

Gustavo de Los Campos

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

83

papers

6,781

citations

36

h-index

82

g-index

97

ext. papers

9,204

ext. citations

5.3

avg, IF

6.2

L-index

#	Paper	IF	Citations
83	Genome-wide regression and prediction with the BGLR statistical package. <i>Genetics</i> , 2014 , 198, 483-95	4	618
82	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. <i>Trends in Plant Science</i> , 2017 , 22, 961-975	13.1	548
81	Whole-genome regression and prediction methods applied to plant and animal breeding. <i>Genetics</i> , 2013 , 193, 327-45	4	544
80	Prediction of genetic values of quantitative traits in plant breeding using pedigree and molecular markers. <i>Genetics</i> , 2010 , 186, 713-24	4	508
79	Predicting quantitative traits with regression models for dense molecular markers and pedigree. <i>Genetics</i> , 2009 , 182, 375-85	4	392
78	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	2.4	336
77	Additive genetic variability and the Bayesian alphabet. <i>Genetics</i> , 2009 , 183, 347-63	4	308
76	A reaction norm model for genomic selection using high-dimensional genomic and environmental data. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 595-607	6	275
75	Genomic prediction in animals and plants: simulation of data, validation, reporting, and benchmarking. <i>Genetics</i> , 2013 , 193, 347-65	4	251
74	Prediction of complex human traits using the genomic best linear unbiased predictor. <i>PLoS Genetics</i> , 2013 , 9, e1003608	6	225
73	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. <i>Genetical Research</i> , 2010 , 92, 295-308	1.1	221
72	Predicting genetic predisposition in humans: the promise of whole-genome markers. <i>Nature Reviews Genetics</i> , 2010 , 11, 880-6	30.1	205
71	Beyond missing heritability: prediction of complex traits. <i>PLoS Genetics</i> , 2011 , 7, e1002051	6	192
70	Genomic heritability: what is it?. <i>PLoS Genetics</i> , 2015 , 11, e1005048	6	183
69	Increased prediction accuracy in wheat breeding trials using a marker \times environment interaction genomic selection model. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 569-82	3.2	155
68	Unraveling additive from nonadditive effects using genomic relationship matrices. <i>Genetics</i> , 2014 , 198, 1759-68	4	101
67	Genomic Selection and Prediction in Plant Breeding. <i>Journal of Crop Improvement</i> , 2011 , 25, 239-261	1.4	100

66	Factors Affecting the Accuracy of Genotype Imputation in Populations from Several Maize Breeding Programs. <i>Crop Science</i> , 2012 , 52, 654-663	2.4	98
65	Can Deep Learning Improve Genomic Prediction of Complex Human Traits?. <i>Genetics</i> , 2018 , 210, 809-819	4	79
64	Bayesian Genomic Prediction with Genotype \times Environment Interaction Kernel Models. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 41-53	3.2	75
63	Predicting grain yield using canopy hyperspectral reflectance in wheat breeding data. <i>Plant Methods</i> , 2017 , 13, 4	5.8	72
62	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	2.4	69
61	Accurate Genomic Prediction of Human Height. <i>Genetics</i> , 2018 , 210, 477-497	4	67
60	Searching for recursive causal structures in multivariate quantitative genetics mixed models. <i>Genetics</i> , 2010 , 185, 633-44	4	64
59	Inferences from genomic models in stratified populations. <i>Genetics</i> , 2012 , 192, 693-704	4	56
58	Genome-wide association study reveals putative regulators of bioenergy traits in <i>Populus deltoides</i> . <i>New Phytologist</i> , 2017 , 213, 799-811	9.8	51
57	Inferring genetic values for quantitative traits non-parametrically. <i>Genetical Research</i> , 2008 , 90, 525-40	1.1	48
56	Assessment of Genetic Heterogeneity in Structured Plant Populations Using Multivariate Whole-Genome Regression Models. <i>Genetics</i> , 2015 , 201, 323-37	4	46
55	A comprehensive genetic approach for improving prediction of skin cancer risk in humans. <i>Genetics</i> , 2012 , 192, 1493-502	4	44
54	Modeling relationships between calving traits: a comparison between standard and recursive mixed models. <i>Genetics Selection Evolution</i> , 2010 , 42, 1	4.9	43
53	Do Molecular Markers Inform About Pleiotropy?. <i>Genetics</i> , 2015 , 201, 23-9	4	42
52	A Pedigree-Based Reaction Norm Model for Prediction of Cotton Yield in Multienvironment Trials. <i>Crop Science</i> , 2015 , 55, 1143-1151	2.4	42
51	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, 1425-38	4	41
50	Transcriptome-Based Prediction of Complex Traits in Maize. <i>Plant Cell</i> , 2020 , 32, 139-151	11.6	38
49	Benchmarking Parametric and Machine Learning Models for Genomic Prediction of Complex Traits. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 3691-3702	3.2	37

48	Heritability of pulmonary function estimated from pedigree and whole-genome markers. <i>Frontiers in Genetics</i> , 2013 , 4, 174	4.5	36
47	Use of Hyperspectral Image Data Outperforms Vegetation Indices in Prediction of Maize Yield. <i>Crop Science</i> , 2017 , 57, 2517-2524	2.4	35
46	Will Big Data Close the Missing Heritability Gap?. <i>Genetics</i> , 2017 , 207, 1135-1145	4	34
45	Complex-Trait Prediction in the Era of Big Data. <i>Trends in Genetics</i> , 2018 , 34, 746-754	8.5	30
44	Genomic models with genotype \times environment interaction for predicting hybrid performance: an application in maize hybrids. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1431-1440	6	29
43	Bayesian analysis and prediction of hybrid performance. <i>Plant Methods</i> , 2019 , 15, 14	5.8	25
42	Diagnosing pregnancy status using infrared spectra and milk composition in dairy cows. <i>Journal of Dairy Science</i> , 2018 , 101, 2496-2505	4	25
41	Incorporating Genetic Heterogeneity in Whole-Genome Regressions Using Interactions. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2015 , 20, 467-490	1.9	24
40	Heat Maps of Hypertension, Diabetes Mellitus, and Smoking in the Continental United States. <i>Circulation: Cardiovascular Quality and Outcomes</i> , 2017 , 10,	5.8	23
39	A data-driven simulation platform to predict cultivars performances under uncertain weather conditions. <i>Nature Communications</i> , 2020 , 11, 4876	17.4	21
38	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , 2017 , 205, 939-953	4	20
37	Imperfect Linkage Disequilibrium Generates Phantom Epistasis (& Perils of Big Data). <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1429-1436	3.2	19
36	Prediction of years of life after diagnosis of breast cancer using omics and omic-by-treatment interactions. <i>European Journal of Human Genetics</i> , 2017 , 25, 538-544	5.3	18
35	Multiple metabolic genetic risk scores and type 2 diabetes risk in three racial/ethnic groups. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2014 , 99, E1814-8	5.6	18
34	Modeling Heterogeneity in the Genetic Architecture of Ethnically Diverse Groups Using Random Effect Interaction Models. <i>Genetics</i> , 2019 , 211, 1395-1407	4	18
33	HaploBlocker: Creation of Subgroup-Specific Haplotype Blocks and Libraries. <i>Genetics</i> , 2019 , 212, 1045-1061	4	17
32	Changes in milk characteristics and fatty acid profile during the estrous cycle in dairy cows. <i>Journal of Dairy Science</i> , 2018 , 101, 9135-9153	4	17
31	Genetic Control of Environmental Variation of Two Quantitative Traits of <i>Drosophila melanogaster</i> Revealed by Whole-Genome Sequencing. <i>Genetics</i> , 2015 , 201, 487-97	4	15

30	Prediction of expected years of life using whole-genome markers. <i>PLoS ONE</i> , 2012 , 7, e40964	3.7	15
29	FW: An R Package for Finlay-Wilkinson Regression that Incorporates Genomic/Pedigree Information and Covariance Structures Between Environments. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 6, 589-97	3.2	15
28	Regularized selection indices for breeding value prediction using hyper-spectral image data. <i>Scientific Reports</i> , 2020 , 10, 8195	4.9	14
27	Phantom Epistasis in Genomic Selection: On the Predictive Ability of Epistatic Models. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3137-3145	3.2	13
26	Sex Disparities in Enrollment in Recent Randomized Clinical Trials of Acute Stroke: A Meta-analysis. <i>JAMA Neurology</i> , 2021 , 78, 666-677	17.2	12
25	Untangling the complex relationships between incident gout risk, serum urate, and its comorbidities. <i>Arthritis Research and Therapy</i> , 2018 , 20, 90	5.7	10
24	Whole-Genome Multi-omic Study of Survival in Patients with Glioblastoma Multiforme. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3627-3636	3.2	10
23	Effectiveness of shrinkage and variable selection methods for the prediction of complex human traits using data from distantly related individuals. <i>Annals of Human Genetics</i> , 2015 , 79, 122-35	2.2	9
22	Performance of four models for eye color prediction in an Italian population sample. <i>Forensic Science International: Genetics</i> , 2019 , 40, 192-200	4.3	8
21	A Scale-Corrected Comparison of Linkage Disequilibrium Levels between Genic and Non-Genic Regions. <i>PLoS ONE</i> , 2015 , 10, e0141216	3.7	8
20	Accelerating forest tree breeding by integrating genomic selection and greenhouse phenotyping. <i>Plant Genome</i> , 2020 , 13, e20048	4.4	8
19	Bayesian functional regression as an alternative statistical analysis of high-throughput phenotyping data of modern agriculture. <i>Plant Methods</i> , 2018 , 14, 46	5.8	7
18	A commentary on Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013 , 14, 894	30.1	7
17	Xylem systems genetics analysis reveals a key regulator of lignin biosynthesis in. <i>Genome Research</i> , 2020 , 30, 1131-1143	9.7	7
16	Assessing the burden of COVID-19 in developing countries: systematic review, meta-analysis and public policy implications. <i>BMJ Global Health</i> , 2022 , 7, e008477	6.6	7
15	BGData - A Suite of R Packages for Genomic Analysis with Big Data. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1377-1383	3.2	6
14	Microarray Gene Expression Dataset Re-analysis Reveals Variability in Influenza Infection and Vaccination. <i>Frontiers in Immunology</i> , 2019 , 10, 2616	8.4	6
13	Optimal breeding-value prediction using a sparse selection index. <i>Genetics</i> , 2021 , 218,	4	6

12	Modelling heterogeneity among fitness functions using random regression. <i>Methods in Ecology and Evolution</i> , 2016 , 7, 70-79	7.7	4
11	Opportunities and limits of combining microbiome and genome data for complex trait prediction. <i>Genetics Selection Evolution</i> , 2021 , 53, 65	4.9	3
10	Age-specific rate of severe and critical SARS-CoV-2 infections estimated with multi-country seroprevalence studies.. <i>BMC Infectious Diseases</i> , 2022 , 22, 311	4	3
9	Breast cancer survival and the expression of genes related to alcohol drinking. <i>PLoS ONE</i> , 2020 , 15, e0223957	3.7	2
8	OCMA: Fast, Memory-Efficient Factorization of Prohibitively Large Relationship Matrices. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 13-19	3.2	1
7	Regularized selection indices for breeding value prediction using hyper-spectral image data		1
6	Multi-generation genomic prediction of maize yield using parametric and non-parametric sparse selection indices. <i>Heredity</i> , 2021 , 127, 423-432	3.6	1
5	Deciphering Sex-Specific Genetic Architectures Using Local Bayesian Regressions. <i>Genetics</i> , 2020 , 215, 231-241	4	0
4	The Genetic Regulation of Alternative Splicing in. <i>Frontiers in Plant Science</i> , 2020 , 11, 590	6.2	0
3	Comparing Genomic Prediction Models by Means of Cross Validation. <i>Frontiers in Plant Science</i> , 2021 , 12, 734512	6.2	0
2	ANOVA-HD: Analysis of variance when both input and output layers are high-dimensional. <i>PLoS ONE</i> , 2020 , 15, e0243251	3.7	0
1	Mapping pleiotropic loci using a fast-sequential testing algorithm. <i>European Journal of Human Genetics</i> , 2021 , 29, 1762-1773	5.3	0