Albrecht E Melchinger

List of Publications by Year
in descending order

315 papers	18,992 citations	9786 73 h-index	20961 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. Euphytica, 2008, 161, 209-228.	1.2	569
2	Genomic and metabolic prediction of complex heterotic traits in hybrid maize. Nature Genetics, 2012, 44, 217-220.	21.4	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. Genetics, 1998, 149, 383-403.	2.9	462
4	Wheat genetic diversity trends during domestication and breeding. Theoretical and Applied Genetics, 2005, 110, 859-864.	3.6	365
5	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.	7.1	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. Genetics, 2000, 154, 1839-1849.	2.9	305
7	Comparison of Mixed-Model Approaches for Association Mapping. Genetics, 2008, 178, 1745-1754.	2.9	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 (*Zea mays* L.). Genetics, 2012, 192, 715-728.	2.9	258
9	Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. G3: Genes, Genomes, Genetics, 2012, 2, 1427-1436.	1.8	242
10	Genetic Similarities among Winter Wheat Cultivars Determined on the Basis of RFLPs, AFLPs, and SSRs and Their Use for Predicting Progeny Variance. Crop Science, 1999, 39, 228-237.	1.8	232
11	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.	3.6	232
12	Quantitative Trait Locus Mapping Based on Resampling in a Vast Maize Testcross Experiment and Its Relevance to Quantitative Genetics for Complex Traits. Genetics, 2004, 167, 485-498.	2.9	231
13	Novel throughput phenotyping platforms in plant genetic studies. Trends in Plant Science, 2007, 12, 433-436.	8.8	220
14	Genetic diversity in European and Mediterranean faba bean germ plasm revealed by RAPD markers. Theoretical and Applied Genetics, 1995, 90, 27-32.	3.6	217
15	Two high-density AFLP® linkage maps of Zea mays L.: analysis of distribution of AFLP markers. Theoretical and Applied Genetics, 1999, 99, 921-935.	3.6	217
16	Comparison of Selection Strategies for Marker€Assisted Backcrossing of a Gene. Crop Science, 1999, 39, 1295-1301.	1.8	206
17	Genome Properties and Prospects of Genomic Prediction of Hybrid Performance in a Breeding Program of Maize. Genetics, 2014, 197, 1343-1355.	2.9	192
18	Use of Molecular Markers in Breeding for Oligogenic Disease Resistance. Plant Breeding, 1990, 104, 1-19.	1.9	191

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19	Optimizing experimental procedures for quantitative evaluation of crop plant performance in high throughput phenotyping systems. Frontiers in Plant Science, 2014, 5, 770.	3.6	187
20	Genomic Predictability of Interconnected Biparental Maize Populations. Genetics, 2013, 194, 493-503.	2.9	180
21	Intraspecific variation of recombination rate in maize. Genome Biology, 2013, 14, R103.	9.6	176
22	Linkage disequilibrium in European elite maize germplasm investigated with SSRs. Theoretical and Applied Genetics, 2005, 111, 723-730.	3.6	167
23	RFLP Mapping in Maize: Quantitative Trait Loci Affecting Testcross Performance of Elite European Flint Lines. Crop Science, 1994, 34, 378-389.	1.8	147
24	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.	5.1	144
25	Genomic prediction of hybrid performance in maize with models incorporating dominance and population specific marker effects. Theoretical and Applied Genetics, 2012, 125, 1181-1194.	3.6	143
26	New Insights into the Genetics of *in Vivo* Induction of Maternal Haploids, the Backbone of Doubled Haploid Technology in Maize. Genetics, 2012, 190, 781-793.	2.9	143
27	Genetic Characterization of CIMMYT Inbred Maize Lines and Open Pollinated Populations Using Large Scale Fingerprinting Methods. Crop Science, 2002, 42, 1832-1840.	1.8	141
28	Quantitative Trait Loci Mapping and The Genetic Basis of Heterosis in Maize and Rice. Genetics, 2008, 180, 1707-1724.	2.9	141
29	High-throughput non-destructive biomass determination during early plant development in maize under field conditions. Field Crops Research, 2011, 121, 268-273.	5.1	139
30	Mapping and characterization of quantitative trait loci affecting resistance against second-generation European corn borer in maize with the aid of RFLPs. Heredity, 1993, 70, 648-659.	2.6	135
31	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.	3.6	132
32	Beyond Genomic Prediction: Combining Different Types of *omics* Data Can Improve Prediction of Hybrid Performance in Maize. Genetics, 2018, 208, 1373-1385.	2.9	130
33	Relationships among Early European Maize Inbreds: II. Comparison of Pedigree and RFLP Data. Crop Science, 1993, 33, 944-950.	1.8	127
34	Doubled haploid technology for line development in maize: technical advances and prospects. Theoretical and Applied Genetics, 2019, 132, 3227-3243.	3.6	126
35	The Role of Epistasis in the Manifestation of Heterosis: A Systems-Oriented Approach. Genetics, 2007, 177, 1815-1825.	2.9	125
36	Genetic diversity for restriction fragment length polymorphisms and heterosis for two diallel sets of maize inbreds. Theoretical and Applied Genetics, 1990, 80, 488-496.	3.6	124

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37	Validation of Dwarf8 polymorphisms associated with flowering time in elite European inbred lines of maize (Zea mays L.). Theoretical and Applied Genetics, 2005, 111, 206-217.	3.6	115
38	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. Genetics, 2014, 198, 3-16.	2.9	114
39	QTL Mapping in Testcrosses of European Flint Lines of Maize: I. Comparison of Different Testers for Forage Yield Traits. Crop Science, 1997, 37, 921-931.	1.8	113
40	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.	1.8	112
41	Relationships among European Barley Germplasm: II. Comparison of RFLP and Pedigree Data. Crop Science, 1994, 34, 1199-1205.	1.8	111
42	Transcriptome-based distance measures for grouping of germplasm and prediction of hybrid performance in maize. Theoretical and Applied Genetics, 2010, 120, 441-450.	3.6	111
43	Use of SSRs for establishing heterotic groups in subtropical maize. Theoretical and Applied Genetics, 2003, 107, 947-957.	3.6	110
44	Overview of Heterosis and Heterotic Groups in Agronomic Crops. CSSA Special Publication - Crop Science Society of America, 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. Journal of Experimental Botany, 2013, 64, 1083-1096.	4.8	107
46	Selection Theory for Marker-Assisted Backcrossing. Genetics, 2005, 170, 909-917.	2.9	99
47	Precision phenotyping of biomass accumulation in triticale reveals temporal genetic patterns of regulation. Scientific Reports, 2013, 3, 2442.	3.3	99
48	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.	3.6	97
49	Genetic structure and diversity of European flint maize populations determined with SSR analyses of individuals and bulks. Theoretical and Applied Genetics, 2005, 111, 906-913.	3.6	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. Genetics, 2007, 177, 1827-1837.	2.9	95
51	Identification of heterotic metabolite QTL in <i>Arabidopsis thaliana</i> RIL and IL populations. Plant Journal, 2009, 59, 777-788.	5.7	95
52	Rapid and accurate identification of in vivo-induced haploid seeds based on oil content in maize. Scientific Reports, 2013, 3, 2129.	3.3	95
53	Doubled Haploids in Tropical Maize: I. Effects of Inducers and Source Germplasm on in vivo Haploid Induction Rates. Crop Science, 2011, 51, 1498-1506.	1.8	94
54	Phylogenetic relationships between cultivated and wild species of the genusBeta revealed by DNA ?fingerprinting?. Theoretical and Applied Genetics, 1993, 86, 449-457.	3.6	93

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55	Trends in genetic diversity among European maize cultivars and their parental components during the past 50 years. Theoretical and Applied Genetics, 2005, 111, 838-845.	3.6	93
56	Genetic Diversity in CIMMYT Nontemperate Maize Germplasm: Landraces, Open Pollinated Varieties, and Inbred Lines. Crop Science, 2008, 48, 617-624.	1.8	93
57	Prediction of single-cross hybrid performance for grain yield and grain dry matter content in maize using AFLP markers associated with QTL. Theoretical and Applied Genetics, 2006, 113, 1037-1047.	3.6	92
58	QTL analysis of early stage heterosis for biomass in Arabidopsis. Theoretical and Applied Genetics, 2010, 120, 227-237.	3.6	90
59	Omics-based hybrid prediction in maize. Theoretical and Applied Genetics, 2017, 130, 1927-1939.	3.6	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. Genetics, 2014, 198, 1717-1734.	2.9	89
61	Recovering Power in Association Mapping Panels with Variable Levels of Linkage Disequilibrium. Genetics, 2014, 197, 375-387.	2.9	89
62	High-resolution mapping of loci conferring resistance to sugarcane mosaic virus in maize using RFLP, SSR, and AFLP markers. Molecular Genetics and Genomics, 1999, 261, 574-581.	2.4	88
63	Genetic diversity for RFLPs in European maize inbreds. Theoretical and Applied Genetics, 1992, 84-84, 672-681.	3.6	86
64	Heterosis for biomass yield and related traits in five hybrids of Arabidopsis thaliana L. Heynh. Heredity, 2003, 91, 36-42.	2.6	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. Crop Science, 2005, 45, 2573-2582.	1.8	86
66	Quantitative Trait Loci Mapping of Resistance to Sugarcane Mosaic Virus in Maize. Phytopathology, 1999, 89, 660-667.	2.2	84
67	Efficiency of Managed-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.	1.8	84
68	Domestication and Breeding of Jatropha curcas L.. Trends in Plant Science, 2016, 21, 1045-1057.	8.8	84
69	Grouping of accessions of Mexican races of maize revisited with SSR markers. Theoretical and Applied Genetics, 2006, 113, 177-185.	3.6	81
70	Genetic diversity in Arabidopsis thaliana L. Heynh. investigated by cleaved amplified polymorphic sequence (CAPS) and inter-simple sequence repeat (ISSR) markers. Molecular Ecology, 2002, 11, 495-505.	3.9	80
71	Relationships among Early European Maize Inbreds: IV. Genetic Diversity Revealed with AFLP Markers and Comparison with RFLP, RAPD, and Pedigree Data. Crop Science, 2000, 40, 783-791.	1.8	79
72	Comparison of mixed-model approaches for association mapping in rapeseed, potato, sugar beet, maize, and Arabidopsis. BMC Genomics, 2009, 10, 94.	2.8	79

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73	Correlation between parental transcriptome and field data for the characterization of heterosis in Zea mays L.. Theoretical and Applied Genetics, 2010, 120, 401-413.	3.6	79
74	QTL Mapping in Testcrosses of Flint Lines of Maize: III. Comparison across Populations for Forage Traits. Crop Science, 1998, 38, 1278-1289.	1.8	76
75	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.	3.6	76
76	Development of Heterotic Groups in Triticale. Crop Science, 2010, 50, 584-590.	1.8	76
77	High congruency of QTL positions for heterosis of grain yield in three crosses of maize. Theoretical and Applied Genetics, 2010, 120, 321-332.	3.6	75
78	Extent and genome-wide distribution of linkage disequilibrium in commercial maize germplasm. Theoretical and Applied Genetics, 2011, 123, 11-20.	3.6	75
79	Genetic diversity among progenitors and elite lines from the Iowa Stiff Stalk Synthetic (BSSS) maize population: comparison of allozyme and RFLP data. Theoretical and Applied Genetics, 1991, 83, 97-107.	3.6	74
80	Title is missing!. Molecular Breeding, 2002, 10, 181-191.	2.1	74
81	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.	2.8	74
82	Optimizing the allocation of resources for genomic selection in one breeding cycle. Theoretical and Applied Genetics, 2013, 126, 2835-2848.	3.6	74
83	Relationships among Early European Maize Inbreds: I. Genetic Diversity among Flint and Dent Lines Revealed by RFLPs. Crop Science, 1992, 32, 1301-1309.	1.8	73
84	Epistasis in an Elite Maize Hybrid and Choice of Generation for Inbred Line Development. Crop Science, 1995, 35, 1272-1281.	1.8	73
85	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.	5.7	73
86	Association mapping for cold tolerance in two large maize inbred panels. BMC Plant Biology, 2016, 16, 127.	3.6	73
87	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.	3.6	70
88	Genome-wide association mapping of flowering time and northern corn leaf blight (Setosphaeria) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	70
89	No Evidence for Epistasis in Hybrid and Per Se Performance of Elite European Flint Maize Inbreds from Generation Means and QTL Analyses. Crop Science, 2005, 45, 2605-2613.	1.8	69
90	Production of Haploids and Doubled Haploids in Maize. Methods in Molecular Biology, 2012, 877, 161-172.	0.9	69

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91	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.	3.6	69
92	Unlocking the Genetic Diversity of Maize Landraces with Doubled Haploids Opens New Avenues for Breeding. PLoS ONE, 2013, 8, e57234.	2.5	68
93	In an elite cross of maize a major quantitative trait locus controls one-fourth of the genetic variation for grain yield. Theoretical and Applied Genetics, 1995, 90, 415-424.	3.6	67
94	QTL Mapping in Testcrosses of European Flint Lines of Maize: II. Comparison of Different Testers for Forage Quality Traits. Crop Science, 1997, 37, 1913-1922.	1.8	66
95	Prospects for Hybrid Breeding in Winter Triticale: I. Heterosis and Combining Ability for Agronomic Traits in European Elite Germplasm. Crop Science, 2005, 45, 1476-1482.	1.8	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. Genetics, 2007, 175, 2009-2017.	2.9	65
97	Genetic basis of resistance to sugarcane mosaic virus in European maize germplasm. Theoretical and Applied Genetics, 1998, 96, 1151-1161.	3.6	63
98	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.	3.6	63
99	QTL mapping of stalk bending strength in a recombinant inbred line maize population. Theoretical and Applied Genetics, 2013, 126, 2257-2266.	3.6	63
100	RFLP analyses of early-maturing European maize germ plasm. Theoretical and Applied Genetics, 1992, 83, 1003-1012.	3.6	62
101	Relationship between European corn borer resistance and concentration of mycotoxins produced by Fusarium spp. in grains of transgenic Bt maize hybrids, their isogenic counterparts, and commercial varieties. Plant Breeding, 2002, 121, 146-154.	1.9	62
102	Population genetic simulation and data analysis with Plabsoft. Euphytica, 2008, 161, 133-139.	1.2	62
103	Marker‑Assisted Backcrossing for Simultaneous Introgression of Two Genes. Crop Science, 2001, 41, 1716-1725.	1.8	61
104	Haploid Fertility in Temperate and Tropical Maize Germplasm. Crop Science, 2012, 52, 623-630.	1.8	61
105	The Genetic Basis of Haploid Induction in Maize Identified with a Novel Genome-Wide Association Method. Genetics, 2016, 202, 1267-1276.	2.9	61
106	Genetic Variation for Resistance to Ear Rots and Mycotoxins Contamination in Early European Maize Inbred Lines. Crop Science, 2009, 49, 2019-2028.	1.8	60
107	Genetic diversity of maize inbred lines within and among heterotic groups revealed by RFLPs. Theoretical and Applied Genetics, 1992, 84, 17-25.	3.6	59
108	Effect of source germplasm and season on the in vivo haploid induction rate in tropical maize. Euphytica, 2011, 180, 219-226.	1.2	59

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109	In Vivo Haploid Induction in Maize: Identification of Haploid Seeds by Their Oil Content. Crop Science, 2014, 54, 1497-1504.	1.8	59
110	Re-evaluation of the prospects of marker-assisted selection for improving insect resistance against Diatraea spp. in tropical maize by cross validation and independent validation. Theoretical and Applied Genetics, 2001, 103, 1059-1067.	3.6	58
111	Genetic diversity in European winter triticale determined with SSR markers and coancestry coefficient. Theoretical and Applied Genetics, 2004, 108, 1385-1391.	3.6	58
112	Multi-trait association mapping in sugar beet (Beta vulgaris L.). Theoretical and Applied Genetics, 2008, 117, 947-954.	3.6	57
113	Genetic diversity in European perennial ryegrass cultivars investigated with RAPD markers. Plant Breeding, 2005, 124, 161-166.	1.9	56
114	Genetic Diversity for RFLPs in European Maize Inbreds: I. Relation to Performance of Flint âœ• Dent Crosses for Forage Traits. Crop Science, 1992, 32, 895-902.	1.8	56
115	Quantifying novel sequence variation and selective advantage in synthetic hexaploid wheats and their backcross-derived lines using SSR markers. Molecular Breeding, 2005, 15, 1-10.	2.1	55
116	Heterosis for Biomass-Related Traits in Arabidopsis Investigated by Quantitative Trait Loci Analysis of the Triple Testcross Design With Recombinant Inbred Lines. Genetics, 2007, 177, 1839-1850.	2.9	55
117	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.	3.6	55
118	QTL mapping for European corn borer resistance (Ostrinia nubilalis Hb.), agronomic and forage quality traits of testcross progenies in early-maturing European maize (Zea mays L.) germplasm. Theoretical and Applied Genetics, 2004, 108, 1545-1554.	3.6	54
119	Genome-wide meta-analysis of maize heterosis reveals the potential role of additive gene expression at pericentromeric loci. BMC Plant Biology, 2014, 14, 88.	3.6	54
120	Hybrid performance and heterosis in spring bread wheat, and their relations to SSR-based genetic distances and coefficients of parentage. Euphytica, 2005, 144, 51-59.	1.2	52
121	Comparison of Linkage Disequilibrium in Elite European Maize Inbred Lines using AFLP and SSR Markers. Molecular Breeding, 2006, 17, 217-226.	2.1	52
122	Development of in vivo haploid inducers for tropical maize breeding programs. Euphytica, 2012, 185, 481-490.	1.2	52
123	Fine mapping of qhir8 affecting in vivo haploid induction in maize. Theoretical and Applied Genetics, 2015, 128, 2507-2515.	3.6	52
124	Accuracy of Genomic Prediction in Synthetic Populations Depending on the Number of Parents, Relatedness, and Ancestral Linkage Disequilibrium. Genetics, 2017, 205, 441-454.	2.9	52
125	European maize landraces made accessible for plant breeding and genome-based studies. Theoretical and Applied Genetics, 2019, 132, 3333-3345.	3.6	52
126	Molecular mapping and gene action of Scm1 and Scm2, two major QTL contributing to SCMV resistance in maize. Plant Breeding, 2000, 119, 299-303.	1.9	51

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127	Development and Validation of Red Root Marker–Based Haploid Inducers in Maize. Crop Science, 2016, 56, 1678-1688.	1.8	50
128	Strategies to Subdivide a Target Population of Environments: Results from the CIMMYT–Led Maize Hybrid Testing Programs in Africa. Crop Science, 2012, 52, 2143-2152.	1.8	49
129	QTL analyses of complex traits with cross validation, bootstrapping and other biometric methods. Euphytica, 2004, 137, 1-11.	1.2	48
130	Mapping quantitative trait loci for freezing tolerance in a recombinant inbred line population of *A*rabidopsis thaliana* accessions Tenela and C24 reveals REVEILLE1 as negative regulator of cold acclimation. Plant, Cell and Environment, 2013, 36, 1256-1267.	5.7	48
131	REML–Based Diallel Analysis. Crop Science, 2011, 51, 470-478.	1.8	47
132	Colchicine Alternatives for Chromosome Doubling in Maize Haploids for Doubled–Haploid Production. Crop Science, 2016, 56, 559-569.	1.8	47
133	QTL mapping of Sclerotinia midstalk-rot resistance in sunflower. Theoretical and Applied Genetics, 2004, 109, 1474-1484.	3.6	44
134	Trends in genetic variance components during 30 years of hybrid maize breeding at the University of Hohenheim. Plant Breeding, 2008, 127, 446-451.	1.9	44
135	Colocalization of QTL for Gibberella Ear Rot Resistance and Low Mycotoxin Contamination in Early European Maize. Crop Science, 2011, 51, 1935-1945.	1.8	44
136	Comparative QTL mapping of resistance to Ustilago maydis across four populations of European flint-maize. Theoretical and Applied Genetics, 1998, 97, 1321-1330.	3.6	43
137	Genetic Diversity and Relationships of Wheat Landraces from Oman Investigated with SSR Markers. Genetic Resources and Crop Evolution, 2006, 53, 1351-1360.	1.6	43
138	Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using a New Mapping Strategy. Genetics, 2007, 176, 563-570.	2.9	43
139	Best linear unbiased prediction and optimum allocation of test resources in maize breeding with doubled haploids. Theoretical and Applied Genetics, 2011, 123, 1-10.	3.6	42
140	Selection on Expected Maximum Haploid Breeding Values Can Increase Genetic Gain in Recurrent Genomic Selection. G3: Genes, Genomes, Genetics, 2018, 8, 1173-1181.	1.8	42
141	Genetic Diversity for RFLPs in European Maize Inbreds. III. Performance of Crosses Within versus Between Heterotic Groups for Grain Traits. Plant Breeding, 1993, 111, 217-226.	1.9	41
142	Development of RGA-CAPS markers and genetic mapping of candidate genes for sugarcane mosaic virus resistance in maize. Theoretical and Applied Genetics, 2002, 105, 355-363.	3.6	41
143	Congruency of Quantitative Trait Loci Detected for Agronomic Traits in Testcrosses of Five Populations of European Maize. Crop Science, 2004, 44, 114-124.	1.8	41
144	Genetic similarity among European winter triticale elite germplasms assessed with AFLP and comparisons with SSR and pedigree data. Plant Breeding, 2005, 124, 154-160.	1.9	41

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145	Selection Strategy for Sorghum Targeting Phosphorus‑limited Environments in West Africa: Analysis of Multi‑environment Experiments. Crop Science, 2012, 52, 2517-2527.	1.8	41
146	Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. Theoretical and Applied Genetics, 2014, 127, 2313-2331.	3.6	41
147	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.	3.6	41
148	Marker-Assisted Breeding of Improved Maternal Haploid Inducers in Maize for the Tropical/Subtropical Regions. Frontiers in Plant Science, 2018, 9, 1527.	3.6	41
149	Optimum prediction of three-way crosses from single crosses in forage maize (Zea mays L.). Theoretical and Applied Genetics, 1987, 74, 339-345.	3.6	40
150	QTL mapping of resistance to Sporisorium reiliana in maize. Theoretical and Applied Genetics, 1999, 99, 593-598.	3.6	40
151	Molecular genetic diversity within and among German ecotypes in comparison to European perennial ryegrass cultivars. Plant Breeding, 2005, 124, 257-262.	1.9	40
152	QTLs for resistance to Setosphaeria turcica in an early maturing DentÃ—Flint maize population. Theoretical and Applied Genetics, 1999, 99, 649-655.	3.6	39
153	QTL mapping of resistance to Sclerotinia midstalk rot in RIL of sunflower population NDBLOSselÃÃ—ÂCM625. Theoretical and Applied Genetics, 2005, 110, 1490-1498.	3.6	39
154	Molecular marker assisted broadening of the Central European heterotic groups in rye with Eastern European germplasm. Theoretical and Applied Genetics, 2010, 120, 291-299.	3.6	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. Theoretical and Applied Genetics, 2017, 130, 2165-2189.	3.6	39
156	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.	3.6	38
157	Characterization of Sudanese pearl millet germplasm for agro-morphological traits and grain nutritional values. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, 35-47.	0.8	38
158	Discovery of beneficial haplotypes for complex traits in maize landraces. Nature Communications, 2020, 11, 4954.	12.8	38
159	Chilling Tolerance of Central European Maize Lines and their Factorial Crosses. Annals of Botany, 2007, 100, 1315-1321.	2.9	37
160	Persistency of Prediction Accuracy and Genetic Gain in Synthetic Populations Under Recurrent Genomic Selection. G3: Genes, Genomes, Genetics, 2017, 7, 801-811.	1.8	37
161	The Length of the Intact Donor Chromosome Segment Around a Target Gene in Marker-Assisted Backcrossing. Genetics, 2001, 157, 1343-1356.	2.9	37
162	Expectation of means and variances of testcrosses produced from from F2 and backcross individuals and their selfed progenies. Heredity, 1987, 59, 105-115.	2.6	36

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163	Identification and validation of QTL for Sclerotinia midstalk rot resistance in sunflower by selective genotyping. Theoretical and Applied Genetics, 2005, 111, 233-242.	3.6	36
164	Identification by suppression subtractive hybridization of genes that are differentially expressed between near-isogenic maize lines in association with sugarcane mosaic virus resistance. Molecular Genetics and Genomics, 2005, 273, 450-461.	2.1	36
165	Near-infrared spectroscopy on combine harvesters to measure maize grain dry matter content and quality parameters. Plant Breeding, 2006, 125, 591-595.	1.9	36
166	Hybrid maize breeding with doubled haploids: I. One-stage versus two-stage selection for testcross performance. Theoretical and Applied Genetics, 2006, 112, 903-912.	3.6	35
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