

Albrecht E Melchinger

List of Publications by Year in descending order

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315
papers

18,992
citations

9756

73
h-index

20900

115
g-index

319
all docs

319
docs citations

319
times ranked

10041
citing authors

#	ARTICLE	IF	CITATIONS
1	BLUP for phenotypic selection in plant breeding and variety testing. <i>Euphytica</i> , 2008, 161, 209-228.	0.6	569
2	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. <i>Nature Genetics</i> , 2012, 44, 217-220.	9.4	532
3	Quantitative Trait Locus (QTL) Mapping Using Different Testers and Independent Population Samples in Maize Reveals Low Power of QTL Detection and Large Bias in Estimates of QTL Effects. <i>Genetics</i> , 1998, 149, 383-403.	1.2	462
4	Wheat genetic diversity trends during domestication and breeding. <i>Theoretical and Applied Genetics</i> , 2005, 110, 859-864.	1.8	365
5	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, 8872-8877.	3.3	340
6	Bias and Sampling Error of the Estimated Proportion of Genotypic Variance Explained by Quantitative Trait Loci Determined From Experimental Data in Maize Using Cross Validation and Validation With Independent Samples. <i>Genetics</i> , 2000, 154, 1839-1849.	1.2	305
7	Comparison of Mixed-Model Approaches for Association Mapping. <i>Genetics</i> , 2008, 178, 1745-1754.	1.2	273
8	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, 715-728.	1.2	258
9	Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1427-1436.	0.8	242
10	Genetic Similarities among Winter Wheat Cultivars Determined on the Basis of RFLPs, AFLPs, and SSRs and Their Use for Predicting Progeny Variance. <i>Crop Science</i> , 1999, 39, 228-237.	0.8	232
11	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, 1289-1299.	1.8	232
12	Quantitative Trait Locus Mapping Based on Resampling in a Vast Maize Testcross Experiment and Its Relevance to Quantitative Genetics for Complex Traits. <i>Genetics</i> , 2004, 167, 485-498.	1.2	231
13	Novel throughput phenotyping platforms in plant genetic studies. <i>Trends in Plant Science</i> , 2007, 12, 433-436.	4.3	220
14	Genetic diversity in European and Mediterranean faba bean germ plasm revealed by RAPD markers. <i>Theoretical and Applied Genetics</i> , 1995, 90, 27-32.	1.8	217
15	Two high-density AFLP® linkage maps of <i>Zea mays</i> L.: analysis of distribution of AFLP markers. <i>Theoretical and Applied Genetics</i> , 1999, 99, 921-935.	1.8	217
16	Comparison of Selection Strategies for Marker-Assisted Backcrossing of a Gene. <i>Crop Science</i> , 1999, 39, 1295-1301.	0.8	206
17	Genome Properties and Prospects of Genomic Prediction of Hybrid Performance in a Breeding Program of Maize. <i>Genetics</i> , 2014, 197, 1343-1355.	1.2	192
18	Use of Molecular Markers in Breeding for Oligogenic Disease Resistance. <i>Plant Breeding</i> , 1990, 104, 1-19.	1.0	191

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19	Optimizing experimental procedures for quantitative evaluation of crop plant performance in high throughput phenotyping systems. <i>Frontiers in Plant Science</i> , 2014, 5, 770.	1.7	187
20	Genomic Predictability of Interconnected Biparental Maize Populations. <i>Genetics</i> , 2013, 194, 493-503.	1.2	180
21	Intraspecific variation of recombination rate in maize. <i>Genome Biology</i> , 2013, 14, R103.	13.9	176
22	Linkage disequilibrium in European elite maize germplasm investigated with SSRs. <i>Theoretical and Applied Genetics</i> , 2005, 111, 723-730.	1.8	167
23	RFLP Mapping in Maize: Quantitative Trait Loci Affecting Testcross Performance of Elite European Flint Lines. <i>Crop Science</i> , 1994, 34, 378-389.	0.8	147
24	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.	2.3	144
25	Genomic prediction of hybrid performance in maize with models incorporating dominance and population specific marker effects. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1181-1194.	1.8	143
26	New Insights into the Genetics of <i>in Vivo</i> Induction of Maternal Haploids, the Backbone of Doubled Haploid Technology in Maize. <i>Genetics</i> , 2012, 190, 781-793.	1.2	143
27	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
28	Quantitative Trait Loci Mapping and The Genetic Basis of Heterosis in Maize and Rice. <i>Genetics</i> , 2008, 180, 1707-1724.	1.2	141
29	High-throughput non-destructive biomass determination during early plant development in maize under field conditions. <i>Field Crops Research</i> , 2011, 121, 268-273.	2.3	139
30	Mapping and characterization of quantitative trait loci affecting resistance against second-generation European corn borer in maize with the aid of RFLPs. <i>Heredity</i> , 1993, 70, 648-659.	1.2	135
31	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, 333-340.	1.8	132
32	Beyond Genomic Prediction: Combining Different Types of <i>omics</i> Data Can Improve Prediction of Hybrid Performance in Maize. <i>Genetics</i> , 2018, 208, 1373-1385.	1.2	130
33	Relationships among Early European Maize Inbreds: II. Comparison of Pedigree and RFLP Data. <i>Crop Science</i> , 1993, 33, 944-950.	0.8	127
34	Doubled haploid technology for line development in maize: technical advances and prospects. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3227-3243.	1.8	126
35	The Role of Epistasis in the Manifestation of Heterosis: A Systems-Oriented Approach. <i>Genetics</i> , 2007, 177, 1815-1825.	1.2	125
36	Genetic diversity for restriction fragment length polymorphisms and heterosis for two diallel sets of maize inbreds. <i>Theoretical and Applied Genetics</i> , 1990, 80, 488-496.	1.8	124

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37	Validation of Dwarf8 polymorphisms associated with flowering time in elite European inbred lines of maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2005, 111, 206-217.	1.8	115
38	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. <i>Genetics</i> , 2014, 198, 3-16.	1.2	114
39	QTL Mapping in Testcrosses of European Flint Lines of Maize: I. Comparison of Different Testers for Forage Yield Traits. <i>Crop Science</i> , 1997, 37, 921-931.	0.8	113
40	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.	0.8	112
41	Relationships among European Barley Germplasm: II. Comparison of RFLP and Pedigree Data. <i>Crop Science</i> , 1994, 34, 1199-1205.	0.8	111
42	Transcriptome-based distance measures for grouping of germplasm and prediction of hybrid performance in maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 441-450.	1.8	111
43	Use of SSRs for establishing heterotic groups in subtropical maize. <i>Theoretical and Applied Genetics</i> , 2003, 107, 947-957.	1.8	110
44	Overview of Heterosis and Heterotic Groups in Agronomic Crops. <i>CSSA Special Publication - Crop Science Society of America</i> , 0, , 29-44.	0.1	109
45	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, 1083-1096.	2.4	107
46	Selection Theory for Marker-Assisted Backcrossing. <i>Genetics</i> , 2005, 170, 909-917.	1.2	99
47	Precision phenotyping of biomass accumulation in triticale reveals temporal genetic patterns of regulation. <i>Scientific Reports</i> , 2013, 3, 2442.	1.6	99
48	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, 133-141.	1.8	97
49	Genetic structure and diversity of European flint maize populations determined with SSR analyses of individuals and bulks. <i>Theoretical and Applied Genetics</i> , 2005, 111, 906-913.	1.8	96
50	Genetic Basis of Heterosis for Growth-Related Traits in Arabidopsis Investigated by Testcross Progenies of Near-Isogenic Lines Reveals a Significant Role of Epistasis. <i>Genetics</i> , 2007, 177, 1827-1837.	1.2	95
51	Identification of heterotic metabolite QTL in <i>Arabidopsis thaliana</i> RIL and IL populations. <i>Plant Journal</i> , 2009, 59, 777-788.	2.8	95
52	Rapid and accurate identification of in vivo-induced haploid seeds based on oil content in maize. <i>Scientific Reports</i> , 2013, 3, 2129.	1.6	95
53	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.	0.8	94
54	Phylogenetic relationships between cultivated and wild species of the genus <i>Beta</i> revealed by DNA fingerprinting?. <i>Theoretical and Applied Genetics</i> , 1993, 86, 449-457.	1.8	93

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55	Trends in genetic diversity among European maize cultivars and their parental components during the past 50 years. <i>Theoretical and Applied Genetics</i> , 2005, 111, 838-845.	1.8	93
56	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
57	Prediction of single-cross hybrid performance for grain yield and grain dry matter content in maize using AFLP markers associated with QTL. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1037-1047.	1.8	92
58	QTL analysis of early stage heterosis for biomass in <i>Arabidopsis</i> . <i>Theoretical and Applied Genetics</i> , 2010, 120, 227-237.	1.8	90
59	Omics-based hybrid prediction in maize. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1927-1939.	1.8	90
60	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, 1717-1734.	1.2	89
61	Recovering Power in Association Mapping Panels with Variable Levels of Linkage Disequilibrium. <i>Genetics</i> , 2014, 197, 375-387.	1.2	89
62	High-resolution mapping of loci conferring resistance to sugarcane mosaic virus in maize using RFLP, SSR, and AFLP markers. <i>Molecular Genetics and Genomics</i> , 1999, 261, 574-581.	2.4	88
63	Genetic diversity for RFLPs in European maize inbreds. <i>Theoretical and Applied Genetics</i> , 1992, 84-84, 672-681.	1.8	86
64	Heterosis for biomass yield and related traits in five hybrids of <i>Arabidopsis thaliana</i> L. Heynh. <i>Heredity</i> , 2003, 91, 36-42.	1.2	86
65	Genetic Diversity among CIMMYT Maize Inbred Lines Investigated with SSR Markers: II. Subtropical, Tropical Midaltitude, and Highland Maize Inbred Lines and their Relationships with Elite U.S. and European Maize. <i>Crop Science</i> , 2005, 45, 2573-2582.	0.8	86
66	Quantitative Trait Loci Mapping of Resistance to Sugarcane Mosaic Virus in Maize. <i>Phytopathology</i> , 1999, 89, 660-667.	1.1	84
67	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.	0.8	84
68	Domestication and Breeding of <i>Jatropha curcas</i> L.. <i>Trends in Plant Science</i> , 2016, 21, 1045-1057.	4.3	84
69	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
70	Genetic diversity in <i>Arabidopsis thaliana</i> L. Heynh. investigated by cleaved amplified polymorphic sequence (CAPS) and inter-simple sequence repeat (ISSR) markers. <i>Molecular Ecology</i> , 2002, 11, 495-505.	2.0	80
71	Relationships among Early European Maize Inbreds: IV. Genetic Diversity Revealed with AFLP Markers and Comparison with RFLP, RAPD, and Pedigree Data. <i>Crop Science</i> , 2000, 40, 783-791.	0.8	79
72	Comparison of mixed-model approaches for association mapping in rapeseed, potato, sugar beet, maize, and <i>Arabidopsis</i> . <i>BMC Genomics</i> , 2009, 10, 94.	1.2	79

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73	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, 401-413.	1.8	79
74	QTL Mapping in Testcrosses of Flint Lines of Maize: III. Comparison across Populations for Forage Traits. <i>Crop Science</i> , 1998, 38, 1278-1289.	0.8	76
75	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, 741-751.	1.8	76
76	Development of Heterotic Groups in Triticale. <i>Crop Science</i> , 2010, 50, 584-590.	0.8	76
77	High congruency of QTL positions for heterosis of grain yield in three crosses of maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 321-332.	1.8	75
78	Extent and genome-wide distribution of linkage disequilibrium in commercial maize germplasm. <i>Theoretical and Applied Genetics</i> , 2011, 123, 11-20.	1.8	75
79	Genetic diversity among progenitors and elite lines from the Iowa Stiff Stalk Synthetic (BSSS) maize population: comparison of allozyme and RFLP data. <i>Theoretical and Applied Genetics</i> , 1991, 83, 97-107.	1.8	74
80	Title is missing!. <i>Molecular Breeding</i> , 2002, 10, 181-191.	1.0	74
81	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.	1.2	74
82	Optimizing the allocation of resources for genomic selection in one breeding cycle. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2835-2848.	1.8	74
83	Relationships among Early European Maize Inbreds: I. Genetic Diversity among Flint and Dent Lines Revealed by RFLPs. <i>Crop Science</i> , 1992, 32, 1301-1309.	0.8	73
84	Epistasis in an Elite Maize Hybrid and Choice of Generation for Inbred Line Development. <i>Crop Science</i> , 1995, 35, 1272-1281.	0.8	73
85	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, 1871-1887.	2.8	73
86	Association mapping for cold tolerance in two large maize inbred panels. <i>BMC Plant Biology</i> , 2016, 16, 127.	1.6	73
87	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, 451-461.	1.8	70
88	Genome-wide association mapping of flowering time and northern corn leaf blight (<i>Setosphaeria</i>) Tj ETQq0 0 0 rgBT Overlock 10 Tf 50	1.6	70
89	No Evidence for Epistasis in Hybrid and Per Se Performance of Elite European Flint Maize Inbreds from Generation Means and QTL Analyses. <i>Crop Science</i> , 2005, 45, 2605-2613.	0.8	69
90	Production of Haploids and Doubled Haploids in Maize. <i>Methods in Molecular Biology</i> , 2012, 877, 161-172.	0.4	69

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91	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, 1901-1913.	1.8	69
92	Unlocking the Genetic Diversity of Maize Landraces with Doubled Haploids Opens New Avenues for Breeding. <i>PLoS ONE</i> , 2013, 8, e57234.	1.1	68
93	In an elite cross of maize a major quantitative trait locus controls one-fourth of the genetic variation for grain yield. <i>Theoretical and Applied Genetics</i> , 1995, 90, 415-424.	1.8	67
94	QTL Mapping in Testcrosses of European Flint Lines of Maize: II. Comparison of Different Testers for Forage Quality Traits. <i>Crop Science</i> , 1997, 37, 1913-1922.	0.8	66
95	Prospects for Hybrid Breeding in Winter Triticale: I. Heterosis and Combining Ability for Agronomic Traits in European Elite Germplasm. <i>Crop Science</i> , 2005, 45, 1476-1482.	0.8	66
96	Analysis of a Triple Testcross Design With Recombinant Inbred Lines Reveals a Significant Role of Epistasis in Heterosis for Biomass-Related Traits in Arabidopsis. <i>Genetics</i> , 2007, 175, 2009-2017.	1.2	65
97	Genetic basis of resistance to sugarcane mosaic virus in European maize germplasm. <i>Theoretical and Applied Genetics</i> , 1998, 96, 1151-1161.	1.8	63
98	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, 2563-2574.	1.8	63
99	QTL mapping of stalk bending strength in a recombinant inbred line maize population. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2257-2266.	1.8	63
100	RFLP analyses of early-maturing European maize germ plasm. <i>Theoretical and Applied Genetics</i> , 1992, 83, 1003-1012.	1.8	62
101	Relationship between European corn borer resistance and concentration of mycotoxins produced by <i>Fusarium</i> spp. in grains of transgenic Bt maize hybrids, their isogenic counterparts, and commercial varieties. <i>Plant Breeding</i> , 2002, 121, 146-154.	1.0	62
102	Population genetic simulation and data analysis with Plabsoft. <i>Euphytica</i> , 2008, 161, 133-139.	0.6	62
103	Marker-Assisted Backcrossing for Simultaneous Introgression of Two Genes. <i>Crop Science</i> , 2001, 41, 1716-1725.	0.8	61
104	Haploid Fertility in Temperate and Tropical Maize Germplasm. <i>Crop Science</i> , 2012, 52, 623-630.	0.8	61
105	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. <i>Genetics</i> , 2016, 202, 1267-1276.	1.2	61
106	Genetic Variation for Resistance to Ear Rots and Mycotoxins Contamination in Early European Maize Inbred Lines. <i>Crop Science</i> , 2009, 49, 2019-2028.	0.8	60
107	Genetic diversity of maize inbred lines within and among heterotic groups revealed by RFLPs. <i>Theoretical and Applied Genetics</i> , 1992, 84, 17-25.	1.8	59
108	Effect of source germplasm and season on the in vivo haploid induction rate in tropical maize. <i>Euphytica</i> , 2011, 180, 219-226.	0.6	59

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109	In Vivo Haploid Induction in Maize: Identification of Haploid Seeds by Their Oil Content. <i>Crop Science</i> , 2014, 54, 1497-1504.	0.8	59
110	Re-evaluation of the prospects of marker-assisted selection for improving insect resistance against <i>Diatraea</i> spp. in tropical maize by cross validation and independent validation. <i>Theoretical and Applied Genetics</i> , 2001, 103, 1059-1067.	1.8	58
111	Genetic diversity in European winter triticale determined with SSR markers and coancestry coefficient. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1385-1391.	1.8	58
112	Multi-trait association mapping in sugar beet (<i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 947-954.	1.8	57
113	Genetic diversity in European perennial ryegrass cultivars investigated with RAPD markers. <i>Plant Breeding</i> , 2005, 124, 161-166.	1.0	56
114	Genetic Diversity for RFLPs in European Maize Inbreds: I. Relation to Performance of Flint \times Dent Crosses for Forage Traits. <i>Crop Science</i> , 1992, 32, 895-902.	0.8	56
115	Quantifying novel sequence variation and selective advantage in synthetic hexaploid wheats and their backcross-derived lines using SSR markers. <i>Molecular Breeding</i> , 2005, 15, 1-10.	1.0	55
116	Heterosis for Biomass-Related Traits in <i>Arabidopsis</i> Investigated by Quantitative Trait Loci Analysis of the Triple Testcross Design With Recombinant Inbred Lines. <i>Genetics</i> , 2007, 177, 1839-1850.	1.2	55
117	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.	1.6	55
118	QTL mapping for European corn borer resistance (<i>Ostrinia nubilalis</i> Hb.), agronomic and forage quality traits of testcross progenies in early-maturing European maize (<i>Zea mays</i> L.) germplasm. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1545-1554.	1.8	54
119	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.	1.6	54
120	Hybrid performance and heterosis in spring bread wheat, and their relations to SSR-based genetic distances and coefficients of parentage. <i>Euphytica</i> , 2005, 144, 51-59.	0.6	52
121	Comparison of Linkage Disequilibrium in Elite European Maize Inbred Lines using AFLP and SSR Markers. <i>Molecular Breeding</i> , 2006, 17, 217-226.	1.0	52
122	Development of in vivo haploid inducers for tropical maize breeding programs. <i>Euphytica</i> , 2012, 185, 481-490.	0.6	52
123	Fine mapping of qhir8 affecting in vivo haploid induction in maize. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2507-2515.	1.8	52
124	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.	1.2	52
125	European maize landraces made accessible for plant breeding and genome-based studies. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3333-3345.	1.8	52
126	Molecular mapping and gene action of Scm1 and Scm2, two major QTL contributing to SCMV resistance in maize. <i>Plant Breeding</i> , 2000, 119, 299-303.	1.0	51

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127	Development and Validation of Red Root Marker-Based Haploid Inducers in Maize. <i>Crop Science</i> , 2016, 56, 1678-1688.	0.8	50
128	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.	0.8	49
129	QTL analyses of complex traits with cross validation, bootstrapping and other biometric methods. <i>Euphytica</i> , 2004, 137, 1-11.	0.6	48
130	Mapping quantitative trait loci for freezing tolerance in a recombinant inbred line population of <i>Zea mays</i> accessions Tenela and C24 reveals REVEILLE1 as negative regulator of cold acclimation. <i>Plant, Cell and Environment</i> , 2013, 36, 1256-1267.	2.8	48
131	REML-Based Diallel Analysis. <i>Crop Science</i> , 2011, 51, 470-478.	0.8	47
132	Colchicine Alternatives for Chromosome Doubling in Maize Haploids for Doubled-Haploid Production. <i>Crop Science</i> , 2016, 56, 559-569.	0.8	47
133	QTL mapping of Sclerotinia midstalk-rot resistance in sunflower. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1474-1484.	1.8	44
134	Trends in genetic variance components during 30 years of hybrid maize breeding at the University of Hohenheim. <i>Plant Breeding</i> , 2008, 127, 446-451.	1.0	44
135	Colocalization of QTL for Gibberella Ear Rot Resistance and Low Mycotoxin Contamination in Early European Maize. <i>Crop Science</i> , 2011, 51, 1935-1945.	0.8	44
136	Comparative QTL mapping of resistance to <i>Ustilago maydis</i> across four populations of European flint-maize. <i>Theoretical and Applied Genetics</i> , 1998, 97, 1321-1330.	1.8	43
137	Genetic Diversity and Relationships of Wheat Landraces from Oman Investigated with SSR Markers. <i>Genetic Resources and Crop Evolution</i> , 2006, 53, 1351-1360.	0.8	43
138	Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. <i>Genetics</i> , 2007, 176, 563-570.	1.2	43
139	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.	1.8	42
140	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.	0.8	42
141	Genetic Diversity for RFLPs in European Maize Inbreds. III. Performance of Crosses Within versus Between Heterotic Groups for Grain Traits. <i>Plant Breeding</i> , 1993, 111, 217-226.	1.0	41
142	Development of RGA-CAPS markers and genetic mapping of candidate genes for sugarcane mosaic virus resistance in maize. <i>Theoretical and Applied Genetics</i> , 2002, 105, 355-363.	1.8	41
143	Congruency of Quantitative Trait Loci Detected for Agronomic Traits in Testcrosses of Five Populations of European Maize. <i>Crop Science</i> , 2004, 44, 114-124.	0.8	41
144	Genetic similarity among European winter triticale elite germplasms assessed with AFLP and comparisons with SSR and pedigree data. <i>Plant Breeding</i> , 2005, 124, 154-160.	1.0	41

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145	Selection Strategy for Sorghum Targeting Phosphorus-limited Environments in West Africa: Analysis of Multi-environment Experiments. <i>Crop Science</i> , 2012, 52, 2517-2527.	0.8	41
146	Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2313-2331.	1.8	41
147	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.	1.8	41
148	Marker-Assisted Breeding of Improved Maternal Haploid Inducers in Maize for the Tropical/Subtropical Regions. <i>Frontiers in Plant Science</i> , 2018, 9, 1527.	1.7	41
149	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, 339-345.	1.8	40
150	QTL mapping of resistance to <i>Sporisorium reilianum</i> in maize. <i>Theoretical and Applied Genetics</i> , 1999, 99, 593-598.	1.8	40
151	Molecular genetic diversity within and among German ecotypes in comparison to European perennial ryegrass cultivars. <i>Plant Breeding</i> , 2005, 124, 257-262.	1.0	40
152	QTLs for resistance to <i>Setosphaeria turcica</i> in an early maturing Dent-Flint maize population. <i>Theoretical and Applied Genetics</i> , 1999, 99, 649-655.	1.8	39
153	QTL mapping of resistance to <i>Sclerotinia</i> midstalk rot in RIL of sunflower population NDBLOSSel-ACM625. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1490-1498.	1.8	39
154	Molecular marker assisted broadening of the Central European heterotic groups in rye with Eastern European germplasm. <i>Theoretical and Applied Genetics</i> , 2010, 120, 291-299.	1.8	39
155	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.	1.8	39
156	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, 301-310.	1.8	38
157	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.	0.4	38
158	Discovery of beneficial haplotypes for complex traits in maize landraces. <i>Nature Communications</i> , 2020, 11, 4954.	5.8	38
159	Chilling Tolerance of Central European Maize Lines and their Factorial Crosses. <i>Annals of Botany</i> , 2007, 100, 1315-1321.	1.4	37
160	Persistency of Prediction Accuracy and Genetic Gain in Synthetic Populations Under Recurrent Genomic Selection. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 801-811.	0.8	37
161	The Length of the Intact Donor Chromosome Segment Around a Target Gene in Marker-Assisted Backcrossing. <i>Genetics</i> , 2001, 157, 1343-1356.	1.2	37
162	Expectation of means and variances of testcrosses produced from F2 and backcross individuals and their selfed progenies. <i>Heredity</i> , 1987, 59, 105-115.	1.2	36

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164	Identification by suppression subtractive hybridization of genes that are differentially expressed between near-isogenic maize lines in association with sugarcane mosaic virus resistance. <i>Molecular Genetics and Genomics</i> , 2005, 273, 450-461.	1.0	36
165	Near-infrared spectroscopy on combine harvesters to measure maize grain dry matter content and quality parameters. <i>Plant Breeding</i> , 2006, 125, 591-595.	1.0	36
166	Hybrid maize breeding with doubled haploids: I. One-stage versus two-stage selection for testcross performance. <i>Theoretical and Applied Genetics</i> , 2006, 112, 903-912.	1.8	35
167	Breeding maize as biogas substrate in Central Europe: I. Quantitative-genetic parameters for testcross performance. <i>Theoretical and Applied Genetics</i> , 2012, 124, 971-980.	1.8	34
168	Optimum design of family structure and allocation of resources in association mapping with lines from multiple crosses. <i>Heredity</i> , 2013, 110, 71-79.	1.2	34
169	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.	0.8	34
170	Evaluation of Near Infra-red Reflectance Spectroscopy for Predicting Grain and Stover Quality Traits in Maize. <i>Plant Breeding</i> , 1986, 97, 20-29.	1.0	33
171	A new test for family-based association mapping with inbred lines from plant breeding programs. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1121-1130.	1.8	33
172	Prediction of single-cross hybrid performance in maize using haplotype blocks associated with QTL for grain yield. <i>Theoretical and Applied Genetics</i> , 2007, 114, 1345-1355.	1.8	33
173	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, 825-833.	1.8	33
174	Epistasis in maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 1986, 72, 231-239.	1.8	32
175	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.	0.8	32
176	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.	0.6	32
177	The Use of DNA Fingerprinting in Ecological Studies of <i>Phragmites australis</i> (Cav.) Trin. ex Steudel. <i>Botanica Acta</i> , 1994, 107, 237-242.	1.6	31
178	Genetic Expectations of Quantitative Trait Loci Main and Interaction Effects Obtained With the Triple Testcross Design and Their Relevance for the Analysis of Heterosis. <i>Genetics</i> , 2008, 178, 2265-2274.	1.2	30
179	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.	1.6	30
180	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. <i>Crop Science</i> , 2014, 54, 1981-1991.	0.8	30

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182	Metabolic robustness in young roots underpins a predictive model of maize hybrid performance in the field. <i>Plant Journal</i> , 2017, 90, 319-329.	2.8	30
183	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.	1.6	29
184	The maize leaf lipidome shows multilevel genetic control and high predictive value for agronomic traits. <i>Scientific Reports</i> , 2013, 3, 2479.	1.6	29
185	Genome-wide association study to identify genomic regions influencing spontaneous fertility in maize haploids. <i>Euphytica</i> , 2019, 215, 138.	0.6	29
186	Congruency of Quantitative Trait Loci Detected for Agronomic Traits in Testcrosses of Five Populations of European Maize. <i>Crop Science</i> , 2004, 44, 114.	0.8	29
187	Comparative Quantitative Trait Loci Mapping of Partial Resistance to Puccinia sorghi Across Four Populations of European Flint Maize. <i>Phytopathology</i> , 1998, 88, 1324-1329.	1.1	28
188	Marker-Assisted Backcrossing for Introgression of a Recessive Gene. <i>Crop Science</i> , 2001, 41, 1485-1494.	0.8	28
189	Comparison of Bt maize hybrids with their non-transgenic counterparts and commercial varieties for resistance to European corn borer and for agronomic traits. <i>Plant Breeding</i> , 2001, 120, 397-403.	1.0	28
190	Influence of genetic background and heterozygosity on meiotic recombination in <i>Arabidopsis thaliana</i> . <i>Genome</i> , 2001, 44, 971-978.	0.9	28
191	Conversion of AFLP fragments tightly linked to SCMV resistance genes Scmv1 and Scmv2 into simple PCR-based markers. <i>Theoretical and Applied Genetics</i> , 2002, 105, 1190-1195.	1.8	28
192	Title is missing!. <i>Molecular Breeding</i> , 2003, 12, 97-106.	1.0	28
193	Association mapping in multiple segregating populations of sugar beet (<i>Beta vulgaris</i> L.). <i>Theoretical and Applied Genetics</i> , 2008, 117, 1167-1179.	1.8	28
194	Unraveling Epistasis With Triple Testcross Progenies of Near-Isogenic Lines. <i>Genetics</i> , 2009, 181, 247-257.	1.2	28
195	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.	1.2	28
196	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.	1.8	28
197	Hybrid maize breeding with doubled haploids: II. Optimum type and number of testers in two-stage selection for general combining ability. <i>Theoretical and Applied Genetics</i> , 2007, 114, 393-402.	1.8	27
198	Hybrid maize breeding with doubled haploids: III. Efficiency of early testing prior to doubled haploid production in two-stage selection for testcross performance. <i>Theoretical and Applied Genetics</i> , 2007, 115, 519-527.	1.8	27

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200	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.	2.9	27
201	Genetic Structure and Diversity among Radish Varieties as Inferred from AFLP and ISSR Analyses. <i>Journal of the American Society for Horticultural Science</i> , 2005, 130, 79-87.	0.5	27
202	Genetic diversity in cornsalad (<i>Valerianella locusta</i>) and related species as determined by AFLP markers. <i>Plant Breeding</i> , 2004, 123, 460-466.	1.0	26
203	Identification of Essentially Derived Varieties Obtained from Biparental Crosses of Homozygous Lines: II. Morphological Distances and Heterosis in Comparison with Simple Sequence Repeat and Amplified Fragment Length Polymorphism Data in Maize. <i>Crop Science</i> , 2005, 45, 1132-1140.	0.8	26
204	Identification of Essentially Derived Varieties Obtained from Biparental Crosses of Homozygous Lines. III. AFLP Data from Maize Inbreds and Comparison with SSR Data. <i>Molecular Breeding</i> , 2006, 17, 111-125.	1.0	26
205	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.	0.8	26
206	Molecular Genetic Diversity among Progenitors and Derived Elite Lines of BSSS and BSCB1 Maize Populations. <i>Crop Science</i> , 2003, 43, 474.	0.8	26
207	Prediction of testcross means and variances among F3 progenies of F1 crosses from testcross means and genetic distances of their parents in maize. <i>Theoretical and Applied Genetics</i> , 1998, 96, 503-512.	1.8	25
208	Two chromosome segments confer multiple potyvirus resistance in maize. <i>Plant Breeding</i> , 2006, 125, 352-356.	1.0	25
209	Effect of N supply on stalk quality in maize hybrids. <i>Field Crops Research</i> , 2010, 118, 208-214.	2.3	25
210	Breeding Potential of European Flint Maize Landraces Evaluated by their Testcross Performance. <i>Crop Science</i> , 2014, 54, 1665-1672.	0.8	25
211	Heterosis and combining ability for grain yield and other agronomic traits in winter triticale. <i>Plant Breeding</i> , 2003, 122, 318-321.	1.0	24
212	Prospects for hybrid breeding in winter triticale: II. Relationship between parental genetic distance and specific combining ability. <i>Plant Breeding</i> , 2006, 125, 331-336.	1.0	24
213	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, 981-988.	1.8	24
214	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. <i>Genetics</i> , 2017, 206, 1611-1619.	1.2	24
215	Small RNA-based prediction of hybrid performance in maize. <i>BMC Genomics</i> , 2018, 19, 371.	1.2	24
216	Optimizing Resource Allocation for Multistage Selection in Plant Breeding with R Package <i><i>Selectiongain</i></i> . <i>Crop Science</i> , 2014, 54, 1413-1418.	0.8	23

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218	Across-years prediction of hybrid performance in maize using genomics. <i>Theoretical and Applied Genetics</i> , 2019, 132, 933-946.	1.8	23
219	Comparison of transcript profiles between near-isogenic maize lines in association with SCMV resistance based on unigene-microarrays. <i>Plant Science</i> , 2006, 170, 159-169.	1.7	22
220	Efficiency gain of marker-assisted backcrossing by sequentially increasing marker densities over generations. <i>Theoretical and Applied Genetics</i> , 2009, 119, 23-32.	1.8	22
221	Identification of key ancestors of modern germplasm in a breeding program of maize. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2545-2553.	1.8	22
222	Genomic selection in biparental populations: assessment of parameters for optimum estimation set design. <i>Plant Breeding</i> , 2015, 134, 623-630.	1.0	22
223	Transcriptome-based prediction of hybrid performance with unbalanced data from a maize breeding programme. <i>Plant Breeding</i> , 2017, 136, 331-337.	1.0	22
224	High-Throughput Precision Phenotyping of the Oil Content of Single Seeds of Various Oilseed Crops. <i>Crop Science</i> , 2018, 58, 670-678.	0.8	22
225	Genomic prediction with multiple biparental families. <i>Theoretical and Applied Genetics</i> , 2020, 133, 133-147.	1.8	22
226	Heterosis and gene effects of multiplicative characters: theoretical relationships and experimental results from <i>Vicia faba</i> L. <i>Theoretical and Applied Genetics</i> , 1994, 88-88, 343-348.	1.8	21
227	Molecular characterization of genetic diversity in European germplasm of perennial ryegrass. <i>Euphytica</i> , 2005, 146, 39-44.	0.6	21
228	Identification of Essentially Derived Varieties Obtained from Biparental Crosses of Homozygous Lines: I. Simple Sequence Repeat Data from Maize Inbreds. <i>Crop Science</i> , 2005, 45, 1120-1131.	0.8	21
229	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.	1.9	21
230	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.	1.7	21
231	Cluster analysis of RFLP data from related maize inbred lines of the BSSS and LSC heterotic groups and comparison with pedigree data. <i>Euphytica</i> , 1992, 60, 139-148.	0.6	20
232	Temporal changes in allele frequencies in two European F2 flint maize populations under modified recurrent full-sib selection. <i>Theoretical and Applied Genetics</i> , 2007, 114, 765-776.	1.8	20
233	Potential causes of linkage disequilibrium in a European maize breeding program investigated with computer simulations. <i>Theoretical and Applied Genetics</i> , 2007, 115, 529-536.	1.8	20
234	Hybrid maize breeding with doubled haploids. IV. Number versus size of crosses and importance of parental selection in two-stage selection for testcross performance. <i>Theoretical and Applied Genetics</i> , 2008, 117, 251-260.	1.8	20

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236	Low validation rate of quantitative trait loci for <i>Gibberella</i> ear rot resistance in European maize. <i>Theoretical and Applied Genetics</i> , 2017, 130, 175-186.	1.8	20
237	Origin of Scm1 and Scm2“ two loci conferring resistance to sugarcane mosaic virus (SCMV) in maize. <i>Theoretical and Applied Genetics</i> , 2000, 100, 934-941.	1.8	19
238	A high-throughput system for genome-wide measurement of genetic recombination in <i>Arabidopsis thaliana</i> based on transgenic markers. <i>Functional and Integrative Genomics</i> , 2000, 1, 200-206.	1.4	19
239	Identification of essentially derived varieties with molecular markers: an approach based on statistical test theory and computer simulations. <i>Theoretical and Applied Genetics</i> , 2005, 111, 598-608.	1.8	19
240	Population structure in sorghum accessions from West Africa differing in race and maturity class. <i>Genetica</i> , 2011, 139, 453-463.	0.5	19
241	Comparison of the observed with the simulated distributions of the parental genome contribution in two marker-assisted backcross programs in rice. <i>Theoretical and Applied Genetics</i> , 2008, 116, 739-744.	1.8	18
242	Inheritance of resistance to <i>Gibberella</i> ear rot and deoxynivalenol contamination in five flint maize crosses. <i>Plant Breeding</i> , 2012, 131, 28-32.	1.0	18
243	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. <i>Genetics</i> , 2018, 210, 1185-1196.	1.2	18
244	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.	1.8	18
245	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.	0.8	17
246	Nitrous Oxide-Induced Chromosome Doubling of Maize Haploids. <i>Crop Science</i> , 2018, 58, 650-659.	0.8	17
247	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.	1.8	17
248	Quality assessment of rapeseed accessions by means of near-infrared spectroscopy on combine harvesters. <i>Plant Breeding</i> , 2007, 126, 329-330.	1.0	16
249	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.	0.6	16
250	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.	1.8	16
251	Variance of the Parental Genome Contribution to Inbred Lines Derived From Biparental Crosses. <i>Genetics</i> , 2007, 176, 477-488.	1.2	15
252	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.	1.0	15

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253	In Vivo Haploid Induction in Maize: Comparison of Different Testing Regimes for Measuring Haploid Induction Rates. <i>Crop Science</i> , 2016, 56, 1127-1135.	0.8	15
254	Optimal allocation of resources in evaluating current sunflower inbred lines for resistance to Sclerotinia. <i>Plant Breeding</i> , 1999, 118, 157-160.	1.0	14
255	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.	0.8	14
256	Optimum allocation of resources for QTL detection using a nested association mapping strategy in maize. <i>Theoretical and Applied Genetics</i> , 2010, 120, 553-561.	1.8	14
257	Optimum allocation of test resources and comparison of breeding strategies for hybrid wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2117-2126.	1.8	14
258	Mean, genetic variance, and usefulness of selfing progenies from intra- and inter-pool crosses in faba beans (<i>Vicia faba</i> L.) and their prediction from parental parameters. <i>Theoretical and Applied Genetics</i> , 1999, 98, 569-580.	1.8	13
259	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.	1.0	13
260	Economic Aspects of Breeding for Yield and Quality Traits in Forage Maize. II. Derivation and Evaluation of Selection Indices. <i>Plant Breeding</i> , 1994, 112, 110-119.	1.0	12
261	Concentration of moniliformin produced by <i>Fusarium</i> species in grains of transgenic Bt maize hybrids compared to their isogenic counterparts and commercial varieties under European corn borer pressure. <i>Plant Breeding</i> , 2003, 122, 322-327.	1.0	12
262	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.	0.8	12
263	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.	1.0	12
264	Genomic prediction of dichotomous traits with Bayesian logistic models. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1133-1143.	1.8	12
265	Calibration and validation of predicted genomic breeding values in an advanced cycle maize population. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3069-3081.	1.8	12
266	Trends in population parameters and best linear unbiased prediction of progeny performance in a European F2 maize population under modified recurrent full-sib selection. <i>Theoretical and Applied Genetics</i> , 2006, 112, 483-491.	1.8	11
267	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, 857-866.	1.8	11
268	The Plabsoft database: a comprehensive database management system for integrating phenotypic and genomic data in academic and commercial plant breeding programs. <i>Euphytica</i> , 2008, 161, 173-179.	0.6	11
269	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.	0.8	11
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272	Targeted BSA mapping of Scmv1 and Scmv2 conferring resistance to SCMV using PstI/MseI compared with EcoRI/MseI AFLP markers. <i>Plant Breeding</i> , 2004, 123, 434-437.	1.0	10
273	Determination of chemical composition and nutritional attributes of silage corn hybrids by near-infrared spectroscopy on chopper: evaluation of traits, sample presentation systems and calibration transferability. <i>Plant Breeding</i> , 2007, 126, 521-526.	1.0	10
274	Doubled haploids in tropical maize: II. Quantitative genetic parameters for testcross performance. <i>Euphytica</i> , 2012, 185, 453-463.	0.6	10
275	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.	0.8	10
276	Prospects for celeriac (<i>Apium graveolens</i> var. <i>rapaceum</i>) improvement by using genetic resources of <i>Apium</i> , as determined by AFLP markers and morphological characterization. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2004, 2, 189-198.	0.4	9
277	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, 1269-1279.	1.8	9
278	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.	0.6	9
279	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, 12, .	0.8	9
280	Marker-Based Prediction of the Parental Genome Contribution to Inbred Lines Derived From Biparental Crosses. <i>Genetics</i> , 2006, 174, 795-803.	1.2	8
281	Efficient genetic value prediction using incomplete omics data. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1211-1222.	1.8	8
282	Modified full-sib selection and best linear unbiased prediction of progeny performance in a European F2 maize population. <i>Plant Breeding</i> , 2006, 125, 248-253.	1.0	7
283	Genetic drift and selection effects of modified recurrent full-sib selection programs in two F2 populations of European flint maize. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1113-1120.	1.8	7
284	An incomplete enumeration algorithm for an exact test of Hardy-Weinberg proportions with multiple alleles. <i>Theoretical and Applied Genetics</i> , 2007, 115, 393-398.	1.8	7
285	Variation and covariation for <i>Gibberella</i> ear rot resistance and agronomic traits in testcrosses of doubled haploid maize lines. <i>Euphytica</i> , 2012, 185, 441-451.	0.6	7
286	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, 2189-2201.	1.8	7
287	Resistance in the leaf and stem of sunflower after infection with two isolates of <i>Phomopsis</i> . <i>Plant Breeding</i> , 1999, 118, 405-410.	1.0	6
288	Linkage disequilibrium in two European F2 flint maize populations under modified recurrent full-sib selection. <i>Theoretical and Applied Genetics</i> , 2007, 115, 289-297.	1.8	6

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289	Genetic variation for resistance and mycotoxin content of European maize inoculated with <i>Fusarium graminearum</i> and <i>F. verticillioides</i> . Cereal Research Communications, 2008, 36, 45-48.	0.8	6
290	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
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308	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.	1.0	3
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