

Jose Crossa

List of Publications by Year in descending order

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454
papers

27,651
citations

4388

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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.	8.8	1,004
2	Prediction of Genetic Values of Quantitative Traits in Plant Breeding Using Pedigree and Molecular Markers. Genetics, 2010, 186, 713-724.	2.9	664
3	Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. Plant Genome, 2012, 5, .	2.8	556
4	Predicting Quantitative Traits With Regression Models for Dense Molecular Markers and Pedigree. Genetics, 2009, 182, 375-385.	2.9	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.	1.8	478
6	A reaction norm model for genomic selection using high-dimensional genomic and environmental data. Theoretical and Applied Genetics, 2014, 127, 595-607.	3.6	439
7	Association Analysis of Historical Bread Wheat Germplasm Using Additive Genetic Covariance of Relatives and Population Structure. Genetics, 2007, 177, 1889-1913.	2.9	426
8	Statistical Analyses of Multilocation Trials. Advances in Agronomy, 1990, , 55-85.	5.2	373
9	Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity, 2014, 112, 48-60.	2.6	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.	1.8	336
11	Semi-parametric genomic-enabled prediction of genetic values using reproducing kernel Hilbert spaces methods. Genetical Research, 2010, 92, 295-308.	0.9	319
12	Additive Main Effects and Multiplicative Interaction Analysis of Two International Maize Cultivar Trials. Crop Science, 1990, 30, 493-500.	1.8	297
13	Breeding schemes for the implementation of genomic selection in wheat (Triticum spp .). Plant Science, 2016, 242, 23-36.	3.6	292
14	High-throughput Phenotyping and Genomic Selection: The Frontiers of Crop Breeding Converge. Journal of Integrative Plant Biology, 2012, 54, 312-320.	8.5	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.	1.8	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.	1.8	253
17	Identification of Drought, Heat, and Combined Drought and Heat Tolerant Donors in Maize. Crop Science, 2013, 53, 1335-1346.	1.8	247
18	Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. G3: Genes, Genomes, Genetics, 2012, 2, 1427-1436.	1.8	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.	1.8	235
20	Biplot Analysis of Genotype \times Environment Interaction: Proceed with Caution. <i>Crop Science</i> , 2009, 49, 1564-1576.	1.8	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.	21.4	219
22	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. <i>Nature Genetics</i> , 2019, 51, 1530-1539.	21.4	216
23	Two Types of GGE Biplots for Analyzing Multi-Environment Trial Data. <i>Crop Science</i> , 2001, 41, 656-663.	1.8	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.	1.8	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.	2.6	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.	2.8	183
27	Genome-enabled prediction of genetic values using radial basis function neural networks. <i>Theoretical and Applied Genetics</i> , 2012, 125, 759-771.	3.6	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.	1.8	171
29	Race non-specific resistance to rust diseases in CIMMYT spring wheats. <i>Euphytica</i> , 2011, 179, 175-186.	1.2	170
30	Bringing wild relatives back into the family: recovering genetic diversity in CIMMYT improved wheat germplasm. <i>Euphytica</i> , 2006, 149, 289-301.	1.2	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.	1.8	164
32	META-R: A software to analyze data from multi-environment plant breeding trials. <i>Crop Journal</i> , 2020, 8, 745-756.	5.2	164
33	Genomic Prediction of Gene Bank Wheat Landraces. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1819-1834.	1.8	159
34	AMMI adjustment for statistical analysis of an international wheat yield trial. <i>Theoretical and Applied Genetics</i> , 1991, 81, 27-37.	3.6	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.	1.6	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.	3.1	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.	1.8	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.	3.6	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.	1.8	141
40	Core Hunter: an algorithm for sampling genetic resources based on multiple genetic measures. <i>BMC Bioinformatics</i> , 2009, 10, 243.	2.6	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.	5.1	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.	2.8	138
43	Agronomic Effects from Chromosome Translocations 7DL.7Ag and 1BL.1RS in Spring Wheat. <i>Crop Science</i> , 1998, 38, 27-33.	1.8	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.	1.2	134
45	High yield potential, shuttle breeding, genetic diversity, and a new international wheat improvement strategy. <i>Euphytica</i> , 2007, 157, 365-384.	1.2	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.	3.6	132
47	Genomic Selection and Prediction in Plant Breeding. <i>Journal of Crop Improvement</i> , 2011, 25, 239-261.	1.7	131
48	Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. <i>Nature Communications</i> , 2020, 11, 4572.	12.8	129
49	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666.	3.6	127
50	Bayesian Genomic Prediction with Genotype \times Environment Interaction Kernel Models. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 41-53.	1.8	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.	5.1	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.	4.3	122
53	A review of deep learning applications for genomic selection. <i>BMC Genomics</i> , 2021, 22, 19.	2.8	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.	1.8	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.	2.8	118
56	Factors Affecting the Accuracy of Genotype Imputation in Populations from Several Maize Breeding Programs. <i>Crop Science</i> , 2012, 52, 654-663.	1.8	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.	4.3	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.	3.6	116
59	Classifying Genetic Resources by Categorical and Continuous Variables. <i>Crop Science</i> , 1998, 38, 1688-1696.	1.8	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.	1.8	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.	3.6	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.	1.8	113
63	A Genomic Bayesian Multi-trait and Multi-environment Model. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2725-2744.	1.8	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.	3.3	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.	3.6	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.	5.1	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.	1.8	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.	5.1	107
69	Predicting grain yield using canopy hyperspectral reflectance in wheat breeding data. <i>Plant Methods</i> , 2017, 13, 4.	4.3	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.	2.8	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.	3.6	106
72	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	27.8	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.	3.6	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.	5.1	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.	3.6	102
76	Phenotyping transgenic wheat for drought resistance. <i>Journal of Experimental Botany</i> , 2012, 63, 1799-1808.	4.8	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.	1.8	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.	3.6	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.	5.1	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.	8.2	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.	0.9	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.	3.6	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.	2.6	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.	1.8	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.	1.8	95
86	Genomic Prediction of Genetic Values for Resistance to Wheat Rusts. <i>Plant Genome</i> , 2012, 5, .	2.8	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.	1.8	94
88	Applications of Machine Learning Methods to Genomic Selection in Breeding Wheat for Rust Resistance. <i>Plant Genome</i> , 2018, 11, 170104.	2.8	94
89	Genomic prediction for grain zinc and iron concentrations in spring wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1595-1605.	3.6	93
90	Genetic Diversity in CIMMYT Nontemperate Maize Germplasm: Landraces, Open Pollinated Varieties, and Inbred Lines. <i>Crop Science</i> , 2008, 48, 617-624.	1.8	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.	1.8	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.	5.1	92
93	META: A Suite of SAS Programs to Analyze Multienvironment Breeding Trials. <i>Agronomy Journal</i> , 2013, 105, 11-19.	1.8	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.	1.8	92
95	Rapid Cycling Genomic Selection in a Multiparental Tropical Maize Population. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2315-2326.	1.8	92
96	Relationships among Bread Wheat International Yield Testing Locations in Dry Areas. <i>Crop Science</i> , 2001, 41, 1461-1469.	1.8	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.	1.8	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.	2.6	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.	3.6	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.	1.8	86
101	Prediction Assessment of Linear Mixed Models for Multienvironment Trials. <i>Crop Science</i> , 2011, 51, 944-954.	1.8	84
102	Interpreting Genotype \times Environment Interaction in Wheat by Partial Least Squares Regression. <i>Crop Science</i> , 1998, 38, 679-689.	1.8	83
103	Biplots of Linear \times Bilinear Models for Studying Crossover Genotype \times Environment Interaction. <i>Crop Science</i> , 2002, 42, 619-633.	1.8	83
104	Dimensions of Diversity in Modern Spring Bread Wheat in Developing Countries from 1965. <i>Crop Science</i> , 2002, 42, 1766-1779.	1.8	82
105	Fast-forward breeding for a food-secure world. <i>Trends in Genetics</i> , 2021, 37, 1124-1136.	6.7	82
106	Grouping of accessions of Mexican races of maize revisited with SSR markers. <i>Theoretical and Applied Genetics</i> , 2006, 113, 177-185.	3.6	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.	1.8	81
108	Sampling Strategies for Conserving Maize Diversity When Forming Core Subsets Using Genetic Markers. <i>Crop Science</i> , 2006, 46, 854-864.	1.8	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.	3.6	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.	3.6	78
112	From Genotype \times Environment Interaction to Gene \times Environment Interaction. <i>Current Genomics</i> , 2012, 13, 225-244.	1.6	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.	1.4	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.	1.8	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.	2.3	77
116	Plant regeneration from immature embryos of 48 elite CIMMYT bread wheats. <i>Theoretical and Applied Genetics</i> , 1996, 92, 163-169.	3.6	76
117	Selection for Resistance to Southwestern Corn Borer Using Marker-Assisted and Conventional Backcrossing. <i>Crop Science</i> , 2002, 42, 1516-1528.	1.8	75
118	Statistical methods for classifying genotypes. <i>Euphytica</i> , 2004, 137, 19-37.	1.2	75
119	Genetic Gains for Grain Yield in CIMMYT Spring Bread Wheat across International Environments. <i>Crop Science</i> , 2012, 52, 1522-1533.	1.8	75
120	Unlocking the genetic diversity of Creole wheats. <i>Scientific Reports</i> , 2016, 6, 23092.	3.3	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.	1.2	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.	2.8	72
123	Plant traits related to yield of wheat in early, late, or continuous drought conditions. <i>Euphytica</i> , 1998, 100, 109-121.	1.2	71
124	Prediction Assessment of Shrinkage Estimators of Multiplicative Models for Multi-Environment Cultivar Trials. <i>Crop Science</i> , 1999, 39, 998-1009.	1.8	71
125	Associations among Twenty Years of International Bread Wheat Yield Evaluation Environments. <i>Crop Science</i> , 2003, 43, 1698-1711.	1.8	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.	1.8	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.	3.6	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.	1.8	69
129	Genomic Prediction Enhanced Sparse Testing for Multi-environment Trials. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2725-2739.	1.8	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.	1.8	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.	2.8	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.	2.1	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.	2.8	66
134	Use of Hyperspectral Image Data Outperforms Vegetation Indices in Prediction of Maize Yield. <i>Crop Science</i> , 2017, 57, 2517-2524.	1.8	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.	2.8	65
136	Differential Adaptation of CIMMYT Bread Wheat to Global High Temperature Environments. <i>Crop Science</i> , 2005, 45, 2443-2453.	1.8	64
137	Analysis of Genetic Factors Influencing the Developmental Rate of Globally Important CIMMYT Wheat Cultivars. <i>Crop Science</i> , 2005, 45, 2113-2119.	1.8	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.	1.4	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.	1.8	63
140	Classification of Peruvian highland maize races using plant traits. <i>Genetic Resources and Crop Evolution</i> , 2008, 55, 151-162.	1.6	62
141	Genomic prediction models for grain yield of spring bread wheat in diverse agro-ecological zones. <i>Scientific Reports</i> , 2016, 6, 27312.	3.3	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.	3.7	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.	5.1	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.	3.3	61

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145	Deep Kernel for Genomic and Near Infrared Predictions in Multi-environment Breeding Trials. G3: Genes, Genomes, Genetics, 2019, 9, 2913-2924.	1.8	61
146	Methodologies for estimating the sample size required for genetic conservation of outbreeding crops. Theoretical and Applied Genetics, 1989, 77, 153-161.	3.6	60
147	Evaluating genetic diversity for heat tolerance traits in Mexican wheat landraces. Genetic Resources and Crop Evolution, 1999, 46, 37-45.	1.6	60
148	Genome-Wide Association Study for Adaptation to Agronomic Plant Density: A Component of High Yield Potential in Spring Wheat. Crop Science, 2015, 55, 2609-2619.	1.8	60
149	A Pedigree-Based Reaction Norm Model for Prediction of Cotton Yield in Multienvironment Trials. Crop Science, 2015, 55, 1143-1151.	1.8	58
150	Hybrid Wheat Prediction Using Genomic, Pedigree, and Environmental Covariables Interaction Models. Plant Genome, 2019, 12, 180051.	2.8	58
151	Performance of Yield and Stability of Advanced Wheat Genotypes under Heat Stress Environments of the Indo-Gangetic Plains. Crop Science, 2007, 47, 1561-1573.	1.8	57
152	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.	5.1	57
153	Gene action of canopy temperature in bread wheat under diverse environments. Theoretical and Applied Genetics, 2010, 120, 1107-1117.	3.6	56
154	Genomic Prediction with Pedigree and Genotype \times Environment Interaction in Spring Wheat Grown in South and West Asia, North Africa, and Mexico. G3: Genes, Genomes, Genetics, 2017, 7, 481-495.	1.8	56
155	Modeling Additive \times Environment and Additive \times Additive \times Environment Using Genetic Covariances of Relatives of Wheat Genotypes. Crop Science, 2007, 47, 311-320.	1.8	55
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