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List of Publications by Year
in descending order

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		11235	23841
315	18,992	73	115
papers	citations	h-index	g-index
319	319	319	11147
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	High-resolution association mapping with libraries of immortalized lines from ancestral landraces. Theoretical and Applied Genetics, 2022, 135, 243-256.	1.8	5
2	Unraveling the potential of phenomic selection within and among diverse breeding material of maize (<i>Zea mays</i> L.). G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	9
3	Genetic diversity of European maize landraces: Dataset on the molecular and phenotypic variation of derived doubled-haploid populations. Data in Brief, 2022, 42, 108164.	0.5	4
4	Theoretical and experimental assessment of genome-based prediction in landraces of allogamous crops. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121797119.	3.3	4
5	Exploiting genetic diversity in two European maize landraces for improving Gibberella ear rot resistance using genomic tools. Theoretical and Applied Genetics, 2021, 134, 793-805.	1.8	18
6	Calibration and validation of predicted genomic breeding values in an advanced cycle maize population. Theoretical and Applied Genetics, 2021, 134, 3069-3081.	1.8	12
7	Optimum breeding strategies using genomic and phenotypic selection for the simultaneous improvement of two traits. Theoretical and Applied Genetics, 2021, 134, 4025-4042.	1.8	5
8	Genomic prediction with multiple biparental families. Theoretical and Applied Genetics, 2020, 133, 133-147.	1.8	22
9	Genetic dissection of maternal influence on in vivo haploid induction in maize. Crop Journal, 2020, 8, 287-298.	2.3	5
10	Discovery of beneficial haplotypes for complex traits in maize landraces. Nature Communications, 2020, 11, 4954.	5.8	38
11	Genome-wide association study to identify genomic regions influencing spontaneous fertility in maize haploids. Euphytica, 2019, 215, 138.	0.6	29
12	European maize landraces made accessible for plant breeding and genome-based studies. Theoretical and Applied Genetics, 2019, 132, 3333-3345.	1.8	52
13	Doubled haploid technology for line development in maize: technical advances and prospects. Theoretical and Applied Genetics, 2019, 132, 3227-3243.	1.8	126
14	Efficient genetic value prediction using incomplete omics data. Theoretical and Applied Genetics, 2019, 132, 1211-1222.	1.8	8
15	Reduced response diversity does not negatively impact wheat climate resilience. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10623-10624.	3.3	11
16	Haploid male fertility and spontaneous chromosome doubling evaluated in a diallel and recurrent selection experiment in maize. Theoretical and Applied Genetics, 2019, 132, 2273-2284.	1.8	17
17	Testcross performance of doubled haploid lines from European flint maize landraces is promising for broadening the genetic base of elite germplasm. Theoretical and Applied Genetics, 2019, 132, 1897-1908.	1.8	28
18	Early diagnosis of ploidy status in doubled haploid production of maize by stomata length and flow cytometry measurements. Plant Breeding, 2019, 138, 266-276.	1.0	13

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19	Progress for testcross performance within the flint heterotic pool of a public maize breeding program since the onset of hybrid breeding. Euphytica, 2019, 215, 1.	0.6	9
20	Across-years prediction of hybrid performance in maize using genomics. Theoretical and Applied Genetics, 2019, 132, 933-946.	1.8	23
21	Beyond Genomic Prediction: Combining Different Types of <i>omics</i> Data Can Improve Prediction of Hybrid Performance in Maize. Genetics, 2018, 208, 1373-1385.	1.2	130
22	Selection on Expected Maximum Haploid Breeding Values Can Increase Genetic Gain in Recurrent Genomic Selection. G3: Genes, Genomes, Genetics, 2018, 8, 1173-1181.	0.8	42
23	Genomic prediction and GWAS of Gibberella ear rot resistance traits in dent and flint lines of a public maize breeding program. Euphytica, 2018, 214, 1.	0.6	32
24	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. Genetics, 2018, 210, 1185-1196.	1.2	18
25	Marker-Assisted Breeding of Improved Maternal Haploid Inducers in Maize for the Tropical/Subtropical Regions. Frontiers in Plant Science, 2018, 9, 1527.	1.7	41
26	Small RNA-based prediction of hybrid performance in maize. BMC Genomics, 2018, 19, 371.	1.2	24
27	Highâ€Throughput Precision Phenotyping of the Oil Content of Single Seeds of Various Oilseed Crops. Crop Science, 2018, 58, 670-678.	0.8	22
28	Nitrous Oxideâ€Induced Chromosome Doubling of Maize Haploids. Crop Science, 2018, 58, 650-659.	0.8	17
29	Parental Expression Variation of Small RNAs Is Negatively Correlated with Grain Yield Heterosis in a Maize Breeding Population. Frontiers in Plant Science, 2018, 9, 13.	1.7	21
30	Metabolic robustness in young roots underpins a predictive model of maize hybrid performance in the field. Plant Journal, 2017, 90, 319-329.	2.8	30
31	Tapping the genetic diversity of landraces in allogamous crops with doubled haploid lines: a case study from European flint maize. Theoretical and Applied Genetics, 2017, 130, 861-873.	1.8	41
32	Transcriptomeâ€based prediction of hybrid performance with unbalanced data from a maize breeding programme. Plant Breeding, 2017, 136, 331-337.	1.0	22
33	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. Genetics, 2017, 206, 1611-1619.	1.2	24
34	Dissection of a major QTL qhir1 conferring maternal haploid induction ability in maize. Theoretical and Applied Genetics, 2017, 130, 1113-1122.	1.8	20
35	Accuracy of Genomic Prediction in Synthetic Populations Depending on the Number of Parents, Relatedness, and Ancestral Linkage Disequilibrium. Genetics, 2017, 205, 441-454.	1.2	52
36	Genomic Prediction Within and Across Biparental Families: Means and Variances of Prediction Accuracy and Usefulness of Deterministic Equations. G3: Genes, Genomes, Genetics, 2017, 7, 3571-3586.	0.8	34

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37	Persistency of Prediction Accuracy and Genetic Gain in Synthetic Populations Under Recurrent Genomic Selection. G3: Genes, Genomes, Genetics, 2017, 7, 801-811.	0.8	37
38	Genotyping-by-sequencing highlights original diversity patterns within a European collection of 1191 maize flint lines, as compared to the maize USDA genebank. Theoretical and Applied Genetics, 2017, 130, 2165-2189.	1.8	39
39	High-throughput platform for automated sorting and selection of single seeds based on time-domain nuclear magnetic resonance (TD-NMR) measurement of oil content. Biosystems Engineering, 2017, 164, 213-220.	1.9	21
40	Omics-based hybrid prediction in maize. Theoretical and Applied Genetics, 2017, 130, 1927-1939.	1.8	90
41	Low validation rate of quantitative trait loci for Gibberella ear rot resistance in European maize. Theoretical and Applied Genetics, 2017, 130, 175-186.	1.8	20
42	Optimum breeding strategies using genomic selection for hybrid breeding in wheat, maize, rye, barley, rice and triticale. Theoretical and Applied Genetics, 2016, 129, 1901-1913.	1.8	69
43	Colchicine Alternatives for Chromosome Doubling in Maize Haploids for Doubledâ€Haploid Production. Crop Science, 2016, 56, 559-569.	0.8	47
44	Development and Validation of Red Root Markerâ€Based Haploid Inducers in Maize. Crop Science, 2016, 56, 1678-1688.	0.8	50
45	In Vivo Haploid Induction in Maize: Comparison of Different Testing Regimes for Measuring Haploid Induction Rates. Crop Science, 2016, 56, 1127-1135.	0.8	15
46	Association mapping for cold tolerance in two large maize inbred panels. BMC Plant Biology, 2016, 16, 127.	1.6	73
47	Domestication and Breeding of Jatropha curcas L.. Trends in Plant Science, 2016, 21, 1045-1057.	4.3	84
48	Silage yield and quality traits in elite maize hybrids and their relationship to elemental concentrations in juvenile plants. Plant Breeding, 2016, 135, 55-62.	1.0	5
49	Prediction of hybrid performance in maize with a ridge regression model employed to DNA markers and mRNA transcription profiles. BMC Genomics, 2016, 17, 262.	1.2	28
50	Selectiongain: an R package for optimizing multi-stage selection. Computational Statistics, 2016, 31, 533-543.	0.8	5
51	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. Genetics, 2016, 202, 1267-1276.	1.2	61
52	Choice of models for QTL mapping with multiple families and design of the training set for prediction of Fusarium resistance traits in maize. Theoretical and Applied Genetics, 2016, 129, 431-444.	1.8	30
53	Controlling Misclassification Rates in Identification of Haploid Seeds from Induction Crosses in Maize with High-Oil Inducers. Crop Science, 2015, 55, 1076-1086.	0.8	10
54	Prediction of deoxynivalenol and zearalenone concentrations in <i>Fusarium graminearum</i> inoculated backcross populations of maize by symptom rating andÂnearâ€infrared spectroscopy. Plant Breeding, 2015, 134, 529-534.	1.0	15

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55	Genomic selection in biparental populations: assessment of parameters for optimum estimation set design. Plant Breeding, 2015, 134, 623-630.	1.0	22
56	Oil Content is Superior to Oil Mass for Identification of Haploid Seeds in Maize Produced with Highâ€Oil Inducers. Crop Science, 2015, 55, 188-195.	0.8	23
57	Genetic diversity of Sudanese pearl millet (Pennisetum glaucum (L.) R. Br.) landraces as revealed by SSR markers, and relationship between genetic and agro-morphological diversity. Genetic Resources and Crop Evolution, 2015, 62, 579-591.	0.8	32
58	Forecasting the accuracy of genomic prediction with different selection targets in the training and prediction set as well as truncation selection. Theoretical and Applied Genetics, 2015, 128, 2189-2201.	1.8	7
59	Shrinkage estimation of the genomic relationship matrix can improve genomic estimated breeding values in the training set. Theoretical and Applied Genetics, 2015, 128, 693-703.	1.8	16
60	Fine mapping of qhir8 affecting in vivo haploid induction in maize. Theoretical and Applied Genetics, 2015, 128, 2507-2515.	1.8	52
61	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. Crop Science, 2014, 54, 1981-1991.	0.8	30
62	In Vivo Haploid Induction in Maize: Identification of Haploid Seeds by Their Oil Content. Crop Science, 2014, 54, 1497-1504.	0.8	59
63	Optimizing Resource Allocation for Multistage Selection in Plant Breeding with R Package <i>Selectiongain</i>. Crop Science, 2014, 54, 1413-1418.	0.8	23
64	Breeding Potential of European Flint Maize Landraces Evaluated by their Testcross Performance. Crop Science, 2014, 54, 1665-1672.	0.8	25
65	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. Genetics, 2014, 198, 1717-1734.	1.2	89
66	Characterization of Sudanese pearl millet germplasm for agro-morphological traits and grain nutritional values. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, 35-47.	0.4	38
67	Recovering Power in Association Mapping Panels with Variable Levels of Linkage Disequilibrium. Genetics, 2014, 197, 375-387.	1.2	89
68	Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. Theoretical and Applied Genetics, 2014, 127, 2313-2331.	1.8	41
69	Optimum allocation of test resources and comparison of breeding strategies for hybrid wheat. Theoretical and Applied Genetics, 2014, 127, 2117-2126.	1.8	14
70	Genome Properties and Prospects of Genomic Prediction of Hybrid Performance in a Breeding Program of Maize. Genetics, 2014, 197, 1343-1355.	1.2	192
71	Identification of key ancestors of modern germplasm in a breeding program of maize. Theoretical and Applied Genetics, 2014, 127, 2545-2553.	1.8	22
72	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. Genetics, 2014, 198, 3-16.	1.2	114

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73	Genome-wide meta-analysis of maize heterosis reveals the potential role of additive gene expression at pericentromeric loci. BMC Plant Biology, 2014, 14, 88.	1.6	54
74	Optimizing experimental procedures for quantitative evaluation of crop plant performance in high throughput phenotyping systems. Frontiers in Plant Science, 2014, 5, 770.	1.7	187
75	High-density genotyping: an overkill for QTL mapping? Lessons learned from a case study in maize and simulations. Theoretical and Applied Genetics, 2013, 126, 2563-2574.	1.8	63
76	Optimizing the allocation of resources for genomic selection in one breeding cycle. Theoretical and Applied Genetics, 2013, 126, 2835-2848.	1.8	74
77	Genomic Predictability of Interconnected Biparental Maize Populations. Genetics, 2013, 194, 493-503.	1.2	180
78	Intraspecific variation of recombination rate in maize. Genome Biology, 2013, 14, R103.	13.9	176
79	The maize leaf lipidome shows multilevel genetic control and high predictive value for agronomic traits. Scientific Reports, 2013, 3, 2479.	1.6	29
80	Genetic diversity analysis of elite European maize (Zea mays L.) inbred lines using AFLP, SSR, and SNP markers reveals ascertainment bias for a subset of SNPs. Theoretical and Applied Genetics, 2013, 126, 133-141.	1.8	97
81	Association mapping for chilling tolerance in elite flint and dent maize inbred lines evaluated in growth chamber and field experiments. Plant, Cell and Environment, 2013, 36, 1871-1887.	2.8	73
82	Optimum design of family structure and allocation of resources in association mapping with lines from multiple crosses. Heredity, 2013, 110, 71-79.	1.2	34
83	High-density linkage mapping of yield components and epistatic interactions in maize with doubled haploid lines from four crosses. Molecular Breeding, 2013, 32, 533-546.	1.0	12
84	Effectiveness of selection at <scp>CIMMYT</scp>'s main maize breeding sites in Mexico for performance at sites in Africa and vice versa. Plant Breeding, 2013, 132, 299-304.	1.0	5
85	Genomic prediction of dichotomous traits with Bayesian logistic models. Theoretical and Applied Genetics, 2013, 126, 1133-1143.	1.8	12
86	QTL mapping of stalk bending strength in a recombinant inbred line maize population. Theoretical and Applied Genetics, 2013, 126, 2257-2266.	1.8	63
87	Rapid and accurate identification of in vivo-induced haploid seeds based on oil content in maize. Scientific Reports, 2013, 3, 2129.	1.6	95
88	Gametophytic and zygotic selection leads to segregation distortion through in vivo induction of a maternal haploid in maize. Journal of Experimental Botany, 2013, 64, 1083-1096.	2.4	107
89	Precision phenotyping of biomass accumulation in triticale reveals temporal genetic patterns of regulation. Scientific Reports, 2013, 3, 2442.	1.6	99
90	Mapping quantitative trait loci for freezing tolerance in a recombinant inbred line population of <i><scp>A</scp>rabidopsis thaliana</i> accessions Tenela and <scp>C24</scp> reveals <scp>REVEILLE1</scp> as negative regulator of cold acclimation. Plant, Cell and Environment, 2013, 36, 1256-1267.	2.8	48

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91	Genomic Prediction of Northern Corn Leaf Blight Resistance in Maize with Combined or Separated Training Sets for Heterotic Groups. G3: Genes, Genomes, Genetics, 2013, 3, 197-203.	0.8	112
92	Unlocking the Genetic Diversity of Maize Landraces with Doubled Haploids Opens New Avenues for Breeding. PLoS ONE, 2013, 8, e57234.	1.1	68
93	Relationship of Line per se and Testcross Performance for Grain Yield of Tropical Maize in Drought and Wellâ€Watered Trials. Crop Science, 2013, 53, 1228-1236.	0.8	11
94	Comparative Quantitative Trait Loci Mapping for Gibberella Ear Rot Resistance and Reduced Deoxynivalenol Contamination across Connected Maize Populations. Crop Science, 2012, 52, 32-43.	0.8	27
95	Haploid Fertility in Temperate and Tropical Maize Germplasm. Crop Science, 2012, 52, 623-630.	0.8	61
96	Genetic Variation among Inbred Lines and Testcrosses of Maize for Early Growth Parameters and Their Relationship to Final Dry Matter Yield. Crop Science, 2012, 52, 1084-1092.	0.8	26
97	Strategies to Subdivide a Target Population of Environments: Results from the CIMMYTâ€Led Maize Hybrid Testing Programs in Africa. Crop Science, 2012, 52, 2143-2152.	0.8	49
98	Selection Strategy for Sorghum Targeting Phosphorusâ€limited Environments in West Africa: Analysis of Multiâ€environment Experiments. Crop Science, 2012, 52, 2517-2527.	0.8	41
99	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
100	Efficiency of Managedâ€Stress Screening of Elite Maize Hybrids under Drought and Low Nitrogen for Yield under Rainfed Conditions in Southern Africa. Crop Science, 2012, 52, 1011-1020.	0.8	84
101	Genome-wide association mapping of leaf metabolic profiles for dissecting complex traits in maize. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8872-8877.	3.3	340
102	Genomic prediction of hybrid performance in maize with models incorporating dominance and population specific marker effects. Theoretical and Applied Genetics, 2012, 125, 1181-1194.	1.8	143
103	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. Nature Genetics, 2012, 44, 217-220.	9.4	532
104	New Insights into the Genetics of<i>in Vivo</i>Induction of Maternal Haploids, the Backbone of Doubled Haploid Technology in Maize. Genetics, 2012, 190, 781-793.	1.2	143
105	Production of Haploids and Doubled Haploids in Maize. Methods in Molecular Biology, 2012, 877, 161-172.	0.4	69
106	Comparison of whole-genome prediction models for traits with contrasting genetic architecture in a diversity panel of maize inbred lines. BMC Genomics, 2012, 13, 452.	1.2	74
107	Association analysis of photoperiodic flowering time genes in west and central African sorghum [Sorghum bicolor (L.) Moench]. BMC Plant Biology, 2012, 12, 32.	1.6	30
108	Genome-wide association mapping of flowering time and northern corn leaf blight (Setosphaeria) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	70

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109	Maximizing the Reliability of Genomic Selection by Optimizing the Calibration Set of Reference Individuals: Comparison of Methods in Two Diverse Groups of Maize Inbreds (<i>Zea mays</i> L.). Genetics, 2012, 192, 715-728.	1.2	258
110	Breeding maize as biogas substrate in Central Europe: I. Quantitative-genetic parameters for testcross performance. Theoretical and Applied Genetics, 2012, 124, 971-980.	1.8	34
111	Breeding maize as biogas substrate in Central Europe: II. Quantitative-genetic parameters for inbred lines and correlations with testcross performance. Theoretical and Applied Genetics, 2012, 124, 981-988.	1.8	24
112	Variation and covariation for Gibberella ear rot resistance and agronomic traits in testcrosses of doubled haploid maize lines. Euphytica, 2012, 185, 441-451.	0.6	7
113	Doubled haploids in tropical maize: II. Quantitative genetic parameters for testcross performance. Euphytica, 2012, 185, 453-463.	0.6	10
114	Development of in vivo haploid inducers for tropical maize breeding programs. Euphytica, 2012, 185, 481-490.	0.6	52
115	Inheritance of resistance to Gibberella ear rot and deoxynivalenol contamination in five flint maize crosses. Plant Breeding, 2012, 131, 28-32.	1.0	18
116	Prediction of grain yield using reflectance spectra of canopy and leaves in maize plants grown under different water regimes. Field Crops Research, 2012, 128, 82-90.	2.3	144
117	Kinetics of methane fermentation yield in biogas reactors: Genetic variation and association with chemical composition in maize. Biomass and Bioenergy, 2012, 37, 132-141.	2.9	27
118	QTL mapping under truncation selection in homozygous lines derived from biparental crosses. Theoretical and Applied Genetics, 2012, 124, 543-553.	1.8	5
119	Partial least squares regression, support vector machine regression, and transcriptome-based distances for prediction of maize hybrid performance with gene expression data. Theoretical and Applied Genetics, 2012, 124, 825-833.	1.8	33
120	Mapping of QTL for resistance to first and second generation of European corn borer using an integrated SNP and SSR linkage map. Euphytica, 2012, 183, 197-206.	0.6	16
121	Determination of Methane Fermentation Yield and its Kinetics by near Infrared Spectroscopy and Chemical Composition in Maize. Journal of Near Infrared Spectroscopy, 2011, 19, 463-477.	0.8	17
122	REMLâ€Based Diallel Analysis. Crop Science, 2011, 51, 470-478.	0.8	47
123	High-throughput non-destructive biomass determination during early plant development in maize under field conditions. Field Crops Research, 2011, 121, 268-273.	2.3	139
124	Effect of source germplasm and season on the in vivo haploid induction rate in tropical maize. Euphytica, 2011, 180, 219-226.	0.6	59
125	Population structure in sorghum accessions from West Africa differing in race and maturity class. Genetica, 2011, 139, 453-463.	0.5	19
126	Best linear unbiased prediction and optimum allocation of test resources in maize breeding with doubled haploids. Theoretical and Applied Genetics, 2011, 123, 1-10.	1.8	42

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127	Extent and genome-wide distribution of linkage disequilibrium in commercial maize germplasm. Theoretical and Applied Genetics, 2011, 123, 11-20.	1.8	75
128	Gene stacking strategies with doubled haploids derived from biparental crosses: theory and simulations assuming a finite number of loci. Theoretical and Applied Genetics, 2011, 123, 1269-1279.	1.8	9
129	Doubled Haploids in Tropical Maize: I. Effects of Inducers and Source Germplasm on in vivo Haploid Induction Rates. Crop Science, 2011, 51, 1498-1506.	0.8	94
130	Colocalization of QTL for Gibberella Ear Rot Resistance and Low Mycotoxin Contamination in Early European Maize. Crop Science, 2011, 51, 1935-1945.	0.8	44
131	Broadening the genetic base of European maize heterotic pools with US Cornbelt germplasm using field and molecular marker data. Theoretical and Applied Genetics, 2010, 120, 301-310.	1.8	38
132	QTL analysis of early stage heterosis for biomass in Arabidopsis. Theoretical and Applied Genetics, 2010, 120, 227-237.	1.8	90
133	Molecular marker assisted broadening of the Central European heterotic groups in rye with Eastern European germplasm. Theoretical and Applied Genetics, 2010, 120, 291-299.	1.8	39
134	Optimum allocation of resources for QTL detection using a nested association mapping strategy in maize. Theoretical and Applied Genetics, 2010, 120, 553-561.	1.8	14
135	Hybrid maize breeding with doubled haploids: V. Selection strategies for testcross performance with variable sizes of crosses and S1 families. Theoretical and Applied Genetics, 2010, 120, 699-708.	1.8	6
136	Correlation between parental transcriptome and field data for the characterization of heterosis in Zea mays L.. Theoretical and Applied Genetics, 2010, 120, 401-413.	1.8	79
137	Variation of the parental genome contribution in segregating populations derived from biparental crosses and its relationship with heterosis of their Design III progenies. Theoretical and Applied Genetics, 2010, 120, 311-319.	1.8	5
138	Transcriptome-based distance measures for grouping of germplasm and prediction of hybrid performance in maize. Theoretical and Applied Genetics, 2010, 120, 441-450.	1.8	111
139	Prediction of hybrid performance in maize using molecular markers and joint analyses of hybrids and parental inbreds. Theoretical and Applied Genetics, 2010, 120, 451-461.	1.8	70
140	High congruency of QTL positions for heterosis of grain yield in three crosses of maize. Theoretical and Applied Genetics, 2010, 120, 321-332.	1.8	75
141	The International Conference on â€œHeterosis in Plantsâ€. Theoretical and Applied Genetics, 2010, 120, 201-203.	1.8	6
142	Dissection of the genetic basis of heterosis in an elite maize hybrid by QTL mapping in an immortalized F2 population. Theoretical and Applied Genetics, 2010, 120, 333-340.	1.8	132
143	Population structure and genetic diversity in a commercial maize breeding program assessed with SSR and SNP markers. Theoretical and Applied Genetics, 2010, 120, 1289-1299.	1.8	232
144	Patterns of molecular and phenotypic diversity in pearl millet [Pennisetum glaucum (L.) R. Br.] from West and Central Africa and their relation to geographical and environmental parameters. BMC Plant Biology, 2010, 10, 216.	1.6	55

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145	Dissecting grain yield pathways and their interactions with grain dry matter content by a two-step correlation approach with maize seedling transcriptome. BMC Plant Biology, 2010, 10, 63.	1.6	29
146	Genetic Variation in Testcrosses and Relationship between Line per se and Testcross Performance for Resistance to Gibberella Ear Rot in Maize. Crop Science, 2010, 50, 1691-1696.	0.8	12
147	Development of Heterotic Groups in Triticale. Crop Science, 2010, 50, 584-590.	0.8	76
148	Effect of N supply on stalk quality in maize hybrids. Field Crops Research, 2010, 118, 208-214.	2.3	25
149	Genetic Variation for Resistance to Ear Rots and Mycotoxins Contamination in Early European Maize Inbred Lines. Crop Science, 2009, 49, 2019-2028.	0.8	60
150	Impact of Genetic Divergence on the Ratio of Variance Due to Specific vs. General Combining Ability in Winter Triticale. Crop Science, 2009, 49, 2119-2122.	0.8	14
151	Unraveling Epistasis With Triple Testcross Progenies of Near-Isogenic Lines. Genetics, 2009, 181, 247-257.	1.2	28
152	Comparison of mixed-model approaches for association mapping in rapeseed, potato, sugar beet, maize, and Arabidopsis. BMC Genomics, 2009, 10, 94.	1.2	79
153	Molecular marker-based prediction of hybrid performance in maize using unbalanced data from multiple experiments with factorial crosses. Theoretical and Applied Genetics, 2009, 118, 741-751.	1.8	76
154	Efficiency gain of marker-assisted backcrossing by sequentially increasing marker densities over generations. Theoretical and Applied Genetics, 2009, 119, 23-32.	1.8	22
155	Identification of heterotic metabolite QTL in <i>Arabidopsis thaliana</i> RIL and IL populations. Plant Journal, 2009, 59, 777-788.	2.8	95
156	Optimum allocation of test resources and relative efficiency of alternative procedures of within-family selection in hybrid breeding. Plant Breeding, 2009, 128, 213-216.	1.0	3
157	A New near Infrared Spectroscopy Sample Presentation Unit for Measuring Feeding Quality of Maize Stover. Journal of Near Infrared Spectroscopy, 2009, 17, 195-201.	0.8	6
158	BLUP for phenotypic selection in plant breeding and variety testing. Euphytica, 2008, 161, 209-228.	0.6	569
159	The Plabsoft database: a comprehensive database management system for integrating phenotypic and genomic data in academic and commercial plant breeding programs. Euphytica, 2008, 161, 173-179.	0.6	11
160	Population genetic simulation and data analysis with Plabsoft. Euphytica, 2008, 161, 133-139.	0.6	62
161	Comparison of the observed with the simulated distributions of the parental genome contribution in two marker-assisted backcross programs in rice. Theoretical and Applied Genetics, 2008, 116, 739-744.	1.8	18
162	Hybrid maize breeding with doubled haploids. IV. Number versus size of crosses and importance of parental selection in two-stage selection for testcross performance. Theoretical and Applied Genetics, 2008, 117, 251-260.	1.8	20

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163	Multi-trait association mapping in sugar beet (Beta vulgaris L.). Theoretical and Applied Genetics, 2008, 117, 947-954.	1.8	57
164	Association mapping in multiple segregating populations of sugar beet (Beta vulgaris L.). Theoretical and Applied Genetics, 2008, 117, 1167-1179.	1.8	28
165	Trends in genetic variance components during 30â€ƒyears of hybrid maize breeding at the University of Hohenheim. Plant Breeding, 2008, 127, 446-451.	1.0	44
166	Feeding quality assessment of fresh maize stover by means of near-infrared spectroscopy with a new sample presentation unit. Plant Breeding, 2008, 127, 214-216.	1.0	2
167	Comparison of Mixed-Model Approaches for Association Mapping. Genetics, 2008, 178, 1745-1754.	1.2	273
168	Genetic Expectations of Quantitative Trait Loci Main and Interaction Effects Obtained With the Triple Testcross Design and Their Relevance for the Analysis of Heterosis. Genetics, 2008, 178, 2265-2274.	1.2	30
169	Precision of Recombination Frequency Estimates After Random Intermating With Finite Population Sizes. Genetics, 2008, 178, 597-600.	1.2	5
170	Quantitative Trait Loci Mapping and The Genetic Basis of Heterosis in Maize and Rice. Genetics, 2008, 180, 1707-1724.	1.2	141
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