Paulino PÃ©rez-RodrÃguez

List of Publications by Year
in descending order

98 papers	8,073 citations	94381 37 h-index	56687 83 g-index
102 all docs	102 docs citations	102 times ranked	5874 citing authors

#	Article	IF	Citations
1	Genome-Wide Regression and Prediction with the BGLR Statistical Package. Genetics, 2014, 198, 483-495.	1.2	1,145
2	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975.	4.3	1,004
3	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. Genetics, 2010, 186, 713-724.	1.2	664
4	PlnTFDB: updated content and new features of the plant transcription factor database. Nucleic Acids Research, 2010, 38, D822-D827.	6.5	635
5	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
6	Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity, 2014, 112, 48-60.	1.2	357
7	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. Nature Genetics, 2019, 51, 1530-1539.	9.4	216
8	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
9	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
10	Genome-enabled prediction of genetic values using radial basis function neural networks. Theoretical and Applied Genetics, 2012, 125, 759-771.	1.8	180
11	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
12	Genomic Prediction of Gene Bank Wheat Landraces. G3: Genes, Genomes, Genetics, 2016, 6, 1819-1834.	0.8	159
13	Genomic Selection and Prediction in Plant Breeding. Journal of Crop Improvement, 2011, 25, 239-261.	0.9	131
14	Bayesian Genomic Prediction with Genotype Ã— Environment Interaction Kernel Models. G3: Genes, Genomes, Genetics, 2017, 7, 41-53.	0.8	126
15	A review of deep learning applications for genomic selection. BMC Genomics, 2021, 22, 19.	1.2	122
16	Genomic Prediction of Genotype Ã— Environment Interaction Kernel Regression Models. Plant Genome, 2016, 9, plantgenome2016.03.0024.	1.6	118
17	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.	0.8	101
18	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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19	Applications of Machine Learning Methods to Genomic Selection in Breeding Wheat for Rust Resistance. Plant Genome, 2018, 11, 170104.	1.6	94
20	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
21	Genomic prediction for grain zinc and iron concentrations in spring wheat. Theoretical and Applied Genetics, 2016, 129, 1595-1605.	1.8	93
22	Genomic-Enabled Prediction in Maize Using Kernel Models with Genotype Ã— Environment Interaction. G3: Genes, Genomes, Genetics, 2017, 7, 1995-2014.	0.8	92
23	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. G3: Genes, Genomes, Genetics, 2017, 7, 2315-2326.	0.8	92
24	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
25	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
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.	1.6	66
27	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
28	Deep Kernel for Genomic and Near Infrared Predictions in Multi-environment Breeding Trials. G3: Genes, Genomes, Genetics, 2019, 9, 2913-2924.	0.8	61
29	A Pedigreeâ€Based Reaction Norm Model for Prediction of Cotton Yield in Multienvironment Trials. Crop Science, 2015, 55, 1143-1151.	0.8	58
30	Hybrid Wheat Prediction Using Genomic, Pedigree, and Environmental Covariables Interaction Models. Plant Genome, 2019, 12, 180051.	1.6	58
31	Empirical Comparison of Tropical Maize Hybrids Selected Through Genomic and Phenotypic Selections. Frontiers in Plant Science, 2019, 10, 1502.	1.7	54
32	Genomic-enabled prediction with classification algorithms. Heredity, 2014, 112, 616-626.	1.2	52
33	Genome-enabled prediction using probabilistic neural network classifiers. BMC Genomics, 2016, 17, 208.	1.2	51
34	A data-driven simulation platform to predict cultivarsâ€™ performances under uncertain weather conditions. Nature Communications, 2020, 11, 4876.	5.8	50
35	Threshold Models for Genome-Enabled Prediction of Ordinal Categorical Traits in Plant Breeding. G3: Genes, Genomes, Genetics, 2015, 5, 291-300.	0.8	47
36	Genomic models with genotypeâ€‰Ã—â€‰environment interaction for predicting hybrid performance: an application in maize hybrids. Theoretical and Applied Genetics, 2017, 130, 1431-1440.	1.8	46

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37	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
38	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
39	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
40	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
41	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
42	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
43	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
44	Incorporating Genetic Heterogeneity in Whole-Genome Regressions Using Interactions. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 467-490.	0.7	32
45	SNP and Haplotype-Based Genomic Selection of Quantitative Traits in Eucalyptus globulus. Plants, 2019, 8, 331.	1.6	32
46	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
47	Target Population of Environments for Wheat Breeding in India: Definition, Prediction and Genetic Gains. Frontiers in Plant Science, 2021, 12, 638520.	1.7	26
48	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
49	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
50	Maize responsiveness to Azospirillum brasilense: Insights into genetic control, heterosis and genomic prediction. PLoS ONE, 2019, 14, e0217571.	1.1	19
51	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
52	Genomic Prediction Models for Count Data. Journal of Agricultural, Biological, and Environmental Statistics, 2015, 20, 533-554.	0.7	18
53	Application of Genomic Selection at the Early Stage of Breeding Pipeline in Tropical Maize. Frontiers in Plant Science, 2021, 12, 685488.	1.7	18
54	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

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55	Multivariate Bayesian Analysis of Onâ€Farm Trials with Multipleâ€Trait and Multipleâ€Environment Data. Agronomy Journal, 2019, 111, 2658-2669.	0.9	17
56	Approximate Genome-Based Kernel Models for Large Data Sets Including Main Effects and Interactions. Frontiers in Genetics, 2020, 11, 567757.	1.1	15
57	Genomeâ€enabled prediction for sparse testing in multiâ€environmental wheat trials. Plant Genome, 2021, 14, e20151.	1.6	15
58	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
59	Genomic prediction of the general combining ability of maize lines (<i>Zea mays</i> L.) and the performance of their single crosses. Plant Breeding, 2018, 137, 379-387.	1.0	14
60	Genomeâ€based prediction of Bayesian linear and nonâ€linear regression models for ordinal data. Plant Genome, 2020, 13, e20021.	1.6	14
61	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
62	Multi-trait genomic-enabled prediction enhances accuracy in multi-year wheat breeding trials. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	13
63	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
64	Assessing combining abilities, genomic data, and genotypeÂÃ— environment interactions to predict hybrid grain sorghum performance. Plant Genome, 2021, 14, e20127.	1.6	12
65	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
66	lme4GS: An R-Package for Genomic Selection. Frontiers in Genetics, 2021, 12, 680569.	1.1	10
67	Response to Early Generation Genomic Selection for Yield in Wheat. Frontiers in Plant Science, 2021, 12, 718611.	1.7	10
68	Invasion of the tropical earthworm<i>Pontoscolex corethrurus</i>(Rhinodrilidae, Oligochaeta) in temperate grasslands. PeerJ, 2016, 4, e2572.	0.9	9
69	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
70	Genome-Wide Association Study for Resistance to Tan Spot in Synthetic Hexaploid Wheat. Plants, 2022, 11, 433.	1.6	8
71	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
72	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

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73	Bayesian Genomic-Enabled Prediction as an Inverse Problem. G3: Genes, Genomes, Genetics, 2014, 4, 1991-2001.	0.8	6
74	A Bayesian Genomic Regression Model with Skew Normal Random Errors. G3: Genes, Genomes, Genetics, 2018, 8, 1771-1785.	0.8	6
75	Beta-Diversity Modeling and Mapping with LiDAR and Multispectral Sensors in a Semi-Evergreen Tropical Forest. Forests, 2019, 10, 419.	0.9	6
76	Bayesian regularized quantile regression: A robust alternative for genome-based prediction of skewed data. Crop Journal, 2020, 8, 713-722.	2.3	5
77	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
78	Host Use and Resource Sharing by Fruit/Seed-Infesting Insects on<i>Schoepfia schreberi</i>(Olacaceae). Environmental Entomology, 2013, 42, 231-239.	0.7	4
79	A Bayesian Decision Theory Approach for Genomic Selection. G3: Genes, Genomes, Genetics, 2018, 8, 3019-3037.	0.8	4
80	Multi-generation genomic prediction of maize yield using parametric and non-parametric sparse selection indices. Heredity, 2021, 127, 423-432.	1.2	4
81	A Comparison of the Adoption of Genomic Selection Across Different Breeding Institutions. Frontiers in Plant Science, 2021, 12, 728567.	1.7	4
82	Artificial Neuronal Networks: A Bayesian Approach Using Parallel Computing. Revista Colombiana De Estadistica, 2018, 41, 173-189.	0.2	2
83	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
84	Bayesian Estimation for the Centered Parameterization of the Skew-Normal Distribution. Revista Colombiana De Estadistica, 2017, 40, 123-140.	0.2	2
85	Genetic diversity in reproductive traits of Braunvieh cattle determined with SNP markers. Veterinary Medicine and Science, 2022, 8, 1709-1720.	0.6	2
86	Integrated genomic and BMI analysis for type 2 diabetes risk assessment. Frontiers in Genetics, 2015, 6, 75.	1.1	1
87	Patterns of Oviposition and Feeding in the Monophagous Fly Anastrepha spatulata (Diptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 1178-1186.	0.7	1
88	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. PLoS ONE, 2019, 14, e0222337.	1.1	1
89	isqg: A Binary Framework for in Silico Quantitative Genetics. G3: Genes, Genomes, Genetics, 2019, 9, 2425-2428.	0.8	1
90	Genetic Diversity and Population Structure for Resistance and Susceptibility to Mastitis in Braunvieh Cattle. Veterinary Sciences, 2021, 8, 329.	0.6	1

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91	IdentificaciÃ³n de cambios en la ciclogÃ©nesis del AtlÃ¡ntico Norte mediante un modelo de mezclas Gaussianas. Tecnologia Y Ciencias Del Agua, 2017, 08, 05-18.	0.1	0
92	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
93	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
94	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
95	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
96	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
97	Pontoscolex corethrurus: A homeless invasive tropical earthworm?. , 2019, 14, e0222337.		0
98	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