

Jose Crossa

List of Publications by Year in descending order

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454
papers

27,651
citations

4370

86
h-index

11581

135
g-index

474
all docs

474
docs citations

474
times ranked

11790
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Selection in Plant Breeding: Methods, Models, and Perspectives. Trends in Plant Science, 2017, 22, 961-975.	4.3	1,004
2	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. Genetics, 2010, 186, 713-724.	1.2	664
3	Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. Plant Genome, 2012, 5, .	1.6	556
4	Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree. Genetics, 2009, 182, 375-385.	1.2	514
5	Genomic Prediction of Breeding Values when Modeling Genotype \times Environment Interaction using Pedigree and Dense Molecular Markers. Crop Science, 2012, 52, 707-719.	0.8	478
6	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
7	Association Analysis of Historical Bread Wheat Germplasm Using Additive Genetic Covariance of Relatives and Population Structure. Genetics, 2007, 177, 1889-1913.	1.2	426
8	Statistical Analyses of Multilocation Trials. Advances in Agronomy, 1990, , 55-85.	2.4	373
9	Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity, 2014, 112, 48-60.	1.2	357
10	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.	0.8	336
11	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. Genetical Research, 2010, 92, 295-308.	0.3	319
12	Additive Main Effects and Multiplicative Interaction Analysis of Two International Maize Cultivar Trials. Crop Science, 1990, 30, 493-500.	0.8	297
13	Breeding schemes for the implementation of genomic selection in wheat (Triticum spp .). Plant Science, 2016, 242, 23-36.	1.7	292
14	High-throughput Phenotyping and Genomic Selection: The Frontiers of Crop Breeding Converge. Journal of Integrative Plant Biology, 2012, 54, 312-320.	4.1	287
15	Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker \times Environment Interaction Genomic Selection Model. G3: Genes, Genomes, Genetics, 2015, 5, 569-582.	0.8	266
16	Genetic Gains in Grain Yield Through Genomic Selection in Eight \times parental Maize Populations under Drought Stress. Crop Science, 2015, 55, 154-163.	0.8	253
17	Identification of Drought, Heat, and Combined Drought and Heat Tolerant Donors in Maize. Crop Science, 2013, 53, 1335-1346.	0.8	247
18	Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. G3: Genes, Genomes, Genetics, 2012, 2, 1427-1436.	0.8	242

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19	Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1903-1926.	0.8	235
20	Biplot Analysis of Genotype \times Environment Interaction: Proceed with Caution. <i>Crop Science</i> , 2009, 49, 1564-1576.	0.8	232
21	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	9.4	219
22	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. <i>Nature Genetics</i> , 2019, 51, 1530-1539.	9.4	216
23	Two Types of GGE Biplots for Analyzing Multi-Environment Trial Data. <i>Crop Science</i> , 2001, 41, 656-663.	0.8	208
24	Comparison Between Linear and Non-parametric Regression Models for Genome-Enabled Prediction in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1595-1605.	0.8	187
25	Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. <i>Heredity</i> , 2015, 114, 291-299.	1.2	187
26	Genomic-Enabled Prediction Based on Molecular Markers and Pedigree Using the Bayesian Linear Regression Package in R. <i>Plant Genome</i> , 2010, 3, 106-116.	1.6	183
27	Genome-enabled prediction of genetic values using radial basis function neural networks. <i>Theoretical and Applied Genetics</i> , 2012, 125, 759-771.	1.8	180
28	Genetic Yield Gains and Changes in Associated Traits of CIMMYT Spring Bread Wheat in a "Historic" Set Representing 30 Years of Breeding. <i>Crop Science</i> , 2012, 52, 1123-1131.	0.8	171
29	Race non-specific resistance to rust diseases in CIMMYT spring wheats. <i>Euphytica</i> , 2011, 179, 175-186.	0.6	170
30	Bringing wild relatives back into the family: recovering genetic diversity in CIMMYT improved wheat germplasm. <i>Euphytica</i> , 2006, 149, 289-301.	0.6	166
31	Evaluation of Genomic Selection Training Population Designs and Genotyping Strategies in Plant Breeding Programs Using Simulation. <i>Crop Science</i> , 2014, 54, 1476-1488.	0.8	164
32	META-R: A software to analyze data from multi-environment plant breeding trials. <i>Crop Journal</i> , 2020, 8, 745-756.	2.3	164
33	Genomic Prediction of Gene Bank Wheat Landraces. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1819-1834.	0.8	159
34	AMMI adjustment for statistical analysis of an international wheat yield trial. <i>Theoretical and Applied Genetics</i> , 1991, 81, 27-37.	1.8	156
35	Wheat genetic resources enhancement by the International Maize and Wheat Improvement Center (CIMMYT). <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 1095-1140.	0.8	155
36	Phylogenetic and Multivariate Analyses To Determine the Effects of Different Tillage and Residue Management Practices on Soil Bacterial Communities. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3685-3691.	1.4	153

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37	Sites Regression and Shifted Multiplicative Model Clustering of Cultivar Trial Sites under Heterogeneity of Error Variances. <i>Crop Science</i> , 1997, 37, 406-415.	0.8	146
38	Effect of Trait Heritability, Training Population Size and Marker Density on Genomic Prediction Accuracy Estimation in 22 bi-parental Tropical Maize Populations. <i>Frontiers in Plant Science</i> , 2017, 8, 1916.	1.7	145
39	Genetic Characterization of CIMMYT Inbred Maize Lines and Open Pollinated Populations Using Large Scale Fingerprinting Methods. <i>Crop Science</i> , 2002, 42, 1832-1840.	0.8	141
40	Core Hunter: an algorithm for sampling genetic resources based on multiple genetic measures. <i>BMC Bioinformatics</i> , 2009, 10, 243.	1.2	138
41	Earliness in wheat: A key to adaptation under terminal and continual high temperature stress in South Asia. <i>Field Crops Research</i> , 2013, 151, 19-26.	2.3	138
42	Multitrait, Random Regression, or Simple Repeatability Model in High-Throughput Phenotyping Data Improve Genomic Prediction for Wheat Grain Yield. <i>Plant Genome</i> , 2017, 10, plantgenome2016.11.0111.	1.6	138
43	Agronomic Effects from Chromosome Translocations 7DL.7Ag and 1BL.1RS in Spring Wheat. <i>Crop Science</i> , 1998, 38, 27-33.	0.8	136
44	A multi-trait multi-environment QTL mixed model with an application to drought and nitrogen stress trials in maize (<i>Zea mays</i> L.). <i>Euphytica</i> , 2008, 161, 241-257.	0.6	134
45	High yield potential, shuttle breeding, genetic diversity, and a new international wheat improvement strategy. <i>Euphytica</i> , 2007, 157, 365-384.	0.6	132
46	The Modern Plant Breeding Triangle: Optimizing the Use of Genomics, Phenomics, and Enviromics Data. <i>Frontiers in Plant Science</i> , 2021, 12, 651480.	1.7	132
47	Genomic Selection and Prediction in Plant Breeding. <i>Journal of Crop Improvement</i> , 2011, 25, 239-261.	0.9	131
48	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.	5.8	129
49	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.	1.7	127
50	Bayesian Genomic Prediction with Genotype \times Environment Interaction Kernel Models. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 41-53.	0.8	126
51	Performance of biofortified spring wheat genotypes in target environments for grain zinc and iron concentrations. <i>Field Crops Research</i> , 2012, 137, 261-267.	2.3	124
52	Long-term consequences of tillage, residue management, and crop rotation on maize/wheat root rot and nematode populations in subtropical highlands. <i>Applied Soil Ecology</i> , 2006, 32, 305-315.	2.1	122
53	A review of deep learning applications for genomic selection. <i>BMC Genomics</i> , 2021, 22, 19.	1.2	122
54	Using Partial Least Squares Regression, Factorial Regression, and AMMI Models for Interpreting Genotype \times Environment Interaction. <i>Crop Science</i> , 1999, 39, 955-967.	0.8	120

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55	Genomic Prediction of Genotype \times Environment Interaction Kernel Regression Models. <i>Plant Genome</i> , 2016, 9, plantgenome2016.03.0024.	1.6	118
56	Factors Affecting the Accuracy of Genotype Imputation in Populations from Several Maize Breeding Programs. <i>Crop Science</i> , 2012, 52, 654-663.	0.8	117
57	Long-term consequences of tillage, residue management, and crop rotation on selected soil micro-flora groups in the subtropical highlands. <i>Applied Soil Ecology</i> , 2008, 38, 197-210.	2.1	116
58	Searching for novel sources of field resistance to Ug99 and Ethiopian stem rust races in durum wheat via association mapping. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1237-1256.	1.8	116
59	Classifying Genetic Resources by Categorical and Continuous Variables. <i>Crop Science</i> , 1998, 38, 1688-1696.	0.8	115
60	Multi-environment Genomic Prediction of Plant Traits Using Deep Learners With Dense Architecture. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3813-3828.	0.8	115
61	Mapping QTLs and QTL \times Environment interaction for CIMMYT maize drought stress program using factorial regression and partial least squares methods. <i>Theoretical and Applied Genetics</i> , 2006, 112, 1009-1023.	1.8	114
62	Modeling Genotype \times Environment Interaction Using Additive Genetic Covariances of Relatives for Predicting Breeding Values of Wheat Genotypes. <i>Crop Science</i> , 2006, 46, 1722-1733.	0.8	113
63	A Genomic Bayesian Multi-trait and Multi-environment Model. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2725-2744.	0.8	113
64	Harnessing genetic potential of wheat germplasm banks through impact-oriented-prebreeding for future food and nutritional security. <i>Scientific Reports</i> , 2018, 8, 12527.	1.6	113
65	Genetic analysis of adult plant, quantitative resistance to stripe rust in wheat cultivar "Stephens"™ in multi-environment trials. <i>Theoretical and Applied Genetics</i> , 2012, 124, 1-11.	1.8	109
66	Response to drought and heat stress on wheat quality, with special emphasis on bread-making quality, in durum wheat. <i>Field Crops Research</i> , 2016, 186, 157-165.	2.3	108
67	Multi-trait, Multi-environment Deep Learning Modeling for Genomic-Enabled Prediction of Plant Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3829-3840.	0.8	108
68	Combining superior agronomic performance and terminal heat tolerance with resistance to spot blotch (<i>Bipolaris sorokiniana</i>) of wheat in the warm humid Gangetic Plains of South Asia. <i>Field Crops Research</i> , 2007, 103, 53-61.	2.3	107
69	Predicting grain yield using canopy hyperspectral reflectance in wheat breeding data. <i>Plant Methods</i> , 2017, 13, 4.	1.9	107
70	Increasing Genomic-Enabled Prediction Accuracy by Modeling Genotype \times Environment Interactions in Kansas Wheat. <i>Plant Genome</i> , 2017, 10, plantgenome2016.12.0130.	1.6	107
71	QTL mapping in three tropical maize populations reveals a set of constitutive and adaptive genomic regions for drought tolerance. <i>Theoretical and Applied Genetics</i> , 2013, 126, 583-600.	1.8	106
72	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	13.7	106

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73	A method for combining molecular markers and phenotypic attributes for classifying plant genotypes. <i>Theoretical and Applied Genetics</i> , 2001, 103, 944-952.	1.8	105
74	Genotype×environment interaction for zinc and iron concentration of wheat grain in eastern Gangetic plains of India. <i>Field Crops Research</i> , 2010, 116, 268-277.	2.3	104
75	Using the shifted multiplicative model to search for “separability” in crop cultivar trials. <i>Theoretical and Applied Genetics</i> , 1992, 84, 161-172.	1.8	102
76	Phenotyping transgenic wheat for drought resistance. <i>Journal of Experimental Botany</i> , 2012, 63, 1799-1808.	2.4	102
77	Extending the Marker × Environment Interaction Model for Genomic-Enabled Prediction and Genome-Wide Association Analysis in Durum Wheat. <i>Crop Science</i> , 2016, 56, 2193-2209.	0.8	101
78	Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1405-1422.	1.8	101
79	The use of unbalanced historical data for genomic selection in an international wheat breeding program. <i>Field Crops Research</i> , 2013, 154, 12-22.	2.3	100
80	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. <i>Food Chemistry</i> , 2017, 237, 499-505.	4.2	100
81	QTL mapping of grain length in rice (<i>Oryza sativa</i> L.) using chromosome segment substitution lines. <i>Genetical Research</i> , 2006, 88, 93-104.	0.3	99
82	Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1415-1430.	1.8	99
83	An assessment of wheat yield sensitivity and breeding gains in hot environments. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20122190.	1.2	97
84	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1231-1247.	0.8	96
85	A Benchmarking Between Deep Learning, Support Vector Machine and Bayesian Threshold Best Linear Unbiased Prediction for Predicting Ordinal Traits in Plant Breeding. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 601-618.	0.8	95
86	Genomic Prediction of Genetic Values for Resistance to Wheat Rusts. <i>Plant Genome</i> , 2012, 5, .	1.6	94
87	Gains in Maize Genetic Improvement in Eastern and Southern Africa: I. CIMMYT Hybrid Breeding Pipeline. <i>Crop Science</i> , 2017, 57, 168-179.	0.8	94
88	Applications of Machine Learning Methods to Genomic Selection in Breeding Wheat for Rust Resistance. <i>Plant Genome</i> , 2018, 11, 170104.	1.6	94
89	Genomic prediction for grain zinc and iron concentrations in spring wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1595-1605.	1.8	93
90	Genetic Diversity in CIMMYT Nontemperate Maize Germplasm: Landraces, Open Pollinated Varieties, and Inbred Lines. <i>Crop Science</i> , 2008, 48, 617-624.	0.8	93

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91	A Sampling Strategy for Conserving Genetic Diversity when Forming Core Subsets. <i>Crop Science</i> , 2005, 45, 1035-1044.	0.8	92
92	Large-scale screening for maize drought resistance using multiple selection criteria evaluated under water-stressed and well-watered environments. <i>Field Crops Research</i> , 2011, 124, 37-45.	2.3	92
93	META: A Suite of SAS Programs to Analyze Multienvironment Breeding Trials. <i>Agronomy Journal</i> , 2013, 105, 11-19.	0.9	92
94	Genomic-Enabled Prediction in Maize Using Kernel Models with Genotype \times Environment Interaction. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1995-2014.	0.8	92
95	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2315-2326.	0.8	92
96	Relationships among Bread Wheat International Yield Testing Locations in Dry Areas. <i>Crop Science</i> , 2001, 41, 1461-1469.	0.8	89
97	Genetic Yield Gains In CIMMYT's International Elite Spring Wheat Yield Trials By Modeling The Genotype \times Environment Interaction. <i>Crop Science</i> , 2017, 57, 789-801.	0.8	89
98	Nonlinear kernels, dominance, and envirotyping data increase the accuracy of genome-based prediction in multi-environment trials. <i>Heredity</i> , 2021, 126, 92-106.	1.2	89
99	Interpreting genotype \times environment interaction in tropical maize using linked molecular markers and environmental covariables. <i>Theoretical and Applied Genetics</i> , 1999, 99, 611-625.	1.8	88
100	Using Factor Analytic Models for Joining Environments and Genotypes without Crossover Genotype \times Environment Interaction. <i>Crop Science</i> , 2008, 48, 1291-1305.	0.8	86
101	Prediction Assessment of Linear Mixed Models for Multienvironment Trials. <i>Crop Science</i> , 2011, 51, 944-954.	0.8	84
102	Interpreting Genotype \times Environment Interaction in Wheat by Partial Least Squares Regression. <i>Crop Science</i> , 1998, 38, 679-689.	0.8	83
103	Biplots of Linear \times Bilinear Models for Studying Crossover Genotype \times Environment Interaction. <i>Crop Science</i> , 2002, 42, 619-633.	0.8	83
104	Dimensions of Diversity in Modern Spring Bread Wheat in Developing Countries from 1965. <i>Crop Science</i> , 2002, 42, 1766-1779.	0.8	82
105	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021, 37, 1124-1136.	2.9	82
106	Grouping of accessions of Mexican races of maize revisited with SSR markers. <i>Theoretical and Applied Genetics</i> , 2006, 113, 177-185.	1.8	81
107	New Deep Learning Genomic-Based Prediction Model for Multiple Traits with Binary, Ordinal, and Continuous Phenotypes. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1545-1556.	0.8	81
108	Sampling Strategies for Conserving Maize Diversity When Forming Core Subsets Using Genetic Markers. <i>Crop Science</i> , 2006, 46, 854-864.	0.8	80

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109	Wheat quality improvement at CIMMYT and the use of genomic selection on it. <i>Applied & Translational Genomics</i> , 2016, 11, 3-8.	2.1	79
110	Statistical genetic considerations for maintaining germ plasm collections. <i>Theoretical and Applied Genetics</i> , 1993, 86, 673-678.	1.8	78
111	Integrating genomic-enabled prediction and high-throughput phenotyping in breeding for climate-resilient bread wheat. <i>Theoretical and Applied Genetics</i> , 2019, 132, 177-194.	1.8	78
112	From Genotype \times Environment Interaction to Gene \times Environment Interaction. <i>Current Genomics</i> , 2012, 13, 225-244.	0.7	78
113	Studying crossover genotype \times environment interaction using linear-bilinear models and mixed models. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2004, 9, 362-380.	0.7	77
114	Associations of Environments in South Asia Based on Spot Blotch Disease of Wheat Caused by <i>Cochliobolus sativus</i> . <i>Crop Science</i> , 2007, 47, 1071-1081.	0.8	77
115	Deep Kernel and Deep Learning for Genome-Based Prediction of Single Traits in Multienvironment Breeding Trials. <i>Frontiers in Genetics</i> , 2019, 10, 1168.	1.1	77
116	Plant regeneration from immature embryos of 48 elite CIMMYT bread wheats. <i>Theoretical and Applied Genetics</i> , 1996, 92, 163-169.	1.8	76
117	Selection for Resistance to Southwestern Corn Borer Using Marker-Assisted and Conventional Backcrossing. <i>Crop Science</i> , 2002, 42, 1516-1528.	0.8	75
118	Statistical methods for classifying genotypes. <i>Euphytica</i> , 2004, 137, 19-37.	0.6	75
119	Genetic Gains for Grain Yield in CIMMYT Spring Bread Wheat across International Environments. <i>Crop Science</i> , 2012, 52, 1522-1533.	0.8	75
120	Unlocking the genetic diversity of Creole wheats. <i>Scientific Reports</i> , 2016, 6, 23092.	1.6	75
121	Assessment of genetic diversity in synthetic hexaploid wheats and their <i>Triticum dicoccum</i> and <i>Aegilops tauschii</i> parents using AFLPs and agronomic traits. <i>Euphytica</i> , 2003, 134, 305-317.	0.6	73
122	Use of Genomic Estimated Breeding Values Results in Rapid Genetic Gains for Drought Tolerance in Maize. <i>Plant Genome</i> , 2017, 10, plantgenome2016.07.0070.	1.6	72
123	Plant traits related to yield of wheat in early, late, or continuous drought conditions. <i>Euphytica</i> , 1998, 100, 109-121.	0.6	71
124	Prediction Assessment of Shrinkage Estimators of Multiplicative Models for Multi-Environment Cultivar Trials. <i>Crop Science</i> , 1999, 39, 998-1009.	0.8	71
125	Associations among Twenty Years of International Bread Wheat Yield Evaluation Environments. <i>Crop Science</i> , 2003, 43, 1698-1711.	0.8	70
126	Improving Maize Grain Yield under Drought Stress and Non-stress Environments in Sub-Saharan Africa using Marker-Assisted Recurrent Selection. <i>Crop Science</i> , 2016, 56, 344-353.	0.8	70

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127	High-throughput phenotyping platforms enhance genomic selection for wheat grain yield across populations and cycles in early stage. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1705-1720.	1.8	70
128	Genetic Gains for Grain Yield in CIMMYT's Semi-Arid Wheat Yield Trials Grown in Suboptimal Environments. <i>Crop Science</i> , 2018, 58, 1890-1898.	0.8	69
129	Genomic Prediction Enhanced Sparse Testing for Multi-environment Trials. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2725-2739.	0.8	68
130	Global Adaptation of Spring Bread and Durum Wheat Lines Near-Isogenic for Major Reduced Height Genes. <i>Crop Science</i> , 2006, 46, 603-613.	0.8	67
131	Association Mapping Reveals Novel Stem Rust Resistance Loci in Durum Wheat at the Seedling Stage. <i>Plant Genome</i> , 2014, 7, plantgenome2013.08.0026.	1.6	67
132	Molecular mapping across three populations reveals a QTL hotspot region on chromosome 3 for secondary traits associated with drought tolerance in tropical maize. <i>Molecular Breeding</i> , 2014, 34, 701-715.	1.0	66
133	Single-Step Genomic and Pedigree Genotype × Environment Interaction Models for Predicting Wheat Lines in International Environments. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0089.	1.6	66
134	Use of Hyperspectral Image Data Outperforms Vegetation Indices in Prediction of Maize Yield. <i>Crop Science</i> , 2017, 57, 2517-2524.	0.8	66
135	Prospects and Challenges of Applied Genomic Selection—A New Paradigm in Breeding for Grain Yield in Bread Wheat. <i>Plant Genome</i> , 2018, 11, 180017.	1.6	65
136	Differential Adaptation of CIMMYT Bread Wheat to Global High Temperature Environments. <i>Crop Science</i> , 2005, 45, 2443-2453.	0.8	64
137	Analysis of Genetic Factors Influencing the Developmental Rate of Globally Important CIMMYT Wheat Cultivars. <i>Crop Science</i> , 2005, 45, 2113-2119.	0.8	63
138	Effect of Leaf Rust on Grain Yield and Yield Traits of Durum Wheats with Race-Specific and Slow-Rusting Resistance to Leaf Rust. <i>Plant Disease</i> , 2006, 90, 1065-1072.	0.7	63
139	Gains in Maize Genetic Improvement in Eastern and Southern Africa: II. CIMMYT Open-Pollinated Variety Breeding Pipeline. <i>Crop Science</i> , 2017, 57, 180-191.	0.8	63
140	Classification of Peruvian highland maize races using plant traits. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 151-162.	0.8	62
141	Genomic prediction models for grain yield of spring bread wheat in diverse agro-ecological zones. <i>Scientific Reports</i> , 2016, 6, 27312.	1.6	62
142	Grain quality traits of commercial durum wheat varieties and their relationships with drought stress and glutenins composition. <i>Journal of Cereal Science</i> , 2017, 75, 1-9.	1.8	62
143	Milling, processing and end-use quality traits of CIMMYT spring bread wheat germplasm under drought and heat stress. <i>Field Crops Research</i> , 2018, 215, 104-112.	2.3	62
144	Genomic-enabled prediction models using multi-environment trials to estimate the effect of genotype × environment interaction on prediction accuracy in chickpea. <i>Scientific Reports</i> , 2018, 8, 11701.	1.6	61

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145	Deep Kernel for Genomic and Near Infrared Predictions in Multi-environment Breeding Trials. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2913-2924.	0.8	61
146	Methodologies for estimating the sample size required for genetic conservation of outbreeding crops. <i>Theoretical and Applied Genetics</i> , 1989, 77, 153-161.	1.8	60
147	Evaluating genetic diversity for heat tolerance traits in Mexican wheat landraces. <i>Genetic Resources and Crop Evolution</i> , 1999, 46, 37-45.	0.8	60
148	Genome-Wide Association Study for Adaptation to Agronomic Plant Density: A Component of High Yield Potential in Spring Wheat. <i>Crop Science</i> , 2015, 55, 2609-2619.	0.8	60
149	A Pedigree-Based Reaction Norm Model for Prediction of Cotton Yield in Multienvironment Trials. <i>Crop Science</i> , 2015, 55, 1143-1151.	0.8	58
150	Hybrid Wheat Prediction Using Genomic, Pedigree, and Environmental Covariables Interaction Models. <i>Plant Genome</i> , 2019, 12, 180051.	1.6	58
151	Performance of Yield and Stability of Advanced Wheat Genotypes under Heat Stress Environments of the Indo-Gangetic Plains. <i>Crop Science</i> , 2007, 47, 1561-1573.	0.8	57
152	The effect of tillage, crop rotation and residue management on maize and wheat growth and development evaluated with an optical sensor. <i>Field Crops Research</i> , 2011, 120, 58-67.	2.3	57
153	Gene action of canopy temperature in bread wheat under diverse environments. <i>Theoretical and Applied Genetics</i> , 2010, 120, 1107-1117.	1.8	56
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