Thomas Lubberstedt

List of Publications by Year
in descending order

211 papers	7,626 citations	47006 47 h-index	79698 73 g-index
217 all docs	217 docs citations	217 times ranked	6345 citing authors

#	Article	IF	Citations
1	Functional markers in plants. Trends in Plant Science, 2003, 8, 554-560.	8.8	640
2	Two high-density AFLPÂ® linkage maps of Zea mays L.: analysis of distribution of AFLP markers. Theoretical and Applied Genetics, 1999, 99, 921-935.	3.6	217
3	From dwarves to giants? Plant height manipulation for biomass yield. Trends in Plant Science, 2009, 14, 454-461.	8.8	195
4	Genome-wide association analysis of seedling root development in maize (Zea mays L.). BMC Genomics, 2015, 16, 47.	2.8	159
5	QTL mapping of vernalization response in perennial ryegrass (Lolium perenne L.) reveals co-location with an orthologue of wheat VRN1. Theoretical and Applied Genetics, 2005, 110, 527-536.	3.6	147
6	Molecular basis of trait correlations. Trends in Plant Science, 2010, 15, 454-461.	8.8	135
7	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
8	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
9	Emerging Avenues for Utilization of Exotic Germplasm. Trends in Plant Science, 2017, 22, 624-637.	8.8	108
10	Analysis of Maize (Zea mays L.) Seedling Roots with the High-Throughput Image Analysis Tool ARIA (Automatic Root Image Analysis). PLoS ONE, 2014, 9, e108255.	2.5	104
11	Novel technologies in doubled haploid line development. Plant Biotechnology Journal, 2017, 15, 1361-1370.	8.3	102
12	The Genetic and Molecular Basis of Plant Resistance to Pathogens. Journal of Genetics and Genomics, 2013, 40, 23-35.	3.9	100
13	Need for multidisciplinary research towards a second green revolution. Current Opinion in Plant Biology, 2005, 8, 337-341.	7.1	97
14	Comparative expression profiling in meristems of inbred-hybrid triplets of maize based on morphological investigations of heterosis for plant height. Plant Molecular Biology, 2006, 63, 21-34.	3.9	97
15	Technological advances in maize breeding: past, present and future. Theoretical and Applied Genetics, 2019, 132, 817-849.	3.6	97
16	Identification of miRNAs and their target genes in developing maize ears by combined small RNA and degradome sequencing. BMC Genomics, 2014, 15, 25.	2.8	94
17	Functional markers in wheat. Current Opinion in Plant Biology, 2007, 10, 211-216.	7.1	92
18	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

#	Article	IF	Citations
19	Genotypic variation and relationships between seedling and adult plant traits in maize (Zea mays L.) inbred lines grown under contrasting nitrogen levels. Euphytica, 2013, 189, 123-133.	1.2	85
20	Quantitative Trait Loci Mapping of Resistance to Sugarcane Mosaic Virus in Maize. Phytopathology, 1999, 89, 660-667.	2.2	84
21	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
22	An Atypical Thioredoxin Imparts Early Resistance to Sugarcane Mosaic Virus in Maize. Molecular Plant, 2017, 10, 483-497.	8.3	79
23	Identification of candidate genes associated with cell wall digestibility and eQTL (expression) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Genomics, 2007, 8, 22.	2.8	77
24	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
25	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics Â Â. Plant Physiology, 2013, 161, 571-582.	4.8	75
26	Accelerating plant breeding. Trends in Plant Science, 2013, 18, 667-672.	8.8	73
27	Combined linkage and association mapping reveals candidates for Scmv1, a major locus involved in resistance to sugarcane mosaic virus (SCMV) in maize. BMC Plant Biology, 2013, 13, 162.	3.6	68
28	The role of cysteine residues of spinach ferredoxin-NADP+ reductase as assessed by site-directed mutagenesis. Biochemistry, 1993, 32, 6374-6380.	2.5	67
29	Genetic characterisation of seed yield and fertility traits in perennial ryegrass (Lolium perenne L.). Theoretical and Applied Genetics, 2008, 117, 781-791.	3.6	67
30	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
31	Analysis of the genetic architecture of maize kernel size traits by combined linkage and association mapping. Plant Biotechnology Journal, 2020, 18, 207-221.	8.3	64
32	Genetic basis of resistance to sugarcane mosaic virus in European maize germplasm. Theoretical and Applied Genetics, 1998, 96, 1151-1161.	3.6	63
33	Nucleotide diversity and linkage disequilibrium in 11 expressed resistance candidate genes in Lolium perenne. BMC Plant Biology, 2007, 7, 43.	3.6	62
34	Frequency, type, and distribution of EST-SSRs from three genotypes of Lolium perenne, and their conservation across orthologous sequences of Festuca arundinacea, Brachypodium distachyon, and Oryza sativa. BMC Plant Biology, 2007, 7, 36.	3.6	60
35	A transcriptome map of perennial ryegrass (Lolium perenne L.). BMC Genomics, 2012, 13, 140.	2.8	60
36	Marker-assisted introgression of qHSR1 to improve maize resistance to head smut. Molecular Breeding, 2012, 30, 1077-1088.	2.1	59

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37	Segments encoding 5'-untranslated leaders of genes for thylakoid proteins contain cis-elements essential for transcription. Plant Journal, 1994, 6, 513-523.	5.7	56
38	An ultra-high-density map as a community resource for discerning the genetic basis of quantitative traits in maize. BMC Genomics, 2015, 16, 1078.	2.8	55
39	Genome-wide association studies of doubled haploid exotic introgression lines for root system architecture traits in maize (Zea mays L.). Plant Science, 2018, 268, 30-38.	3.6	55
40	Genotypic variation for root architecture traits in seedlings of maize (<i>Zea mays</i> L.) inbred lines. Plant Breeding, 2012, 131, 465-478.	1.9	54
41	GWAS and WGCNA uncover hub genes controlling salt tolerance in maize (Zea mays L.) seedlings. Theoretical and Applied Genetics, 2021, 134, 3305-3318.	3.6	54
42	Development and mapping of a public reference set of SSR markers in Lolium perenne L.. Molecular Ecology Notes, 2005, 5, 951-957.	1.7	52
43	Vernalization Response in Perennial Ryegrass (Lolium perenne L.) Involves Orthologues of Diploid Wheat (Triticum monococcum) VRN1 and Rice (Oryza sativa) Hd1. Plant Molecular Biology, 2006, 60, 481-494.	3.9	52
44	Comprehensive phenotypic analysis and quantitative trait locus identification for grain mineral concentration, content, and yield in maize (Zea mays L.). Theoretical and Applied Genetics, 2015, 128, 1777-1789.	3.6	52
45	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
46	Characterization of phenylpropanoid pathway genes within European maize (Zea mays L.) inbreds. BMC Plant Biology, 2008, 8, 2.	3.6	51
47	Genetic variation, population structure, and linkage disequilibrium in European elite germplasm of perennial ryegrass. Plant Science, 2011, 181, 412-420.	3.6	51
48	High levels of linkage disequilibrium and associations with forage quality at a Phenylalanine Ammonia-Lyase locus in European maize (Zea mays L.) inbreds. Theoretical and Applied Genetics, 2006, 114, 307-319.	3.6	50
49	Validation of candidate genes putatively associated with resistance to SCMV and MDMV in maize (Zea) Tj ETQq1 1 0.784314 rgBT /Ove	3.6	50
50	Genomics-assisted breeding â€" A revolutionary strategy for crop improvement. Journal of Integrative Agriculture, 2017, 16, 2674-2685.	3.5	50
51	QTL Mapping of Low-Temperature Germination Ability in the Maize IBM Syn4 RIL Population. PLoS ONE, 2016, 11, e0152795.	2.5	50
52	Development and mapping of DArT markers within the Festuca - Lolium complex. BMC Genomics, 2009, 10, 473.	2.8	49
53	The Role of Plastids in the Expression of Nuclear Genes for Thylakoid Proteins Studied with Chimeric [beta]-Glucuronidase Gene Fusions. Plant Physiology, 1994, 105, 1355-1364.	4.8	47
54	Saturation of two chromosome regions conferring resistance to SCMV with SSR and AFLP markers by targeted BSA. Theoretical and Applied Genetics, 2003, 106, 485-493.	3.6	46

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55	Development and application of functional markers in maize. Euphytica, 2005, 146, 101-108.	1.2	46
56	Quantitative Trait Locus Analysis for Deep-Sowing Germination Ability in the Maize IBM Syn10 DH Population. Frontiers in Plant Science, 2017, 8, 813.	3.6	44
57	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
58	Evidence that the plastid signal and light operate via the samecis-acting elements in the promoters of nuclear genes for plastid proteins. Molecular Genetics and Genomics, 1996, 252, 631-639.	2.4	42
59	EST-derived SSR markers used as anchor loci for the construction of a consensus linkage map in ryegrass (Lolium spp.). BMC Plant Biology, 2010, 10, 177.	3.6	42
60	Genomic prediction of seedling root length in maize (<i>Zea mays</i> L.). Plant Journal, 2015, 83, 903-912.	5.7	42
61	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
62	Nucleotide diversity and linkage disequilibrium of nine genes with putative effects on flowering time in perennial ryegrass (Lolium perenne L.). Plant Science, 2011, 180, 228-237.	3.6	41
63	QTL mapping of resistance to Sporisorium reiliana in maize. Theoretical and Applied Genetics, 1999, 99, 593-598.	3.6	40
64	Comparison of maize brown-midrib isogenic lines by cellular UV-microspectrophotometry and comparative transcript profiling. Plant Molecular Biology, 2006, 62, 697-714.	3.9	40
65	Genome-wide association mapping in a diverse spring barley collection reveals the presence of QTL hotspots and candidate genes for root and shoot architecture traits at seedling stage. BMC Plant Biology, 2019, 19, 216.	3.6	40
66	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
67	QTL mapping for haploid male fertility by a segregation distortion method and fine mapping of a key QTL qhmf4 in maize. Theoretical and Applied Genetics, 2017, 130, 1349-1359.	3.6	39
68	The Impact of Genetic Relationship and Linkage Disequilibrium on Genomic Selection. PLoS ONE, 2015, 10, e0132379.	2.5	37
69	Haploid differentiation in maize kernels based on fluorescence imaging. Plant Breeding, 2016, 135, 439-445.	1.9	37
70	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
71	Probing the role of lysine 116 and lysine 244 in the spinach ferredoxin-NADP+ reductase by site-directed mutagenesis.. Journal of Biological Chemistry, 1991, 266, 17760-17763.	3.4	36
72	Genetic and physical fine mapping of Scmv2, a potyvirus resistance gene in maize. Theoretical and Applied Genetics, 2010, 120, 1621-1634.	3.6	35

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73	Species-Specific Detection of the Maize Pathogens Sporisorium reiliana and Ustilago maydis by Dot Blot Hybridization and PCR-Based Assays. Plant Disease, 1999, 83, 390-395.	1.4	34
74	Association analysis of single nucleotide polymorphisms in candidate genes with root traits in maize (Zea mays L.) seedlings. Plant Science, 2014, 224, 9-19.	3.6	34
75	Regenerating Agricultural Landscapes with Perennial Groundcover for Intensive Crop Production. Agronomy, 2019, 9, 458.	3.0	34
76	Auxin Binding Protein 1 Reinforces Resistance to Sugarcane Mosaic Virus in Maize. Molecular Plant, 2017, 10, 1357-1360.	8.3	33
77	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEMâ€DH) Lines. Plant Genome, 2018, 11, 170083.	2.8	33
78	Polymorphisms in O-methyltransferase genes are associated with stover cell wall digestibility in European maize (Zea maysL.). BMC Plant Biology, 2010, 10, 27.	3.6	32
79	Genome-Wide Identification and Analysis of Drought-Responsive Genes and MicroRNAs in Tobacco. International Journal of Molecular Sciences, 2015, 16, 5714-5740.	4.1	32
80	Gibberellins Promote Brassinosteroids Action and Both Increase Heterosis for Plant Height in Maize (Zea mays L.). Frontiers in Plant Science, 2017, 8, 1039.	3.6	32
81	QTL Mapping in Three Connected Populations Reveals a Set of Consensus Genomic Regions for Low Temperature Germination Ability in Zea mays L.. Frontiers in Plant Science, 2018, 9, 65.	3.6	32
82	Promoters from Genes for Plastid Proteins Possess Regions with Different Sensitivities toward Red and Blue Light. Plant Physiology, 1994, 104, 997-1006.	4.8	31
83	Expressed sequence tag-derived microsatellite markers of perennial ryegrass (Lolium perenne L.). Molecular Breeding, 2008, 21, 533-548.	2.1	31
84	New Insights into the Genetics of Haploid Male Fertility in Maize. Crop Science, 2017, 57, 637-647.	1.8	31
85	Breeding Maize Maternal Haploid Inducers. Plants, 2020, 9, 614.	3.5	31
86	Polymorphisms in monolignol biosynthetic genes are associated with biomass yield and agronomic traits in European maize (Zea mays L.). BMC Plant Biology, 2010, 10, 12.	3.6	30
87	Application of doubled haploids for target gene fixation in backcross programmes of maize. Plant Breeding, 2012, 131, 449-452.	1.9	30
88	Overcoming self-incompatibility in grasses: a pathway to hybrid breeding. Theoretical and Applied Genetics, 2016, 129, 1815-1829.	3.6	30
89	Application of microsatellites from maize to teosinte and other relatives of maize. Plant Breeding, 1998, 117, 447-450.	1.9	29
90	Functional markers in wheat: technical and economic aspects. Molecular Breeding, 2008, 22, 319-328.	2.1	29

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91	Comparative Quantitative Trait Loci Mapping of Partial Resistance to Puccinia sorghi Across Four Populations of European Flint Maize. Phytopathology, 1998, 88, 1324-1329.	2.2	28
92	Influence of genetic background and heterozygosity on meiotic recombination in<i>Arabidopsis thaliana</i>. Genome, 2001, 44, 971-978.	2.0	28
93	Conversion of AFLP fragments tightly linked to SCMV resistance genes Scmv1 and Scmv2 into simple PCR-based markers. Theoretical and Applied Genetics, 2002, 105, 1190-1195.	3.6	28
94	Selection of Haploid Maize Kernels from Hybrid Kernels for Plant Breeding Using Near-Infrared Spectroscopy and SIMCA Analysis. Applied Spectroscopy, 2012, 66, 447-450.	2.2	28
95	Interacting cis elements in the plastocyanin promoter from spinach ensure regulated high-level expression. Molecular Genetics and Genomics, 1994, 242, 602-613.	2.4	27
96	Analysis of sugarcane mosaic virus resistance in maize in an isogenic dihybrid crossing scheme and implications for breeding potyvirus-resistant maize hybrids. Genome, 2006, 49, 1274-1282.	2.0	27
97	Genetic diversity in cornsalad (Valerianella locusta) and related species as determined by AFLP markers. Plant Breeding, 2004, 123, 460-466.	1.9	26
98	QTL analysis of crown rust resistance in perennial ryegrass under conditions of natural and artificial infection. Plant Breeding, 2007, 126, 347-352.	1.9	26
99	Identification of genetically linked RGAs by BAC screening in maize and implications for gene cloning, mapping and MAS. Theoretical and Applied Genetics, 2003, 106, 1171-1177.	3.6	25
100	Two chromosome segments confer multiple potyvirus resistance in maize. Plant Breeding, 2006, 125, 352-356.	1.9	25
101	Comparative sequence analysis of VRN1 alleles of Lolium perenne with the co-linear regions in barley, wheat, and rice. Molecular Genetics and Genomics, 2011, 286, 433-447.	2.1	25
102	Heterosis in Early Maize Ear Inflorescence Development: A Genome-Wide Transcription Analysis for Two Maize Inbred Lines and Their Hybrid. International Journal of Molecular Sciences, 2014, 15, 13892-13915.	4.1	25
103	Maize Doubled Haploids. , 0, , 123-166.		25
104	Brassinosteroid and gibberellin control of seedling traits in maize (Zea mays L.). Plant Science, 2017, 263, 132-141.	3.6	25
105	Heterosis-related genes under different planting densities in maize. Journal of Experimental Botany, 2018, 69, 5077-5087.	4.8	25
106	Identification of novel <i>brown midrib</i> genes in maize by tests of allelism. Plant Breeding, 2010, 129, 724-726.	1.9	23
107	A Diallel Analysis of a Maize Donor Population Response to In Vivo Maternal Haploid Induction: I. Inducibility. Crop Science, 2018, 58, 1830-1837.	1.8	23
108	Haplotype structure in commercial maize breeding programs in relation to key founder lines. Theoretical and Applied Genetics, 2020, 133, 547-561.	3.6	23

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109	Comparison of transcript profiles between near-isogenic maize lines in association with SCMV resistance based on unigene-microarrays. Plant Science, 2006, 170, 159-169.	3.6	22
110	Prospects for Hybrid Breeding in Bioenergy Grasses. Bioenergy Research, 2012, 5, 10-19.	3.9	22
111	Construction of two Lolium perenne BAC libraries and identification of BACs containing candidate genes for disease resistance and forage quality. Molecular Breeding, 2006, 19, 15-23.	2.1	21
112	Haploid Strategies for Functional Validation of Plant Genes. Trends in Biotechnology, 2015, 33, 611-620.	9.3	21
113	Nucleotide diversity and linkage disequilibrium in five Lolium perenne genes with putative role in shoot morphology. Plant Science, 2010, 179, 194-201.	3.6	20
114	Weighing in on a method to discriminate maize haploid from hybrid seed. Plant Breeding, 2015, 134, 283-285.	1.9	20
115	Association analysis of genes involved in maize (Zea mays L.) root development with seedling and agronomic traits under contrasting nitrogen levels. Plant Molecular Biology, 2015, 88, 133-147.	3.9	20
116	Generation of Maize (<i>Zea mays</i>) Doubled Haploids via Traditional Methods. Current Protocols in Plant Biology, 2017, 2, 147-157.	2.8	20
117	Origin of Scm1 and Scm2â€“ two loci conferring resistance to sugarcane mosaic virus (SCMV) in maize. Theoretical and Applied Genetics, 2000, 100, 934-941.	3.6	19
118	A high-throughput system for genome-wide measurement of genetic recombination in Arabidopsis thaliana based on transgenic markers. Functional and Integrative Genomics, 2000, 1, 200-206.	3.5	19
119	Genotypic and phenotypic characterization of isogenic doubled haploid exotic introgression lines in maize. Molecular Breeding, 2012, 30, 1001-1016.	2.1	19
120	Turning Maize Cobs into a Valuable Feedstock. Bioenergy Research, 2012, 5, 20-31.	3.9	19
121	Impact of Spontaneous Haploid Genome Doubling in Maize Breeding. Plants, 2020, 9, 369.	3.5	19
122	Functional Markers in Resistance Breeding. Progress in Botany Fortschritte Der Botanik, 2008, , 61-87.	0.3	18
123	GWASpro: a high-performance genome-wide association analysis server. Bioinformatics, 2019, 35, 2512-2514.	4.1	18
124	Association mapping for root system architecture traits under two nitrogen conditions in germplasm enhancement of maize doubled haploid lines. Crop Journal, 2020, 8, 213-226.	5.2	18
125	Mapping of QTL and identification of candidate genes conferring spontaneous haploid genome doubling in maize (Zea mays L.). Plant Science, 2020, 293, 110337.	3.6	18
126	Genetic and physical fine mapping of the novel brown midrib gene bm6 in maize (Zea mays L.) to a 180Âkb region on chromosome 2. Theoretical and Applied Genetics, 2012, 125, 1223-1235.	3.6	17

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127	Effects of ZmHIPP on lead tolerance in maize seedlings: Novel ideas for soil bioremediation. Journal of Hazardous Materials, 2022, 430, 128457.	12.4	17
128	Mapping of QTL for resistance to powdery mildew and resistance gene analogues in perennial ryegrass. Plant Breeding, 2008, 127, 368-375.	1.9	16
129	Integrating a genome-wide association study with transcriptomic analysis to detect genes controlling grain drying rate in maize (Zea may, L.). Theoretical and Applied Genetics, 2020, 133, 623-634.	3.6	16
130	Genetic and agronomic assessment of cob traits in corn under low and normal nitrogen management conditions. Theoretical and Applied Genetics, 2015, 128, 1231-1242.	3.6	15
131	Genome-wide comparative analysis of digital gene expression tag profiles during maize ear development. Genomics, 2015, 106, 52-60.	2.9	15
132	Association of single nucleotide polymorphisms in LpIRI1 gene with freezing tolerance traits in perennial ryegrass. Euphytica, 2015, 204, 523-534.	1.2	15
133	Haploid and Doubled Haploid Techniques in Perennial Ryegrass (Lolium perenne L.) to Advance Research and Breeding. Agronomy, 2016, 6, 60.	3.0	15
134	Identification of quantitative trait loci for leafâ€related traits in an IBM Syn10 DH maize population across three environments. Plant Breeding, 2018, 137, 127-138.	1.9	15
135	QTL Mapping Low-Temperature Germination Ability in the Maize IBM Syn10 DH Population. Plants, 2022, 11, 214.	3.5	15
136	Low Level of Linkage Disequilibrium at the COMT (Caffeic Acid O-methyl Transferase) Locus in European Maize (Zea mays L.). Genetic Resources and Crop Evolution, 2007, 54, 139-148.	1.6	14
137	Fine mapping a self-fertility locus in perennial ryegrass. Theoretical and Applied Genetics, 2018, 131, 817-827.	3.6	14
138	Genetic dissection of haploid male fertility in maize (<i>Zea mays </i>L.). Plant Breeding, 2019, 138, 259-265.	1.9	14
139	Mapping of QTL for Grain Yield Components Based on a DH Population in Maize. Scientific Reports, 2020, 10, 7086.	3.3	14
140	Genomic prediction of maternal haploid induction rate in maize. Plant Genome, 2020, 13, e20014.	2.8	14
141	Assessing plant performance in the Enviratron. Plant Methods, 2019, 15, 117.	4.3	13
142	GWAS and transcriptome analysis reveal MADS26 involved in seed germination ability in maize. Theoretical and Applied Genetics, 2022, 135, 1717-1730.	3.6	13
143	Cross-species amplification of 105 Lolium perenne SSR loci in 23 species within the Poaceae. Molecular Ecology Notes, 2007, 7, 1155-1161.	1.7	12
144	Genetic dissection of stalk lodging-related traits using an IBM Syn10 DH population in maize across three environments (Zea mays L.). Molecular Genetics and Genomics, 2019, 294, 1277-1288.	2.1	12

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145	Stability Analysis of Kernel Quality Traits in Exoticâ€Derived Doubled Haploid Maize Lines. Plant Genome, 2019, 12, 170114.	2.8	12
146	QTL mapping of spontaneous haploid genome doubling using genotyping-by-sequencing in maize (Zea) Tj ETQq0 0 0 rgBT /Overlock 10	3.6	12
147	Characterization of Sugarcane Mosaic Virus Scmv1 and Scmv2 Resistance Regions by Regional Association Analysis in Maize. PLoS ONE, 2015, 10, e0140617.	2.5	12
148	Getting the â€˜MOSTâ€™ out of crop improvement. Trends in Plant Science, 2015, 20, 372-379.	8.8	11
149	Genetic dissection of maize seedling traits in an IBM Syn10 DH population under the combined stress of lead and cadmium. Molecular Genetics and Genomics, 2021, 296, 1057-1070.	2.1	11
150	Paper Roll Culture and Assessment of Maize Root Parameters. Bio-protocol, 2016, 6, .	0.4	11
151	Identification of Candidate Genes for Self-Compatibility in Perennial Ryegrass (Lolium perenne L.). Frontiers in Plant Science, 2021, 12, 707901.	3.6	11
152	Targeted BSA mapping of Scmv1 and Scmv2 conferring resistance to SCMV using PstI/MseI compared with EcoRI/MseI AFLP markers. Plant Breeding, 2004, 123, 434-437.	1.9	10
153	Characterization of European forage maize lines for stover composition and associations with polymorphisms within O-methyltransferase genes. Plant Science, 2012, 185-186, 281-287.	3.6	10
154	Gametophytic Selfâ€Incompatibility Is Operative in <i>Miscanthus sinensis</i> (Poaceae) and Is Affected by Pistil Age. Crop Science, 2017, 57, 1948-1956.	1.8	10
155	Quantitative trait loci mapping of forage stover quality traits in six mapping populations derived from European elite maize germplasm. Plant Breeding, 2018, 137, 139-147.	1.9	10
156	Genetic mapping of QTL for maize leaf width combining RIL and IF2 populations. PLoS ONE, 2017, 12, e0189441.	2.5	10
157	Prospects for celeriac (Apium graveolensvar.rapaceum) improvement by using genetic resources ofApium, as determined by AFLP markers and morphological characterization. Plant Genetic Resources: Characterisation and Utilisation, 2004, 2, 189-198.	0.8	9
158	Duplicate marker loci can result in incorrect locus orders on linkage maps. Theoretical and Applied Genetics, 2004, 109, 305-316.	3.6	9
159	Association analysis of five candidate genes with plant height and dry matter yield in perennial ryegrass. Plant Breeding, 2015, 134, 454-460.	1.9	9
160	Major locus for spontaneous haploid genome doubling detected by a caseâ€"control GWAS in exotic maize germplasm. Theoretical and Applied Genetics, 2021, 134, 1423-1434.	3.6	9
161	Mapping a New Source of Self-fertility in Perennial Ryegrass (Lolium perenne L.). Plant Breeding and Biotechnology, 2013, 1, 385-395.	0.9	9
162	Simultaneous Selection of Sweet-Waxy Corn Ideotypes Appealing to Hybrid Seed Producers, Growers, and Consumers in Thailand. Agronomy, 2022, 12, 87.	3.0	9

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163	Genetic and Morphometric Analysis of Cob Architecture and Biomass-Related Traits in the Intermated B73â€‰Ã—â€‰Mo17 Recombinant Inbred Lines of Maize. Bioenergy Research, 2013, 6, 903-916.	3.9	8
164	Genetic architecture of plant height in maize phenotypeâ€selected introgression families. Plant Breeding, 2016, 135, 429-438.	1.9	8
165	QTL analysis of deepâ€sowing tolerance during seed germination in the maize IBM Syn4 RIL population. Plant Breeding, 2020, 139, 1125-1134.	1.9	8
166	Characterization and practical use of self-compatibility in outcrossing grass species. Annals of Botany, 2021, 127, 841-852.	2.9	8
167	Variation in the Vernalization Response of a Geographically Diverse Collection of Timothy Genotypes. Crop Science, 2011, 51, 2689-2697.	1.8	7
168	Identification of genomic loci associated with crown rust resistance in perennial ryegrass (Lolium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	7
169	Significant Variation for Bio-oil Compounds After Pyrolysis/Gas Chromatographyâ€"Mass Spectrometry of Cobs and Stover Among Five Near-Isogenic Brown Midrib Hybrids in Maize. Bioenergy Research, 2014, 7, 693-701.	3.9	7
170	Variability in Prolificacy, Total Carotenoids, Lutein, and Zeaxanthin of Yellow Small-Ear Waxy Corn Germplasm. International Journal of Agronomy, 2020, 2020, 1-12.	1.2	7
171	Function of Genetic Material: Genes Involved in Quantitative and Qualitative Resistance. Progress in Botany Fortschritte Der Botanik, 2002, , 80-105.	0.3	7
172	Evidence that the plastid signal and light operate via the same. Molecular Genetics and Genomics, 1996, 252, 631.	2.4	7
173	Germplasm enhancement of maize: a look into haploid induction and chromosomal doubling of haploids from temperateâ€adapted tropical sources. Plant Breeding, 2016, 135, 593-597.	1.9	6
174	Tracing the signature of Peronosclerospora maydis in maize seeds. Australasian Plant Pathology, 2016, 45, 73-82.	1.0	6
175	Quantitative trait loci mapping of forage agronomic traits in six mapping populations derived from European elite maize germplasm. Plant Breeding, 2018, 137, 370-378.	1.9	6
176	Association between SCMV Resistance and Macroarray-based Expression Patterns in Maize Inbreds. Molecular Breeding, 2005, 16, 173-184.	2.1	5
177	The Pic19 NBS-LRR gene family members are closely linked to Scmv1, but not involved in maize resistance to sugarcane mosaic virus. Genome, 2008, 51, 673-684.	2.0	5
178	Mapping of quantitative trait loci/locus conferring resistance to foxtail mosaic virus in maize using the intermated B73â€ƒÃ—â€ƒMo17 population. Plant Breeding, 2010, 129, 721-723.	1.9	5
179	Prospects and Limitations for Development and Application of Functional Markers in Plants. , 2013, , 329-346.		5
180	Extensive genetic diversity and low linkage disequilibrium within the COMT locus in maize exotic populations. Plant Science, 2014, 221-222, 69-80.	3.6	5

#	ARTICLE	IF	CITATIONS
181	Validation of two models for selfâ€incompatibility in autotetraploid perennial ryegrass using high resolution meltingâ€based markers. Plant Breeding, 2014, 133, 765-770.	1.9	5
182	The Genetics and Genomics of Virus Resistance in Maize. Compendium of Plant Genomes, 2018, , 185-200.	0.5	5
183	A diallel analysis of a maize donor population response to in vivo maternal haploid induction: II. Haploid male fertility. Crop Science, 2020, 60, 873-882.	1.8	5
184	Breeding for Prolificacy, Total Carotenoids and Resistance to Downy Mildew in Small-Ear Waxy Corn by Modified Mass Selection. Agronomy, 2021, 11, 1793.	3.0	5
185	Influence of genetic background and heterozygosity on meiotic recombination in <i>Arabidopsis thaliana</i>. Genome, 2001, 44, 971-978.	2.0	5
186	"PolyMin": software for identification of the minimum number of polymorphisms required for haplotype and genotype differentiation. BMC Bioinformatics, 2009, 10, 176.	2.6	4
187	Classification approaches for sorting maize (<i>Zea mays</i> subsp. <i>mays</i>) haploids using singleâ€kernel nearâ€infrared spectroscopy. Plant Breeding, 2020, 139, 1103-1112.	1.9	4
188	Mapping of QTL for kernel abortion caused by in vivo haploid induction in maize (Zea mays L.). PLoS ONE, 2020, 15, e0228411.	2.5	4
189	QTL Mapping for Haploid Inducibility Using Genotyping by Sequencing in Maize. Plants, 2022, 11, 878.	3.5	4
190	Selection Gain of Maize Haploid Inducers for the Tropical Savanna Environments. Plants, 2021, 10, 2812.	3.5	4
191	Protocols for In Vivo Doubled Haploid (DH) Technology in Maize Breeding: From Haploid Inducer Development to Haploid Genome Doubling. Methods in Molecular Biology, 2022, 2484, 213-235.	0.9	4
192	QTL mapping of improving forage maize starch degradability in European elite maize germplasm. Plant Breeding, 2019, 138, 524-533.	1.9	3
193	Pattern of inheritance of a selfâ€fertility gene in an autotetraploid perennial ryegrass (Lolium perenne) Tj ETQq1 1 0.784314 rgBT /Over	1.9	3
194	Investigating the Effect of the Interaction of Maize Inducer and Donor Backgrounds on Haploid Induction Rates. Plants, 2022, 11, 1527.	3.5	3
195	Genetic and Quantitative Trait Locus Analysis for Bio-Oil Compounds after Fast Pyrolysis in Maize Cobs. PLoS ONE, 2016, 11, e0145845.	2.5	2
196	MYO, a Candidate Gene for Haploid Induction in Maize Causes Male Sterility. Plants, 2020, 9, 773.	3.5	2
197	Usefulness of temperate-adapted maize lines developed by doubled haploid and single-seed descent methods. Theoretical and Applied Genetics, 2022, 135, 1829-1841.	3.6	2
198	Combining data sets for maize root seedling traits increases the power of GWAS and genomic prediction accuracies. Journal of Experimental Botany, 0, , .	4.8	2

#	Article	IF	Citations
199	PollenCALC: Software for estimation of pollen compatibility of self-incompatible allo- and autotetraploid species. BMC Bioinformatics, 2012, 13, 125.	2.6	1
200	Parent Selection â€" Usefulness and Prediction of Hybrid Performance. , 2013, , 349-368.		1
201	Increasing Seed Viability of Maize Haploid Inducing Lines by Genetic and Nonâ€Genetic Approaches. Crop Science, 2016, 56, 1940-1947.	1.8	1
202	Genetic variation of seedling traits responded to brassinosteroid and gibberellin inhibitors in maize (Zea mays) doubled haploid lines. Plant Breeding, 2020, 139, 870-882.	1.9	1
203	Exploring the potential usefulness of U.S. maize expired Plant Variety Protection Act lines for maize breeding in subâ€Saharan Africa. Crop Science, 2020, 60, 2251-2265.	1.8	1
204	Function of genetic material: From genomics to functional markers in maize. , 2006, , 53-74.		1
205	Molecular characterization of the spinach G-box binding protein family. Physiologia Plantarum, 1998, 103, 415-425.	5.2	0
206	Estimation of Temporal Allele Frequency Changes in Ryegrass Populations Selected for Axillary Tiller Development. , 2013, , 81-87.		0
207	Utilization of Reduced Haploid Vigor for Phenomic Discrimination of Haploid and Diploid Maize Seedlings. The Plant Phenome Journal, 2019, 2, 1-10.	2.0	0
208	QTL Mapping of Forage Traits. , 2002, , 585-600.		0
209	Application of Genomics to Plant Breeding. , 2010, , 494-527.		0
210	Maize Zmcyp710a8 Mutant as a Tool to Decipher the Function of Stigmasterol in Plant Metabolism. Frontiers in Plant Science, 2021, 12, 732216.	3.6	0
211	Application Of Genomics To Forage CROP Breeding For Quality Traits. , 2007, , 281-306.		0