JosÃ© Crossa

List of Publications by Year
in descending order

573 papers	30,517 citations	4351 88 h-index	10969 139 g-index
614 all docs	614 docs citations	614 times ranked	23561 citing authors

#	Article	IF	Citations
1	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975.	9.1	1,094
2	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. Genetics, 2010, 186, 713-724.	2.9	677
3	Autoantibodies against IL-17A, IL-17F, and IL-22 in patients with chronic mucocutaneous candidiasis and autoimmune polyendocrine syndrome type I. Journal of Experimental Medicine, 2010, 207, 291-297.	8.8	674
4	Genomic Selection in Wheat Breeding using Genotypingâ€byâ€Sequencing. Plant Genome, 2012, 5, .	3.2	571
5	Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree. Genetics, 2009, 182, 375-385.	2.9	528
6	A reaction norm model for genomic selection using high-dimensional genomic and environmental data. Theoretical and Applied Genetics, 2014, 127, 595-607.	3.7	467
7	Statistical Analyses of Multilocation Trials. Advances in Agronomy, 1990, , 55-85.	3.7	383
8	Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity, 2014, 112, 48-60.	2.7	371
9	Canopy Temperature and Vegetation Indices from High-Throughput Phenotyping Improve Accuracy of Pedigree and Genomic Selection for Grain Yield in Wheat. G3: Genes, Genomes, Genetics, 2016, 6, 2799-2808.	1.9	354
10	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. Genetical Research, 2010, 92, 295-308.	0.9	326
11	Breeding schemes for the implementation of genomic selection in wheat (Triticum spp .). Plant Science, 2016, 242, 23-36.	3.8	312
12	Additive Main Effects and Multiplicative Interaction Analysis of Two International Maize Cultivar Trials. Crop Science, 1990, 30, 493-500.	1.9	309
13	Highâ€throughput Phenotyping and Genomic Selection: The Frontiers of Crop Breeding Converge^F. Journal of Integrative Plant Biology, 2012, 54, 312-320.	9.2	292
14	Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker Ã— Environment Interaction Genomic Selection Model. G3: Genes, Genomes, Genetics, 2015, 5, 569-582.	1.9	279
15	Genetic Gains in Grain Yield Through Genomic Selection in Eight Biâ€parental Maize Populations under Drought Stress. Crop Science, 2015, 55, 154-163.	1.9	262
16	Identification of Drought, Heat, and Combined Drought and Heat Tolerant Donors in Maize. Crop Science, 2013, 53, 1335-1346.	1.9	250
17	Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. G3: Genes, Genomes, Genetics, 2012, 2, 1427-1436.	1.9	246
18	Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 1903-1926.	1.9	244

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19	Biplot Analysis of Genotype Ã— Environment Interaction: Proceed with Caution. Crop Science, 2009, 49, 1564-1576.	1.9	239
20	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. Nature Genetics, 2019, 51, 1530-1539.	20.4	233
21	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. Nature Genetics, 2019, 51, 857-864.	20.4	231
22	Two Types of GGE Biplots for Analyzing Multiâ€Environment Trial Data. Crop Science, 2001, 41, 656-663.	1.9	223
23	Comparison Between Linear and Non-parametric Regression Models for Genome-Enabled Prediction in Wheat. G3: Genes, Genomes, Genetics, 2012, 2, 1595-1605.	1.9	197
24	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.	2.7	193
25	META-R: A software to analyze data from multi-environment plant breeding trials. Crop Journal, 2020, 8, 745-756.	5.3	189
26	Genome-enabled prediction of genetic values using radial basis function neural networks. Theoretical and Applied Genetics, 2012, 125, 759-771.	3.7	188
27	Genomicâ€Enabled Prediction Based on Molecular Markers and Pedigree Using the Bayesian Linear Regression Package in R. Plant Genome, 2010, 3, 106-116.	3.2	187
28	Regional brain contents of serotonin, dopamine and their metabolites in the selectively bred high- and low-alcohol drinking lines of rats. Alcohol, 1989, 6, 317-320.	2.0	176
29	Race non-specific resistance to rust diseases in CIMMYT spring wheats. Euphytica, 2011, 179, 175-186.	1.2	176
30	Genetic Yield Gains and Changes in Associated Traits of CIMMYT Spring Bread Wheat in a â€œHistoricâ€•Set Representing 30 Years of Breeding. Crop Science, 2012, 52, 1123-1131.	1.9	175
31	Evaluation of Genomic Selection Training Population Designs and Genotyping Strategies in Plant Breeding Programs Using Simulation. Crop Science, 2014, 54, 1476-1488.	1.9	175
32	Bringing wild relatives back into the family: recovering genetic diversity in CIMMYT improved wheat germplasm. Euphytica, 2006, 149, 289-301.	1.2	168
33	Genomic Prediction of Gene Bank Wheat Landraces. G3: Genes, Genomes, Genetics, 2016, 6, 1819-1834.	1.9	167
34	Phylogenetic and Multivariate Analyses To Determine the Effects of Different Tillage and Residue Management Practices on Soil Bacterial Communities. Applied and Environmental Microbiology, 2010, 76, 3685-3691.	3.2	159
35	AMMI adjustment for statistical analysis of an international wheat yield trial. Theoretical and Applied Genetics, 1991, 81, 27-37.	3.7	158
36	Wheat genetic resources enhancement by the International Maize and Wheat Improvement Center (CIMMYT). Genetic Resources and Crop Evolution, 2008, 55, 1095-1140.	1.6	158

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37	The Modern Plant Breeding Triangle: Optimizing the Use of Genomics, Phenomics, and Enviromics Data. Frontiers in Plant Science, 2021, 12, 651480.	3.8	153
38	Sites Regression and Shifted Multiplicative Model Clustering of Cultivar Trial Sites under Heterogeneity of Error Variances. Crop Science, 1997, 37, 406-415.	1.9	151
39	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.	3.8	151
40	Core Hunter: an algorithm for sampling genetic resources based on multiple genetic measures. BMC Bioinformatics, 2009, 10, 243.	2.7	146
41	Multitrait, Random Regression, or Simple Repeatability Model in Highâ€Throughput Phenotyping Data Improve Genomic Prediction for Wheat Grain Yield. Plant Genome, 2017, 10, plantgenome2016.11.0111.	3.2	146
42	A review of deep learning applications for genomic selection. BMC Genomics, 2021, 22, 19.	2.9	145
43	Earliness in wheat: A key to adaptation under terminal and continual high temperature stress in South Asia. Field Crops Research, 2013, 151, 19-26.	5.2	144
44	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. Nature Communications, 2020, 11, 4572.	13.2	144
45	Genetic Characterization of CIMMYT Inbred Maize Lines and Open Pollinated Populations Using Large Scale Fingerprinting Methods. Crop Science, 2002, 42, 1832-1840.	1.9	142
46	Energy saving electrochromic windows from bistable low-HOMO level conjugated polymers. Energy and Environmental Science, 2016, 9, 117-122.	32.2	141
47	A multi-trait multi-environment QTL mixed model with an application to drought and nitrogen stress trials in maize (Zea maysÂL.). Euphytica, 2008, 161, 241-257.	1.2	139
48	High yield potential, shuttle breeding, genetic diversity, and a new international wheat improvement strategy. Euphytica, 2007, 157, 365-384.	1.2	137
49	Agronomic Effects from Chromosome Translocations 7DL.7Ag and 1BL.1RS in Spring Wheat. Crop Science, 1998, 38, 27-33.	1.9	136
50	Genomic Selection and Prediction in Plant Breeding. Journal of Crop Improvement, 2011, 25, 239-261.	1.6	134
51	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. Frontiers in Plant Science, 2016, 7, 1666.	3.8	132
52	Performance of biofortified spring wheat genotypes in target environments for grain zinc and iron concentrations. Field Crops Research, 2012, 137, 261-267.	5.2	129
53	Bayesian Genomic Prediction with Genotype Ã— Environment Interaction Kernel Models. G3: Genes, Genomes, Genetics, 2017, 7, 41-53.	1.9	129
54	Long-term consequences of tillage, residue management, and crop rotation on maize/wheat root rot and nematode populations in subtropical highlands. Applied Soil Ecology, 2006, 32, 305-315.	4.4	125

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55	Using Partial Least Squares Regression, Factorial Regression, and AMMI Models for Interpreting Genotype Ã— Environment Interaction. Crop Science, 1999, 39, 955-967.	1.9	124
56	Genomic Prediction of Genotype Ã— Environment Interaction Kernel Regression Models. Plant Genome, 2016, 9, plantgenome2016.03.0024.	3.2	123
57	Multi-environment Genomic Prediction of Plant Traits Using Deep Learners With Dense Architecture. G3: Genes, Genomes, Genetics, 2018, 8, 3813-3828.	1.9	123
58	A chickpea genetic variation map based on the sequencing of 3,366 genomes. Nature, 2021, 599, 622-627.	36.2	122
59	FDA-Approved Drugs with Potent In Vitro Antiviral Activity against Severe Acute Respiratory Syndrome Coronavirus 2. Pharmaceuticals, 2020, 13, 443.	3.9	121
60	Factors Affecting the Accuracy of Genotype Imputation in Populations from Several Maize Breeding Programs. Crop Science, 2012, 52, 654-663.	1.9	119
61	A Genomic Bayesian Multi-trait and Multi-environment Model. G3: Genes, Genomes, Genetics, 2016, 6, 2725-2744.	1.9	119
62	Increasing Genomicâ€Enabled Prediction Accuracy by Modeling Genotype Ã— Environment Interactions in Kansas Wheat. Plant Genome, 2017, 10, plantgenome2016.12.0130.	3.2	119
63	Modeling Genotype Ã— Environment Interaction Using Additive Genetic Covariances of Relatives for Predicting Breeding Values of Wheat Genotypes. Crop Science, 2006, 46, 1722-1733.	1.9	118
64	Long-term consequences of tillage, residue management, and crop rotation on selected soil micro-flora groups in the subtropical highlands. Applied Soil Ecology, 2008, 38, 197-210.	4.4	118
65	Searching for novel sources of field resistance to Ug99 and Ethiopian stem rust races in durum wheat via association mapping. Theoretical and Applied Genetics, 2013, 126, 1237-1256.	3.7	117
66	Harnessing genetic potential of wheat germplasm banks through impact-oriented-prebreeding for future food and nutritional security. Scientific Reports, 2018, 8, 12527.	3.4	117
67	Classifying Genetic Resources by Categorical and Continuous Variables. Crop Science, 1998, 38, 1688-1696.	1.9	116
68	The Japanese Clinical Practice Guidelines for Management of Sepsis and Septic Shock 2020 (J-SSCG) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.9	115
69	Mapping QTLs and QTLÂÃ—Âenvironment interaction for CIMMYT maize drought stress program using factorial regression and partial least squares methods. Theoretical and Applied Genetics, 2006, 112, 1009-1023.	3.7	114
70	Response to drought and heat stress on wheat quality, with special emphasis on bread-making quality, in durum wheat. Field Crops Research, 2016, 186, 157-165.	5.2	113
71	Multi-trait, Multi-environment Deep Learning Modeling for Genomic-Enabled Prediction of Plant Traits. G3: Genes, Genomes, Genetics, 2018, 8, 3829-3840.	1.9	113
72	Genetic analysis of adult plant, quantitative resistance to stripe rust in wheat cultivar â€˜Stephensâ€™ in multi-environment trials. Theoretical and Applied Genetics, 2012, 124, 1-11.	3.7	110

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73	QTL mapping in three tropical maize populations reveals a set of constitutive and adaptive genomic regions for drought tolerance. Theoretical and Applied Genetics, 2013, 126, 583-600.	3.7	110
74	Predicting grain yield using canopy hyperspectral reflectance in wheat breeding data. Plant Methods, 2017, 13, 4.	4.5	110
75	GenotypeÃ—environment interaction for zinc and iron concentration of wheat grain in eastern Gangetic plains of India. Field Crops Research, 2010, 116, 268-277.	5.2	109
76	An epigenomic roadmap to induced pluripotency reveals DNA methylation as a reprogramming modulator. Nature Communications, 2014, 5, 5619.	13.2	109
77	A method for combining molecular markers and phenotypic attributes for classifying plant genotypes. Theoretical and Applied Genetics, 2001, 103, 944-952.	3.7	108
78	Combining superior agronomic performance and terminal heat tolerance with resistance to spot blotch (Bipolaris sorokiniana) of wheat in the warm humid Gangetic Plains of South Asia. Field Crops Research, 2007, 103, 53-61.	5.2	107
79	Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes. Theoretical and Applied Genetics, 2018, 131, 1405-1422.	3.7	106
80	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. G3: Genes, Genomes, Genetics, 2019, 9, 1231-1247.	1.9	106
81	Variability in iron, zinc and phytic acid content in a worldwide collection of commercial durum wheat cultivars and the effect of reduced irrigation on these traits. Food Chemistry, 2017, 237, 499-505.	8.4	104
82	The use of unbalanced historical data for genomic selection in an international wheat breeding program. Field Crops Research, 2013, 154, 12-22.	5.2	103
83	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.	1.9	103
84	Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. Theoretical and Applied Genetics, 2017, 130, 1415-1430.	3.7	103
85	A Benchmarking Between Deep Learning, Support Vector Machine and Bayesian Threshold Best Linear Unbiased Prediction for Predicting Ordinal Traits in Plant Breeding. G3: Genes, Genomes, Genetics, 2019, 9, 601-618.	1.9	103
86	Using the shifted multiplicative model to search for â€œseparabilityâ€• in crop cultivar trials. Theoretical and Applied Genetics, 1992, 84, 161-172.	3.7	102
87	Applications of Machine Learning Methods to Genomic Selection in Breeding Wheat for Rust Resistance. Plant Genome, 2018, 11, 170104.	3.2	102
88	QTL mapping of grain length in rice (Oryza sativa L.) using chromosome segment substitution lines. Genetical Research, 2006, 88, 93-104.	0.9	101
89	Gains in Maize Genetic Improvement in Eastern and Southern Africa: I. CIMMYT Hybrid Breeding Pipeline. Crop Science, 2017, 57, 168-179.	1.9	100
90	An assessment of wheat yield sensitivity and breeding gains in hot environments. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20122190.	2.8	99

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91	Genomic prediction for grain zinc and iron concentrations in spring wheat. Theoretical and Applied Genetics, 2016, 129, 1595-1605.	3.7	98
92	Genomic-Enabled Prediction in Maize Using Kernel Models with Genotype Ã— Environment Interaction. G3: Genes, Genomes, Genetics, 2017, 7, 1995-2014.	1.9	98
93	Nonlinear kernels, dominance, and envirotyping data increase the accuracy of genome-based prediction in multi-environment trials. Heredity, 2021, 126, 92-106.	2.7	98
94	Genomic Prediction of Genetic Values for Resistance to Wheat Rusts. Plant Genome, 2012, 5, .	3.2	97
95	A Sampling Strategy for Conserving Genetic Diversity when Forming Core Subsets. Crop Science, 2005, 45, 1035-1044.	1.9	95
96	Genetic Diversity in CIMMYT Nontemperate Maize Germplasm: Landraces, Open Pollinated Varieties, and Inbred Lines. Crop Science, 2008, 48, 617-624.	1.9	95
97	Large-scale screening for maize drought resistance using multiple selection criteria evaluated under water-stressed and well-watered environments. Field Crops Research, 2011, 124, 37-45.	5.2	94
98	META: A Suite of SAS Programs to Analyze Multienvironment Breeding Trials. Agronomy Journal, 2013, 105, 11-19.	1.9	94
99	Using Factor Analytic Models for Joining Environments and Genotypes without Crossover Genotype Ã— Environment Interaction. Crop Science, 2008, 48, 1291-1305.	1.9	93
100	Interpreting genotypeâ€…Ã—â€…environment interaction in tropical maize using linked molecular markers and environmental covariables. Theoretical and Applied Genetics, 1999, 99, 611-625.	3.7	92
101	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. G3: Genes, Genomes, Genetics, 2017, 7, 2315-2326.	1.9	92
102	Genetic Yield Gains In CIMMYT's International Elite Spring Wheat Yield Trials By Modeling The Genotype Ã— Environment Interaction. Crop Science, 2017, 57, 789-801.	1.9	91
103	Relationships among Bread Wheat International Yield Testing Locations in Dry Areas. Crop Science, 2001, 41, 1461-1469.	1.9	89
104	Fast-forward breeding for a food-secure world. Trends in Genetics, 2021, 37, 1124-1136.	6.9	88
105	Biplots of Linearâ€Bilinear Models for Studying Crossover Genotype Ã— Environment Interaction. Crop Science, 2002, 42, 619-633.	1.9	87
106	Prediction Assessment of Linear Mixed Models for Multienvironment Trials. Crop Science, 2011, 51, 944-954.	1.9	86
107	New Deep Learning Genomic-Based Prediction Model for Multiple Traits with Binary, Ordinal, and Continuous Phenotypes. G3: Genes, Genomes, Genetics, 2019, 9, 1545-1556.	1.9	85
108	Interpreting Genotype âœ• Environment Interaction in Wheat by Partial Least Squares Regression. Crop Science, 1998, 38, 679-689.	1.9	84

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109	Dimensions of Diversity in Modern Spring Bread Wheat in Developing Countries from 1965. Crop Science, 2002, 42, 1766-1779.	1.9	82
110	Sampling Strategies for Conserving Maize Diversity When Forming Core Subsets Using Genetic Markers. Crop Science, 2006, 46, 854-864.	1.9	82
111	Dynamics of dikes versus cone sheets in volcanic systems. Journal of Geophysical Research: Solid Earth, 2014, 119, 6178-6192.	3.4	82
112	Grouping of accessions of Mexican races of maize revisited with SSR markers. Theoretical and Applied Genetics, 2006, 113, 177-185.	3.7	81
113	Integrating genomic-enabled prediction and high-throughput phenotyping in breeding for climate-resilient bread wheat. Theoretical and Applied Genetics, 2019, 132, 177-194.	3.7	81
114	Studying crossover genotype Ã— environment interaction using linear-bilinear models and mixed models. Journal of Agricultural, Biological, and Environmental Statistics, 2004, 9, 362-380.	1.5	80
115	Genetic Gains for Grain Yield in CIMMYT Spring Bread Wheat across International Environments. Crop Science, 2012, 52, 1522-1533.	1.9	80
116	Wheat quality improvement at CIMMYT and the use of genomic selection on it. Applied & Translational Genomics, 2016, 11, 3-8.	2.2	80
117	Statistical genetic considerations for maintaining germ plasm collections. Theoretical and Applied Genetics, 1993, 86, 673-678.	3.7	79
118	Plant regeneration from immature embryos of 48 elite CIMMYT bread wheats. Theoretical and Applied Genetics, 1996, 92, 163-169.	3.7	79
119	Deep Kernel and Deep Learning for Genome-Based Prediction of Single Traits in Multienvironment Breeding Trials. Frontiers in Genetics, 2019, 10, 1168.	2.3	79
120	From Genotype Ã— Environment Interaction to Gene Ã— Environment Interaction. Current Genomics, 2012, 13, 225-244.	1.6	78
121	Associations of Environments in South Asia Based on Spot Blotch Disease of Wheat Caused by Cochliobolus sativus. Crop Science, 2007, 47, 1071-1081.	1.9	77
122	Unlocking the genetic diversity of Creole wheats. Scientific Reports, 2016, 6, 23092.	3.4	77
123	Genomic Prediction Enhanced Sparse Testing for Multi-environment Trials. G3: Genes, Genomes, Genetics, 2020, 10, 2725-2739.	1.9	77
124	Statistical methods for classifying genotypes. Euphytica, 2004, 137, 19-37.	1.2	76
125	Improving Maize Grain Yield under Drought Stress and Nonâ€stress Environments in Subâ€Saharan Africa using Markerâ€Assisted Recurrent Selection. Crop Science, 2016, 56, 344-353.	1.9	76
126	Selection for Resistance to Southwestern Corn Borer Using Markerâ€Assisted and Conventional Backcrossing. Crop Science, 2002, 42, 1516-1528.	1.9	75

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127	Use of Genomic Estimated Breeding Values Results in Rapid Genetic Gains for Drought Tolerance in Maize. Plant Genome, 2017, 10, plantgenome2016.07.0070.	3.2	75
128	Genetic Gains for Grain Yield in CIMMYT's Semiâ€Arid Wheat Yield Trials Grown in Suboptimal Environments. Crop Science, 2018, 58, 1890-1898.	1.9	74
129	Plant traits related to yield of wheat in early, late, or continuous drought conditions. Euphytica, 1998, 100, 109-121.	1.2	73
130	Assessment of genetic diversity in synthetic hexaploid wheats and their Triticum dicoccum and Aegilops tauschii parents using AFLPs and agronomic traits. Euphytica, 2003, 134, 305-317.	1.2	73
131	Prediction Assessment of Shrinkage Estimators of Multiplicative Models for Multiâ€Environment Cultivar Trials. Crop Science, 1999, 39, 998-1009.	1.9	72
132	High-throughput phenotyping platforms enhance genomic selection for wheat grain yield across populations and cycles in early stage. Theoretical and Applied Genetics, 2019, 132, 1705-1720.	3.7	72
133	Use of Hyperspectral Image Data Outperforms Vegetation Indices in Prediction of Maize Yield. Crop Science, 2017, 57, 2517-2524.	1.9	71
134	Associations among Twenty Years of International Bread Wheat Yield Evaluation Environments. Crop Science, 2003, 43, 1698-1711.	1.9	70
135	Prospects and Challenges of Applied Genomic Selectionâ€”A New Paradigm in Breeding for Grain Yield in Bread Wheat. Plant Genome, 2018, 11, 180017.	3.2	70
136	Global Adaptation of Spring Bread and Durum Wheat Lines Nearâ€Isogenic for Major Reduced Height Genes. Crop Science, 2006, 46, 603-613.	1.9	69
137	Molecular mapping across three populations reveals a QTL hotspot region on chromosome 3 for secondary traits associated with drought tolerance in tropical maize. Molecular Breeding, 2014, 34, 701-715.	2.1	68
138	Singleâ€Step Genomic and Pedigree Genotype Ã— Environment Interaction Models for Predicting Wheat Lines in International Environments. Plant Genome, 2017, 10, plantgenome2016.09.0089.	3.2	68
139	Deep Kernel for Genomic and Near Infrared Predictions in Multi-environment Breeding Trials. G3: Genes, Genomes, Genetics, 2019, 9, 2913-2924.	1.9	68
140	Association Mapping Reveals Novel Stem Rust Resistance Loci in Durum Wheat at the Seedling Stage. Plant Genome, 2014, 7, plantgenome2013.08.0026.	3.2	67
141	Differential Adaptation of CIMMYT Bread Wheat to Global High Temperature Environments. Crop Science, 2005, 45, 2443-2453.	1.9	66
142	Effect of Leaf Rust on Grain Yield and Yield Traits of Durum Wheats with Race-Specific and Slow-Rusting Resistance to Leaf Rust. Plant Disease, 2006, 90, 1065-1072.	1.5	66
143	Gains in Maize Genetic Improvement in Eastern and Southern Africa: II. CIMMYT Openâ€Pollinated Variety Breeding Pipeline. Crop Science, 2017, 57, 180-191.	1.9	66
144	<i>EnvRtype</i>: a software to interplay enviromics and quantitative genomics in agriculture. G3: Genes, Genomes, Genetics, 2021, 11, .	1.9	66

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145	Directional Charge Transport in Layered Twoâ€Dimensional Triazineâ€Based Graphitic Carbon Nitride. Angewandte Chemie - International Edition, 2019, 58, 9394-9398.	14.8	65
146	Immigrantsâ€™ utilization of specialist mental healthcare according to age, country of origin, and migration history: a nation-wide register study in Norway. Social Psychiatry and Psychiatric Epidemiology, 2017, 52, 679-687.	3.4	64
147	Grain quality traits of commercial durum wheat varieties and their relationships with drought stress and glutenins composition. Journal of Cereal Science, 2017, 75, 1-9.	3.7	64
148	Milling, processing and end-use quality traits of CIMMYT spring bread wheat germplasm under drought and heat stress. Field Crops Research, 2018, 215, 104-112.	5.2	64
149	Analysis of Genetic Factors Influencing the Developmental Rate of Globally Important CIMMYT Wheat Cultivars. Crop Science, 2005, 45, 2113-2119.	1.9	63
150	Genomic-enabled prediction models using multi-environment trials to estimate the effect of genotypeâ€‰Ã—â€‰environment interaction on prediction accuracy in chickpea. Scientific Reports, 2018, 8, 11701.	3.4	63
151	Evaluating genetic diversity for heat tolerance traits in Mexican wheat landraces. Genetic Resources and Crop Evolution, 1999, 46, 37-45.	1.6	62
152	Genomic prediction models for grain yield of spring bread wheat in diverse agro-ecological zones. Scientific Reports, 2016, 6, 27312.	3.4	62
153	Methodologies for estimating the sample size required for genetic conservation of outbreeding crops. Theoretical and Applied Genetics, 1989, 77, 153-161.	3.7	61
154	Clinical Characteristics and Genotype-phenotype Correlation in 62 Patients with X-linked Agammaglobulinemia. Journal of Clinical Immunology, 2010, 30, 121-131.	3.8	61
155	Genetic architecture of maize chlorotic mottle virus and maize lethal necrosis through GWAS, linkage analysis and genomic prediction in tropical maize germplasm. Theoretical and Applied Genetics, 2019, 132, 2381-2399.	3.7	61
156	Genomeâ€Wide Association Study for Adaptation to Agronomic Plant Density: A Component of High Yield Potential in Spring Wheat. Crop Science, 2015, 55, 2609-2619.	1.9	60
157	A Pedigreeâ€Based Reaction Norm Model for Prediction of Cotton Yield in Multienvironment Trials. Crop Science, 2015, 55, 1143-1151.	1.9	60
158	Hybrid Wheat Prediction Using Genomic, Pedigree, and Environmental Covariables Interaction Models. Plant Genome, 2019, 12, 180051.	3.2	60
159	Prediction of genetic values of quantitative traits with epistatic effects in plant breeding populations. Heredity, 2012, 109, 313-319.	2.7	59
160	Performance of Yield and Stability of Advanced Wheat Genotypes under Heat Stress Environments of the Indoâ€Gangetic Plains. Crop Science, 2007, 47, 1561-1573.	1.9	58
161	The effect of tillage, crop rotation and residue management on maize and wheat growth and development evaluated with an optical sensor. Field Crops Research, 2011, 120, 58-67.	5.2	58
162	Empirical Comparison of Tropical Maize Hybrids Selected Through Genomic and Phenotypic Selections. Frontiers in Plant Science, 2019, 10, 1502.	3.8	58

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163	Modeling Additive Ã— Environment and Additive Ã— Additive Ã— Environment Using Genetic Covariances of Relatives of Wheat Genotypes. Crop Science, 2007, 47, 311-320.	1.9	57
164	Gene action of canopy temperature in bread wheat under diverse environments. Theoretical and Applied Genetics, 2010, 120, 1107-1117.	3.7	57
165	Gene effects and heterosis for grain iron and zinc density in pearl millet (Pennisetum glaucum (L.) R.) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	57
166	Pattern-induced expectation bias in visual anticipation of action outcomes. Acta Psychologica, 2015, 161, 45-53.	1.5	57
167	Identifying QTLs and Epistasis in Structured Plant Populations Using Adaptive Mixed LASSO. Journal of Agricultural, Biological, and Environmental Statistics, 2011, 16, 170-184.	1.5	56
168	Genomic Prediction with Pedigree and Genotype Ã— Environment Interaction in Spring Wheat Grown in South and West Asia, North Africa, and Mexico. G3: Genes, Genomes, Genetics, 2017, 7, 481-495.	1.9	56
169	Genomic-enabled prediction with classification algorithms. Heredity, 2014, 112, 616-626.	2.7	55
170	The Paleogeographic and Stratigraphic Distribution of Ceratopsids (Ornithischia) in the Upper Judith River Group of Western Canada. Palaios, 1998, 13, 160.	1.4	54
171	Physiological factors associated with genotype by environment interaction in wheat. Field Crops Research, 2002, 75, 139-160.	5.2	54
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