64	Bayesian Genomic Prediction with Genotype Ã— Environment Interaction Kernel Models. G3: Genes, Genomes, Genetics, 2017, 7, 41-53.	0.8	126
65	Bayesian Estimation for the Centered Parameterization of the Skew-Normal Distribution. Revista Colombiana De Estadistica, 2017, 40, 123-140.	0.2	2
66	Identificación de cambios en la ciclogénesis del Atlántico Norte mediante un modelo de mezclas Gaussianas. Tecnologia Y Ciencias Del Agua, 2017, 08, 05-18.	0.1	0
67	Extending the Marker Ã— Environment Interaction Model for Genomic‐Enabled Prediction and Genome‐Wide Association Analysis in Durum Wheat. Crop Science, 2016, 56, 2193-2209.	0.8	101
68	Genomic Prediction of Genotype Ã— Environment Interaction Kernel Regression Models. Plant Genome, 2016, 9, plantgenome2016.03.0024.	1.6	118
69	Plant Proteins Are Smaller Because They Are Encoded by Fewer Exons than Animal Proteins. Genomics, Proteomics and Bioinformatics, 2016, 14, 357-370.	3.0	43
70	Genomic prediction for grain zinc and iron concentrations in spring wheat. Theoretical and Applied Genetics, 2016, 129, 1595-1605.	1.8	93
71	Genomic Prediction of Gene Bank Wheat Landraces. G3: Genes, Genomes, Genetics, 2016, 6, 1819-1834.	0.8	159
72	Genome-enabled prediction using probabilistic neural network classifiers. BMC Genomics, 2016, 17, 208.	1.2	51

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73	Nest site selection and nutritional provision through excreta: a form of parental care in a tropical endogeic earthworm. PeerJ, 2016, 4, e2032.	0.9	5
74	Invasion of the tropical earthworm *Pontoscolex corethrurus* (Rhinodrilidae, Oligochaeta) in temperate grasslands. PeerJ, 2016, 4, e2572.	0.9	9
75	Incorporating Genetic Heterogeneity in Whole-Genome Regressions Using Interactions. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 467-490.	0.7	32
76	A Pedigreeâ€Based Reaction Norm Model for Prediction of Cotton Yield in Multienvironment Trials. Crop Science, 2015, 55, 1143-1151.	0.8	58
77	Selection of the Bandwidth Parameter in a Bayesian Kernel Regression Model for Genomic-Enabled Prediction. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 512-532.	0.7	38
78	Effectiveness of Shrinkage and Variable Selection Methods for the Prediction of Complex Human Traits using Data from Distantly Related Individuals. Annals of Human Genetics, 2015, 79, 122-135.	0.3	14
79	Threshold Models for Genome-Enabled Prediction of Ordinal Categorical Traits in Plant Breeding. G3: Genes, Genomes, Genetics, 2015, 5, 291-300.	0.8	47
80	Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. Heredity, 2015, 114, 291-299.	1.2	187
81	Integrated genomic and BMI analysis for type 2 diabetes risk assessment. Frontiers in Genetics, 2015, 6, 75.	1.1	1
82	Genomic Prediction Models for Count Data. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 533-554.	0.7	18
83	Asexual propagation of Pinus leiophylla Schiede ex Schltdl. et Cham.. Revista Chapingo, Serie Ciencias Forestales Y Del Ambiente, 2015, XXI, 81-95.	0.1	8
84	Genomic-enabled prediction with classification algorithms. Heredity, 2014, 112, 616-626.	1.2	52
85	Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity, 2014, 112, 48-60.	1.2	357
86	Bayesian Genomic-Enabled Prediction as an Inverse Problem. G3: Genes, Genomes, Genetics, 2014, 4, 1991-2001.	0.8	6
87	A reaction norm model for genomic selection using high-dimensional genomic and environmental data. Theoretical and Applied Genetics, 2014, 127, 595-607.	1.8	439
88	Genome-Wide Regression and Prediction with the BGLR Statistical Package. Genetics, 2014, 198, 483-495.	1.2	1,145
89	Host Use and Resource Sharing by Fruit/Seed-Infesting Insects on *Schoepfia schreberi* (Olacaceae). Environmental Entomology, 2013, 42, 231-239.	0.7	4
90	Technical Note: An R package for fitting Bayesian regularized neural networks with applications in animal breeding1. Journal of Animal Science, 2013, 91, 3522-3531.	0.2	43

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91	Comparison Between Linear and Non-parametric Regression Models for Genome-Enabled Prediction in Wheat. G3: Genes, Genomes, Genetics, 2012, 2, 1595-1605.	0.8	187
92	Genome-enabled prediction of genetic values using radial basis function neural networks. Theoretical and Applied Genetics, 2012, 125, 759-771.	1.8	180
93	Mathematical modeling and comparison of protein size distribution in different plant, animal, fungal and microbial species reveals a negative correlation between protein size and protein number, thus providing insight into the evolution of proteomes. BMC Research Notes, 2012, 5, 85.	0.6	93
94	Genomic Selection and Prediction in Plant Breeding. Journal of Crop Improvement, 2011, 25, 239-261.	0.9	131
95	A growth phenotyping pipeline for <i>Arabidopsis thaliana</i> integrating image analysis and rosette area modeling for robust quantification of genotype effects. New Phytologist, 2011, 191, 895-907.	3.5	178
96	PlnTFDB: updated content and new features of the plant transcription factor database. Nucleic Acids Research, 2010, 38, D822-D827.	6.5	635
97	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. Genetics, 2010, 186, 713-724.	1.2	664
98	A Goodness-of-Fit Test for the Gumbel Distribution Based on Kullbackâ€"Leibler Information. Communications in Statistics - Theory and Methods, 2009, 38, 842-855.	0.6	17