

Albrecht E Melchinger

List of Publications by Year in Descending Order

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

313
papers

14,894
citations

64
h-index

102
g-index

319
ext. papers

17,075
ext. citations

4.3
avg, IF

6.46
L-index

#	Paper	IF	Citations
313	Unraveling the potential of phenomic selection within and among diverse breeding material of maize (<i>Zea mays</i> L.).. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	1
312	Genetic diversity of European maize landraces: Dataset on the molecular and phenotypic variation of derived doubled-haploid populations.. <i>Data in Brief</i> , 2022 , 42, 108164	1.2	
311	Theoretical and experimental assessment of genome-based prediction in landraces of allogamous crops.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2121797119	11.5	119
310	High-resolution association mapping with libraries of immortalized lines from ancestral landraces. <i>Theoretical and Applied Genetics</i> , 2021 , 1	6	2
309	Optimum breeding strategies using genomic and phenotypic selection for the simultaneous improvement of two traits. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 4025-4042	6	0
308	Calibration and validation of predicted genomic breeding values in an advanced cycle maize population. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 3069-3081	6	5
307	Exploiting genetic diversity in two European maize landraces for improving <i>Gibberella</i> ear rot resistance using genomic tools. <i>Theoretical and Applied Genetics</i> , 2021 , 134, 793-805	6	7
306	Genetic dissection of maternal influence on in vivo haploid induction in maize. <i>Crop Journal</i> , 2020 , 8, 287-298	4.6	1
305	Discovery of beneficial haplotypes for complex traits in maize landraces. <i>Nature Communications</i> , 2020 , 11, 4954	17.4	17
304	Genomic prediction with multiple biparental families. <i>Theoretical and Applied Genetics</i> , 2020 , 133, 133-147		14
303	European maize landraces made accessible for plant breeding and genome-based studies. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 3333-3345	6	22
302	Doubled haploid technology for line development in maize: technical advances and prospects. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 3227-3243	6	52
301	Efficient genetic value prediction using incomplete omics data. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 1211-1222	6	7
300	Reduced response diversity does not negatively impact wheat climate resilience. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 10623-10624	11.5	9
299	Haploid male fertility and spontaneous chromosome doubling evaluated in a diallel and recurrent selection experiment in maize. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 2273-2284	6	10
298	Testcross performance of doubled haploid lines from European flint maize landraces is promising for broadening the genetic base of elite germplasm. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 1897-1908	6	15
297	Early diagnosis of ploidy status in doubled haploid production of maize by stomata length and flow cytometry measurements. <i>Plant Breeding</i> , 2019 , 138, 266-276	2.4	9

296	Progress for testcross performance within the flint heterotic pool of a public maize breeding program since the onset of hybrid breeding. <i>Euphytica</i> , 2019 , 215, 1	2.1	7
295	Genome-wide association study to identify genomic regions influencing spontaneous fertility in maize haploids. <i>Euphytica</i> , 2019 , 215, 138	2.1	20
294	Across-years prediction of hybrid performance in maize using genomics. <i>Theoretical and Applied Genetics</i> , 2019 , 132, 933-946	6	13
293	Beyond Genomic Prediction: Combining Different Types of Data Can Improve Prediction of Hybrid Performance in Maize. <i>Genetics</i> , 2018 , 208, 1373-1385	4	66
292	Selection on Expected Maximum Haploid Breeding Values Can Increase Genetic Gain in Recurrent Genomic Selection. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 1173-1181	3.2	18
291	Nitrous Oxide-Induced Chromosome Doubling of Maize Haploids. <i>Crop Science</i> , 2018 , 58, 650-659	2.4	12
290	Parental Expression Variation of Small RNAs Is Negatively Correlated with Grain Yield Heterosis in a Maize Breeding Population. <i>Frontiers in Plant Science</i> , 2018 , 9, 13	6.2	13
289	Genomic prediction and GWAS of Gibberella ear rot resistance traits in dent and flint lines of a public maize breeding program. <i>Euphytica</i> , 2018 , 214, 1	2.1	23
288	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. <i>Genetics</i> , 2018 , 210, 1185-1196	4	14
287	Marker-Assisted Breeding of Improved Maternal Haploid Inducers in Maize for the Tropical/Subtropical Regions. <i>Frontiers in Plant Science</i> , 2018 , 9, 1527	6.2	17
286	Small RNA-based prediction of hybrid performance in maize. <i>BMC Genomics</i> , 2018 , 19, 371	4.5	13
285	High-Throughput Precision Phenotyping of the Oil Content of Single Seeds of Various Oilseed Crops. <i>Crop Science</i> , 2018 , 58, 670-678	2.4	17
284	Metabolic robustness in young roots underpins a predictive model of maize hybrid performance in the field. <i>Plant Journal</i> , 2017 , 90, 319-329	6.9	24
283	Tapping the genetic diversity of landraces in allogamous crops with doubled haploid lines: a case study from European flint maize. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 861-873	6	26
282	Transcriptome-based prediction of hybrid performance with unbalanced data from a maize breeding programme. <i>Plant Breeding</i> , 2017 , 136, 331-337	2.4	15
281	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. <i>Genetics</i> , 2017 , 206, 1611-1619	4	21
280	Dissection of a major QTL qhir1 conferring maternal haploid induction ability in maize. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1113-1122	6	11
279	Accuracy of Genomic Prediction in Synthetic Populations Depending on the Number of Parents, Relatedness, and Ancestral Linkage Disequilibrium. <i>Genetics</i> , 2017 , 205, 441-454	4	41

278	Genomic Prediction Within and Across Biparental Families: Means and Variances of Prediction Accuracy and Usefulness of Deterministic Equations. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3571-3586	3.2	22
277	Persistency of Prediction Accuracy and Genetic Gain in Synthetic Populations Under Recurrent Genomic Selection. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 801-811	3.2	22
276	Genotyping-by-sequencing highlights original diversity patterns within a European collection of 1191 maize flint lines, as compared to the maize USDA genebank. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 2165-2189	6	24
275	High-throughput platform for automated sorting and selection of single seeds based on time-domain nuclear magnetic resonance (TD-NMR) measurement of oil content. <i>Biosystems Engineering</i> , 2017 , 164, 213-220	4.8	13
274	Omics-based hybrid prediction in maize. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1927-1939	6	54
273	Low validation rate of quantitative trait loci for Gibberella ear rot resistance in European maize. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 175-186	6	15
272	Domestication and Breeding of <i>Jatropha curcas</i> L. <i>Trends in Plant Science</i> , 2016 , 21, 1045-1057	13.1	54
271	Silage yield and quality traits in elite maize hybrids and their relationship to elemental concentrations in juvenile plants. <i>Plant Breeding</i> , 2016 , 135, 55-62	2.4	2
270	Prediction of hybrid performance in maize with a ridge regression model employed to DNA markers and mRNA transcription profiles. <i>BMC Genomics</i> , 2016 , 17, 262	4.5	21
269	Selectiongain: an R package for optimizing multi-stage selection. <i>Computational Statistics</i> , 2016 , 31, 533-543		2
268	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. <i>Genetics</i> , 2016 , 202, 1267-76	4	43
267	Choice of models for QTL mapping with multiple families and design of the training set for prediction of Fusarium resistance traits in maize. <i>Theoretical and Applied Genetics</i> , 2016 , 129, 431-44	6	24
266	Optimum breeding strategies using genomic selection for hybrid breeding in wheat, maize, rye, barley, rice and triticale. <i>Theoretical and Applied Genetics</i> , 2016 , 129, 1901-13	6	53
265	Colchicine Alternatives for Chromosome Doubling in Maize Haploids for Doubled-Haploid Production. <i>Crop Science</i> , 2016 , 56, 559-569	2.4	31
264	Development and Validation of Red Root Marker-Based Haploid Inducers in Maize. <i>Crop Science</i> , 2016 , 56, 1678-1688	2.4	33
263	In Vivo Haploid Induction in Maize: Comparison of Different Testing Regimes for Measuring Haploid Induction Rates. <i>Crop Science</i> , 2016 , 56, 1127-1135	2.4	10
262	Association mapping for cold tolerance in two large maize inbred panels. <i>BMC Plant Biology</i> , 2016 , 16, 127	5.3	46
261	Forecasting the accuracy of genomic prediction with different selection targets in the training and prediction set as well as truncation selection. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 2189-201	6	7

260	Shrinkage estimation of the genomic relationship matrix can improve genomic estimated breeding values in the training set. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 693-703	6	11
259	Fine mapping of qhir8 affecting in vivo haploid induction in maize. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 2507-15	6	37
258	Controlling Misclassification Rates in Identification of Haploid Seeds from Induction Crosses in Maize with High-Oil Inducers. <i>Crop Science</i> , 2015 , 55, 1076-1086	2.4	9
257	Overview of Heterosis and Heterotic Groups in Agronomic Crops. <i>CSSA Special Publication - Crop Science Society of America</i> , 2015 , 29-44		57
256	Prediction of deoxynivalenol and zearalenone concentrations in <i>Fusarium graminearum</i> inoculated backcross populations of maize by symptom rating and near-infrared spectroscopy. <i>Plant Breeding</i> , 2015 , 134, 529-534	2.4	10
255	Genomic selection in biparental populations: assessment of parameters for optimum estimation set design. <i>Plant Breeding</i> , 2015 , 134, 623-630	2.4	22
254	Oil Content is Superior to Oil Mass for Identification of Haploid Seeds in Maize Produced with High-Oil Inducers. <i>Crop Science</i> , 2015 , 55, 188-195	2.4	18
253	Genetic diversity of Sudanese pearl millet (<i>Pennisetum glaucum</i> (L.) R. Br.) landraces as revealed by SSR markers, and relationship between genetic and agro-morphological diversity. <i>Genetic Resources and Crop Evolution</i> , 2015 , 62, 579-591	2	25
252	Optimizing experimental procedures for quantitative evaluation of crop plant performance in high throughput phenotyping systems. <i>Frontiers in Plant Science</i> , 2014 , 5, 770	6.2	104
251	Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 2313-31	6	33
250	Optimum allocation of test resources and comparison of breeding strategies for hybrid wheat. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 2117-26	6	10
249	Genome properties and prospects of genomic prediction of hybrid performance in a breeding program of maize. <i>Genetics</i> , 2014 , 197, 1343-55	4	125
248	Identification of key ancestors of modern germplasm in a breeding program of maize. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 2545-53	6	18
247	Usefulness of multiparental populations of maize (<i>Zea mays</i> L.) for genome-based prediction. <i>Genetics</i> , 2014 , 198, 3-16	4	84
246	Genome-wide meta-analysis of maize heterosis reveals the potential role of additive gene expression at pericentromeric loci. <i>BMC Plant Biology</i> , 2014 , 14, 88	5.3	25
245	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. <i>Crop Science</i> , 2014 , 54, 1981-1991	2.4	21
244	In Vivo Haploid Induction in Maize: Identification of Haploid Seeds by Their Oil Content. <i>Crop Science</i> , 2014 , 54, 1497-1504	2.4	42
243	Optimizing Resource Allocation for Multistage Selection in Plant Breeding with R Package Selectiongain. <i>Crop Science</i> , 2014 , 54, 1413-1418	2.4	14

242	Breeding Potential of European Flint Maize Landraces Evaluated by their Testcross Performance. <i>Crop Science</i> , 2014 , 54, 1665-1672	2.4	20
241	Linkage disequilibrium with linkage analysis of multiline crosses reveals different multiallelic QTL for hybrid performance in the flint and dent heterotic groups of maize. <i>Genetics</i> , 2014 , 198, 1717-34	4	58
240	Characterization of Sudanese pearl millet germplasm for agro-morphological traits and grain nutritional values. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014 , 12, 35-47	1	28
239	Recovering power in association mapping panels with variable levels of linkage disequilibrium. <i>Genetics</i> , 2014 , 197, 375-87	4	58
238	High-density genotyping: an overkill for QTL mapping? Lessons learned from a case study in maize and simulations. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 2563-74	6	51
237	Optimizing the allocation of resources for genomic selection in one breeding cycle. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 2835-48	6	57
236	Genomic predictability of interconnected biparental maize populations. <i>Genetics</i> , 2013 , 194, 493-503	4	142
235	Intraspecific variation of recombination rate in maize. <i>Genome Biology</i> , 2013 , 14, R103	18.3	134
234	The maize leaf lipidome shows multilevel genetic control and high predictive value for agronomic traits. <i>Scientific Reports</i> , 2013 , 3, 2479	4.9	22
233	Genetic diversity analysis of elite European maize (<i>Zea mays</i> L.) inbred lines using AFLP, SSR, and SNP markers reveals ascertainment bias for a subset of SNPs. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 133-41	6	67
232	Association mapping for chilling tolerance in elite flint and dent maize inbred lines evaluated in growth chamber and field experiments. <i>Plant, Cell and Environment</i> , 2013 , 36, 1871-87	8.4	53
231	Optimum design of family structure and allocation of resources in association mapping with lines from multiple crosses. <i>Heredity</i> , 2013 , 110, 71-9	3.6	32
230	Relationship of Line per se and Testcross Performance for Grain Yield of Tropical Maize in Drought and Well-Watered Trials. <i>Crop Science</i> , 2013 , 53, 1228-1236	2.4	9
229	High-density linkage mapping of yield components and epistatic interactions in maize with doubled haploid lines from four crosses. <i>Molecular Breeding</i> , 2013 , 32, 533-546	3.4	9
228	Effectiveness of selection at CIMMYT's main maize breeding sites in Mexico for performance at sites in Africa and vice versa. <i>Plant Breeding</i> , 2013 , 132, 299-304	2.4	4
227	Genomic prediction of dichotomous traits with Bayesian logistic models. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 1133-43	6	10
226	QTL mapping of stalk bending strength in a recombinant inbred line maize population. <i>Theoretical and Applied Genetics</i> , 2013 , 126, 2257-66	6	36
225	Rapid and accurate identification of in vivo-induced haploid seeds based on oil content in maize. <i>Scientific Reports</i> , 2013 , 3, 2129	4.9	71

224	Gametophytic and zygotic selection leads to segregation distortion through in vivo induction of a maternal haploid in maize. <i>Journal of Experimental Botany</i> , 2013 , 64, 1083-96	7	73
223	Precision phenotyping of biomass accumulation in triticale reveals temporal genetic patterns of regulation. <i>Scientific Reports</i> , 2013 , 3, 2442	4.9	84
222	Mapping quantitative trait loci for freezing tolerance in a recombinant inbred line population of <i>Arabidopsis thaliana</i> accessions Tenela and C24 reveals REVEILLE1 as negative regulator of cold acclimation. <i>Plant, Cell and Environment</i> , 2013 , 36, 1256-67	8.4	33
221	Genomic prediction of northern corn leaf blight resistance in maize with combined or separated training sets for heterotic groups. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 197-203	3.2	83
220	Unlocking the genetic diversity of maize landraces with doubled haploids opens new avenues for breeding. <i>PLoS ONE</i> , 2013 , 8, e57234	3.7	53
219	Kinetics of methane fermentation yield in biogas reactors: Genetic variation and association with chemical composition in maize. <i>Biomass and Bioenergy</i> , 2012 , 37, 132-141	5.3	24
218	QTL mapping under truncation selection in homozygous lines derived from biparental crosses. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 543-53	6	5
217	Partial least squares regression, support vector machine regression, and transcriptome-based distances for prediction of maize hybrid performance with gene expression data. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 825-33	6	25
216	Mapping of QTL for resistance to first and second generation of European corn borer using an integrated SNP and SSR linkage map. <i>Euphytica</i> , 2012 , 183, 197-206	2.1	12
215	Genomic prediction of hybrid performance in maize with models incorporating dominance and population specific marker effects. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 1181-94	6	105
214	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. <i>Nature Genetics</i> , 2012 , 44, 217-20	36.3	424
213	New insights into the genetics of in vivo induction of maternal haploids, the backbone of doubled haploid technology in maize. <i>Genetics</i> , 2012 , 190, 781-93	4	98
212	Production of haploids and doubled haploids in maize. <i>Methods in Molecular Biology</i> , 2012 , 877, 161-72	1.4	58
211	Comparison of whole-genome prediction models for traits with contrasting genetic architecture in a diversity panel of maize inbred lines. <i>BMC Genomics</i> , 2012 , 13, 452	4.5	61
210	Association analysis of photoperiodic flowering time genes in west and central African sorghum [<i>Sorghum bicolor</i> (L.) Moench]. <i>BMC Plant Biology</i> , 2012 , 12, 32	5.3	28
209	Genome-wide association mapping of flowering time and northern corn leaf blight (<i>Setosphaeria turcica</i>) resistance in a vast commercial maize germplasm set. <i>BMC Plant Biology</i> , 2012 , 12, 56	5.3	55
208	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.). <i>Genetics</i> , 2012 , 192, 715-28	4	193
207	Breeding maize as biogas substrate in Central Europe: I. Quantitative-genetic parameters for testcross performance. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 971-80	6	30

206	Breeding maize as biogas substrate in Central Europe: II. Quantitative-genetic parameters for inbred lines and correlations with testcross performance. <i>Theoretical and Applied Genetics</i> , 2012 , 124, 981-8	6	24
205	Variation and covariation for Gibberella ear rot resistance and agronomic traits in testcrosses of doubled haploid maize lines. <i>Euphytica</i> , 2012 , 185, 441-451	2.1	6
204	Doubled haploids in tropical maize: II. Quantitative genetic parameters for testcross performance. <i>Euphytica</i> , 2012 , 185, 453-463	2.1	9
203	Development of in vivo haploid inducers for tropical maize breeding programs. <i>Euphytica</i> , 2012 , 185, 481-490	2.1	30
202	Inheritance of resistance to Gibberella ear rot and deoxynivalenol contamination in five flint maize crosses. <i>Plant Breeding</i> , 2012 , 131, 28-32	2.4	13
201	Prediction of grain yield using reflectance spectra of canopy and leaves in maize plants grown under different water regimes. <i>Field Crops Research</i> , 2012 , 128, 82-90	5.5	118
200	Comparative Quantitative Trait Loci Mapping for Gibberella Ear Rot Resistance and Reduced Deoxynivalenol Contamination across Connected Maize Populations. <i>Crop Science</i> , 2012 , 52, 32-43	2.4	22
199	Haploid Fertility in Temperate and Tropical Maize Germplasm. <i>Crop Science</i> , 2012 , 52, 623-630	2.4	39
198	Genetic Variation among Inbred Lines and Testcrosses of Maize for Early Growth Parameters and Their Relationship to Final Dry Matter Yield. <i>Crop Science</i> , 2012 , 52, 1084-1092	2.4	23
197	Strategies to Subdivide a Target Population of Environments: Results from the CIMMYT-Led Maize Hybrid Testing Programs in Africa. <i>Crop Science</i> , 2012 , 52, 2143-2152	2.4	42
196	Selection Strategy for Sorghum Targeting Phosphorus-limited Environments in West Africa: Analysis of Multi-environment Experiments. <i>Crop Science</i> , 2012 , 52, 2517-2527	2.4	39
195	Effectiveness of genomic prediction of maize hybrid performance in different breeding populations and environments. <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 1427-36	3.2	166
194	Efficiency of Managed-Stress Screening of Elite Maize Hybrids under Drought and Low Nitrogen for Yield under Rainfed Conditions in Southern Africa. <i>Crop Science</i> , 2012 , 52, 1011-1020	2.4	76
193	Genome-wide association mapping of leaf metabolic profiles for dissecting complex traits in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 8872-7	11.5	260
192	Determination of Methane Fermentation Yield and its Kinetics by near Infrared Spectroscopy and Chemical Composition in Maize. <i>Journal of Near Infrared Spectroscopy</i> , 2011 , 19, 463-477	1.5	14
191	REML-Based Diallel Analysis. <i>Crop Science</i> , 2011 , 51, 470-478	2.4	36
190	High-throughput non-destructive biomass determination during early plant development in maize under field conditions. <i>Field Crops Research</i> , 2011 , 121, 268-273	5.5	109
189	Effect of source germplasm and season on the in vivo haploid induction rate in tropical maize. <i>Euphytica</i> , 2011 , 180, 219-226	2.1	41

188	Population structure in sorghum accessions from West Africa differing in race and maturity class. <i>Genetica</i> , 2011 , 139, 453-63	1.5	12
187	Best linear unbiased prediction and optimum allocation of test resources in maize breeding with doubled haploids. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 1-10	6	17
186	Extent and genome-wide distribution of linkage disequilibrium in commercial maize germplasm. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 11-20	6	61
185	Gene stacking strategies with doubled haploids derived from biparental crosses: theory and simulations assuming a finite number of loci. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 1269-79	6	8
184	Doubled Haploids in Tropical Maize: I. Effects of Inducers and Source Germplasm on in vivo Haploid Induction Rates. <i>Crop Science</i> , 2011 , 51, 1498-1506	2.4	62
183	Colocalization of QTL for Gibberella Ear Rot Resistance and Low Mycotoxin Contamination in Early European Maize. <i>Crop Science</i> , 2011 , 51, 1935-1945	2.4	38
182	Genetic Variation in Testcrosses and Relationship between Line per se and Testcross Performance for Resistance to Gibberella Ear Rot in Maize. <i>Crop Science</i> , 2010 , 50, 1691-1696	2.4	10
181	Development of Heterotic Groups in Triticale. <i>Crop Science</i> , 2010 , 50, 584-590	2.4	64
180	Effect of N supply on stalk quality in maize hybrids. <i>Field Crops Research</i> , 2010 , 118, 208-214	5.5	16
179	Broadening the genetic base of European maize heterotic pools with US Cornbelt germplasm using field and molecular marker data. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 301-10	6	34
178	QTL analysis of early stage heterosis for biomass in Arabidopsis. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 227-37	6	80
177	Molecular marker assisted broadening of the Central European heterotic groups in rye with Eastern European germplasm. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 291-9	6	34
176	Optimum allocation of resources for QTL detection using a nested association mapping strategy in maize. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 553-61	6	14
175	Hybrid maize breeding with doubled haploids: V. Selection strategies for testcross performance with variable sizes of crosses and S(1) families. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 699-708	6	5
174	Correlation between parental transcriptome and field data for the characterization of heterosis in <i>Zea mays</i> L. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 401-13	6	52
173	Variation of the parental genome contribution in segregating populations derived from biparental crosses and its relationship with heterosis of their Design III progenies. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 311-9	6	5
172	Transcriptome-based distance measures for grouping of germplasm and prediction of hybrid performance in maize. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 441-50	6	82
171	Prediction of hybrid performance in maize using molecular markers and joint analyses of hybrids and parental inbreds. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 451-61	6	53

170	High congruency of QTL positions for heterosis of grain yield in three crosses of maize. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 321-32	6	62
169	Dissection of the genetic basis of heterosis in an elite maize hybrid by QTL mapping in an immortalized F2 population. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 333-40	6	99
168	Population structure and genetic diversity in a commercial maize breeding program assessed with SSR and SNP markers. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 1289-99	6	193
167	Patterns of molecular and phenotypic diversity in pearl millet [<i>Pennisetum glaucum</i> (L.) R. Br.] from West and Central Africa and their relation to geographical and environmental parameters. <i>BMC Plant Biology</i> , 2010 , 10, 216	5.3	46
166	Dissecting grain yield pathways and their interactions with grain dry matter content by a two-step correlation approach with maize seedling transcriptome. <i>BMC Plant Biology</i> , 2010 , 10, 63	5.3	27
165	Impact of Genetic Divergence on the Ratio of Variance Due to Specific vs. General Combining Ability in Winter Triticale. <i>Crop Science</i> , 2009 , 49, 2119-2122	2.4	12
164	Unraveling epistasis with triple testcross progenies of near-isogenic lines. <i>Genetics</i> , 2009 , 181, 247-57	4	24
163	Comparison of mixed-model approaches for association mapping in rapeseed, potato, sugar beet, maize, and Arabidopsis. <i>BMC Genomics</i> , 2009 , 10, 94	4.5	62
162	Molecular marker-based prediction of hybrid performance in maize using unbalanced data from multiple experiments with factorial crosses. <i>Theoretical and Applied Genetics</i> , 2009 , 118, 741-51	6	56
161	Efficiency gain of marker-assisted backcrossing by sequentially increasing marker densities over generations. <i>Theoretical and Applied Genetics</i> , 2009 , 119, 23-32	6	21
160	Identification of heterotic metabolite QTL in Arabidopsis thaliana RIL and IL populations. <i>Plant Journal</i> , 2009 , 59, 777-88	6.9	84
159	Optimum allocation of test resources and relative efficiency of alternative procedures of within-family selection in hybrid breeding. <i>Plant Breeding</i> , 2009 , 128, 213-216	2.4	3
158	A New near Infrared Spectroscopy Sample Presentation Unit for Measuring Feeding Quality of Maize Stover. <i>Journal of Near Infrared Spectroscopy</i> , 2009 , 17, 195-201	1.5	4
157	Genetic Variation for Resistance to Ear Rots and Mycotoxins Contamination in Early European Maize Inbred Lines. <i>Crop Science</i> , 2009 , 49, 2019-2028	2.4	44
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144	Multi-trait association mapping in sugar beet (<i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008 , 117, 947-54	6	50
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121	Comparison of linkage maps from F2 and three times intermated generations in two populations of European flint maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2006 , 113, 857-66	6	11
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8	Use of Molecular Markers in Breeding for Oligogenic Disease Resistance. <i>Plant Breeding</i> , 1990 , 104, 1-19	2.4	157
7	Genetic diversity for restriction fragment length polymorphisms and heterosis for two diallel sets of maize inbreds. <i>Theoretical and Applied Genetics</i> , 1990 , 80, 488-96	6	101
6	Optimum prediction of three-way crosses from single crosses in forage maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 1987 , 74, 339-45	6	38
5	Expectation of means and variances of testcrosses produced from from F2 and backcross individuals and their selfed progenies. <i>Heredity</i> , 1987 , 59, 105-115	3.6	29
4	Epistasis in Maize (<i>Zea mays</i> L.) III. Comparison of Single and Three-Way Crosses for Forage Traits. <i>Plant Breeding</i> , 1987 , 98, 185-193	2.4	3
3	Epistasis in maize (<i>Zea mays</i> L.) : 2. Genetic effects in crosses among early flint and dent inbred lines determined by three methods. <i>Theoretical and Applied Genetics</i> , 1986 , 72, 231-9	6	27
2	Evaluation of Near Infra-red Reflectance Spectroscopy for Predicting Grain and Stover Quality Traits in Maize. <i>Plant Breeding</i> , 1986 , 97, 20-29	2.4	32
1	Omics-based Hybrid Prediction in Maize		2