

# Thomas Lubberstedt

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2646445/publications.pdf>

Version: 2024-02-01

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	QTL Mapping Low-Temperature Germination Ability in the Maize IBM Syn10 DH Population. <i>Plants</i> , 2022, 11, 214.	3.5	15
2	Effects of ZmHIPP on lead tolerance in maize seedlings: Novel ideas for soil bioremediation. <i>Journal of Hazardous Materials</i> , 2022, 430, 128457.	12.4	17
3	Usefulness of temperate-adapted maize lines developed by doubled haploid and single-seed descent methods. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1829-1841.	3.6	2
4	QTL Mapping for Haploid Inducibility Using Genotyping by Sequencing in Maize. <i>Plants</i> , 2022, 11, 878.	3.5	4
5	GWAS and transcriptome analysis reveal MADS26 involved in seed germination ability in maize. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1717-1730.	3.6	13
6	Simultaneous Selection of Sweet-Waxy Corn Ideotypes Appealing to Hybrid Seed Producers, Growers, and Consumers in Thailand. <i>Agronomy</i> , 2022, 12, 87.	3.0	9
7	Protocols for In Vivo Doubled Haploid (DH) Technology in Maize Breeding: From Haploid Inducer Development to Haploid Genome Doubling. <i>Methods in Molecular Biology</i> , 2022, 2484, 213-235.	0.9	4
8	Investigating the Effect of the Interaction of Maize Inducer and Donor Backgrounds on Haploid Induction Rates. <i>Plants</i> , 2022, 11, 1527.	3.5	3
9	Major locus for spontaneous haploid genome doubling detected by a caseâ€“control GWAS in exotic maize germplasm. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1423-1434.	3.6	9
10	Characterization and practical use of self-compatibility in outcrossing grass species. <i>Annals of Botany</i> , 2021, 127, 841-852.	2.9	8
11	Genetic dissection of maize seedling traits in an IBM Syn10 DH population under the combined stress of lead and cadmium. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1057-1070.	2.1	11
12	GWAS and WGCNA uncover hub genes controlling salt tolerance in maize ( <i>Zea mays</i> L.) seedlings. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3305-3318.	3.6	54
13	Breeding for Prolificacy, Total Carotenoids and Resistance to Downy Mildew in Small-Ear Waxy Corn by Modified Mass Selection. <i>Agronomy</i> , 2021, 11, 1793.	3.0	5
14	Identification of Candidate Genes for Self-Compatibility in Perennial Ryegrass ( <i>Lolium perenne</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 707901.	3.6	11
15	Maize <i>Zmcp710a8</i> Mutant as a Tool to Decipher the Function of Stigmasterol in Plant Metabolism. <i>Frontiers in Plant Science</i> , 2021, 12, 732216.	3.6	0
16	Selection Gain of Maize Haploid Inducers for the Tropical Savanna Environments. <i>Plants</i> , 2021, 10, 2812.	3.5	4
17	Analysis of the genetic architecture of maize kernel size traits by combined linkage and association mapping. <i>Plant Biotechnology Journal</i> , 2020, 18, 207-221.	8.3	64
18	Pattern of inheritance of a selfâ€“fertility gene in an autotetraploid perennial ryegrass ( <i>Lolium perenne</i> ) Tj ETQq0 0 0,rgBT /Overlock 10 T	1.98	3

#	ARTICLE	IF	CITATIONS
19	Association mapping for root system architecture traits under two nitrogen conditions in germplasm enhancement of maize doubled haploid lines. <i>Crop Journal</i> , 2020, 8, 213-226.	5.2	18
20	Integrating a genome-wide association study with transcriptomic analysis to detect genes controlling grain drying rate in maize ( <i>Zea mays</i> , L.). <i>Theoretical and Applied Genetics</i> , 2020, 133, 623-634.	3.6	16
21	Mapping of QTL and identification of candidate genes conferring spontaneous haploid genome doubling in maize ( <i>Zea mays</i> L.). <i>Plant Science</i> , 2020, 293, 110337.	3.6	18
22	Haplotype structure in commercial maize breeding programs in relation to key founder lines. <i>Theoretical and Applied Genetics</i> , 2020, 133, 547-561.	3.6	23
23	Genetic variation of seedling traits responded to brassinosteroid and gibberellin inhibitors in maize ( <i>Zea mays</i> ) doubled haploid lines. <i>Plant Breeding</i> , 2020, 139, 870-882.	1.9	1
24	Classification approaches for sorting maize ( <i>Zea mays</i> subsp. <i>mays</i> ) haploids using single-kernel near-infrared spectroscopy. <i>Plant Breeding</i> , 2020, 139, 1103-1112.	1.9	4
25	QTL analysis of deep-sowing tolerance during seed germination in the maize IBM Syn4 RIL population. <i>Plant Breeding</i> , 2020, 139, 1125-1134.	1.9	8
26	Variability in Prolificacy, Total Carotenoids, Lutein, and Zeaxanthin of Yellow Small-Ear Waxy Corn Germplasm. <i>International Journal of Agronomy</i> , 2020, 2020, 1-12.	1.2	7
27	Exploring the potential usefulness of U.S. maize expired Plant Variety Protection Act lines for maize breeding in sub-Saharan Africa. <i>Crop Science</i> , 2020, 60, 2251-2265.	1.8	1
28	Mapping of QTL for Grain Yield Components Based on a DH Population in Maize. <i>Scientific Reports</i> , 2020, 10, 7086.	3.3	14
29	Genomic prediction of maternal haploid induction rate in maize. <i>Plant Genome</i> , 2020, 13, e20014.	2.8	14
30	Breeding Maize Maternal Haploid Inducers. <i>Plants</i> , 2020, 9, 614.	3.5	31
31	Impact of Spontaneous Haploid Genome Doubling in Maize Breeding. <i>Plants</i> , 2020, 9, 369.	3.5	19
32	MYO, a Candidate Gene for Haploid Induction in Maize Causes Male Sterility. <i>Plants</i> , 2020, 9, 773.	3.5	2
33	Mapping of QTL for kernel abortion caused by in vivo haploid induction in maize ( <i>Zea mays</i> L.). <i>PLoS ONE</i> , 2020, 15, e0228411.	2.5	4
34	A diallel analysis of a maize donor population response to in vivo maternal haploid induction: II. Haploid male fertility. <i>Crop Science</i> , 2020, 60, 873-882.	1.8	5
35	QTL mapping of spontaneous haploid genome doubling using genotyping-by-sequencing in maize ( <i>Zea</i> ) Tj ETQq1 1.0,784314 rgBT /O	3.6	12
36	Assessing plant performance in the Enviratron. <i>Plant Methods</i> , 2019, 15, 117.	4.3	13

#	ARTICLE	IF	CITATIONS
37	QTL mapping of improving forage maize starch degradability in European elite maize germplasm. <i>Plant Breeding</i> , 2019, 138, 524-533.	1.9	3
38	Regenerating Agricultural Landscapes with Perennial Groundcover for Intensive Crop Production. <i>Agronomy</i> , 2019, 9, 458.	3.0	34
39	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. <i>BMC Plant Biology</i> , 2019, 19, 216.	3.6	40
40	Genetic dissection of stalk lodging-related traits using an IBM Syn10 DH population in maize across three environments ( <i>Zea mays</i> L.). <i>Molecular Genetics and Genomics</i> , 2019, 294, 1277-1288.	2.1	12
41	Utilization of Reduced Haploid Vigor for Phenomic Discrimination of Haploid and Diploid Maize Seedlings. <i>The Plant Phenome Journal</i> , 2019, 2, 1-10.	2.0	0
42	Stability Analysis of Kernel Quality Traits in Exoticâ€Derived Doubled Haploid Maize Lines. <i>Plant Genome</i> , 2019, 12, 170114.	2.8	12
43	Genetic dissection of haploid male fertility in maize ( <i>Zea mays</i> L.). <i>Plant Breeding</i> , 2019, 138, 259-265.	1.9	14
44	Technological advances in maize breeding: past, present and future. <i>Theoretical and Applied Genetics</i> , 2019, 132, 817-849.	3.6	97
45	GWASpro: a high-performance genome-wide association analysis server. <i>Bioinformatics</i> , 2019, 35, 2512-2514.	4.1	18
46	Identification of quantitative trait loci for leafâ€related traits in an IBM Syn10 DH maize population across three environments. <i>Plant Breeding</i> , 2018, 137, 127-138.	1.9	15
47	Quantitative trait loci mapping of forage stover quality traits in six mapping populations derived from European elite maize germplasm. <i>Plant Breeding</i> , 2018, 137, 139-147.	1.9	10
48	Genome-wide association studies of doubled haploid exotic introgression lines for root system architecture traits in maize ( <i>Zea mays</i> L.). <i>Plant Science</i> , 2018, 268, 30-38.	3.6	55
49	Fine mapping a self-fertility locus in perennial ryegrass. <i>Theoretical and Applied Genetics</i> , 2018, 131, 817-827.	3.6	14
50	The Genetics and Genomics of Virus Resistance in Maize. <i>Compendium of Plant Genomes</i> , 2018, , 185-200.	0.5	5
51	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEMâ€DH) Lines. <i>Plant Genome</i> , 2018, 11, 170083.	2.8	33
52	Quantitative trait loci mapping of forage agronomic traits in six mapping populations derived from European elite maize germplasm. <i>Plant Breeding</i> , 2018, 137, 370-378.	1.9	6
53	A Diallel Analysis of a Maize Donor Population Response to In Vivo Maternal Haploid Induction: I. Inducibility. <i>Crop Science</i> , 2018, 58, 1830-1837.	1.8	23
54	Heterosis-related genes under different planting densities in maize. <i>Journal of Experimental Botany</i> , 2018, 69, 5077-5087.	4.8	25

#	ARTICLE	IF	CITATIONS
55	QTL Mapping in Three Connected Populations Reveals a Set of Consensus Genomic Regions for Low Temperature Germination Ability in <i>Zea mays</i> L.. <i>Frontiers in Plant Science</i> , 2018, 9, 65.	3.6	32
56	An Atypical Thioredoxin Imparts Early Resistance to Sugarcane Mosaic Virus in Maize. <i>Molecular Plant</i> , 2017, 10, 483-497.	8.3	79
57	Emerging Avenues for Utilization of Exotic Germplasm. <i>Trends in Plant Science</i> , 2017, 22, 624-637.	8.8	108
58	QTL mapping for haploid male fertility by a segregation distortion method and fine mapping of a key QTL <i>qhmf4</i> in maize. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1349-1359.	3.6	39
59	New Insights into the Genetics of Haploid Male Fertility in Maize. <i>Crop Science</i> , 2017, 57, 637-647.	1.8	31
60	Generation of Maize ( <i>Zea mays</i> ) Doubled Haploids via Traditional Methods. <i>Current Protocols in Plant Biology</i> , 2017, 2, 147-157.	2.8	20
61	Brassinosteroid and gibberellin control of seedling traits in maize ( <i>Zea mays</i> L.). <i>Plant Science</i> , 2017, 263, 132-141.	3.6	25
62	Auxin Binding Protein 1 Reinforces Resistance to Sugarcane Mosaic Virus in Maize. <i>Molecular Plant</i> , 2017, 10, 1357-1360.	8.3	33
63	Novel technologies in doubled haploid line development. <i>Plant Biotechnology Journal</i> , 2017, 15, 1361-1370.	8.3	102
64	Genomics-assisted breeding â€œ A revolutionary strategy for crop improvement. <i>Journal of Integrative Agriculture</i> , 2017, 16, 2674-2685.	3.5	50
65	Quantitative Trait Locus Analysis for Deep-Sowing Germination Ability in the Maize IBM Syn10 DH Population. <i>Frontiers in Plant Science</i> , 2017, 8, 813.	3.6	44
66	Gibberellins Promote Brassinosteroids Action and Both Increase Heterosis for Plant Height in Maize ( <i>Zea mays</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1039.	3.6	32
67	Gametophytic Self-Incompatibility Is Operative in <i>Miscanthus sinensis</i> (Poaceae) and Is Affected by Pistil Age. <i>Crop Science</i> , 2017, 57, 1948-1956.	1.8	10
68	Genetic mapping of QTL for maize leaf width combining RIL and IF2 populations. <i>PLoS ONE</i> , 2017, 12, e0189441.	2.5	10
69	Haploid and Doubled Haploid Techniques in Perennial Ryegrass ( <i>Lolium perenne</i> L.) to Advance Research and Breeding. <i>Agronomy</i> , 2016, 6, 60.	3.0	15
70	Genetic and Quantitative Trait Locus Analysis for Bio-Oil Compounds after Fast Pyrolysis in Maize Cobs. <i>PLoS ONE</i> , 2016, 11, e0145845.	2.5	2
71	Haploid differentiation in maize kernels based on fluorescence imaging. <i>Plant Breeding</i> , 2016, 135, 439-445.	1.9	37
72	Increasing Seed Viability of Maize Haploid Inducing Lines by Genetic and Non-Genetic Approaches. <i>Crop Science</i> , 2016, 56, 1940-1947.	1.8	1

#	ARTICLE	IF	CITATIONS
73	Overcoming self-incompatibility in grasses: a pathway to hybrid breeding. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1815-1829.	3.6	30
74	Germplasm enhancement of maize: a look into haploid induction and chromosomal doubling of haploids from temperate-adapted tropical sources. <i>Plant Breeding</i> , 2016, 135, 593-597.	1.9	6
75	Genetic architecture of plant height in maize phenotype-selected introgression families. <i>Plant Breeding</i> , 2016, 135, 429-438.	1.9	8
76	Tracing the signature of <i>Peronosclerospora maydis</i> in maize seeds. <i>Australasian Plant Pathology</i> , 2016, 45, 73-82.	1.0	6
77	QTL Mapping of Low-Temperature Germination Ability in the Maize IBM Syn4 RIL Population. <i>PLoS ONE</i> , 2016, 11, e0152795.	2.5	50
78	Paper Roll Culture and Assessment of Maize Root Parameters. <i>Bio-protocol</i> , 2016, 6, .	0.4	11
79	An ultra-high-density map as a community resource for discerning the genetic basis of quantitative traits in maize. <i>BMC Genomics</i> , 2015, 16, 1078.	2.8	55
80	Association analysis of five candidate genes with plant height and dry matter yield in perennial ryegrass. <i>Plant Breeding</i> , 2015, 134, 454-460.	1.9	9
81	Weighing in on a method to discriminate maize haploid from hybrid seed. <i>Plant Breeding</i> , 2015, 134, 283-285.	1.9	20
82	Genomic prediction of seedling root length in maize ( <i>Zea mays</i> L.). <i>Plant Journal</i> , 2015, 83, 903-912.	5.7	42
83	The Impact of Genetic Relationship and Linkage Disequilibrium on Genomic Selection. <i>PLoS ONE</i> , 2015, 10, e0132379.	2.5	37
84	Genetic and agronomic assessment of cob traits in corn under low and normal nitrogen management conditions. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1231-1242.	3.6	15
85	Genome-wide association analysis of seedling root development in maize ( <i>Zea mays</i> L.). <i>BMC Genomics</i> , 2015, 16, 47.	2.8	159
86	Association analysis of genes involved in maize ( <i>Zea mays</i> L.) root development with seedling and agronomic traits under contrasting nitrogen levels. <i>Plant Molecular Biology</i> , 2015, 88, 133-147.	3.9	20
87	Getting the "MOST" out of crop improvement. <i>Trends in Plant Science</i> , 2015, 20, 372-379.	8.8	11
88	Genome-Wide Identification and Analysis of Drought-Responsive Genes and MicroRNAs in Tobacco. <i>International Journal of Molecular Sciences</i> , 2015, 16, 5714-5740.	4.1	32
89	Genome-wide comparative analysis of digital gene expression tag profiles during maize ear development. <i>Genomics</i> , 2015, 106, 52-60.	2.9	15
90	Haploid Strategies for Functional Validation of Plant Genes. <i>Trends in Biotechnology</i> , 2015, 33, 611-620.	9.3	21

#	ARTICLE	IF	CITATIONS
91	Comprehensive phenotypic analysis and quantitative trait locus identification for grain mineral concentration, content, and yield in maize ( <i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 2015, 128, 1777-1789.	3.6	52
92	Association of single nucleotide polymorphisms in LpIR1 gene with freezing tolerance traits in perennial ryegrass. <i>Euphytica</i> , 2015, 204, 523-534.	1.2	15
93	Characterization of Sugarcane Mosaic Virus Scmv1 and Scmv2 Resistance Regions by Regional Association Analysis in Maize. <i>PLoS ONE</i> , 2015, 10, e0140617.	2.5	12
94	Heterosis in Early Maize Ear Inflorescence Development: A Genome-Wide Transcription Analysis for Two Maize Inbred Lines and Their Hybrid. <i>International Journal of Molecular Sciences</i> , 2014, 15, 13892-13915.	4.1	25
95	Significant Variation for Bio-oil Compounds After Pyrolysis/Gas Chromatography-Mass Spectrometry of Cobs and Stover Among Five Near-Isogenic Brown Midrib Hybrids in Maize. <i>Bioenergy Research</i> , 2014, 7, 693-701.	3.9	7
96	Association analysis of single nucleotide polymorphisms in candidate genes with root traits in maize ( <i>Zea mays</i> L.) seedlings. <i>Plant Science</i> , 2014, 224, 9-19.	3.6	34
97	Identification of miRNAs and their target genes in developing maize ears by combined small RNA and degradome sequencing. <i>BMC Genomics</i> , 2014, 15, 25.	2.8	94
98	Extensive genetic diversity and low linkage disequilibrium within the COMT locus in maize exotic populations. <i>Plant Science</i> , 2014, 221-222, 69-80.	3.6	5
99	Validation of two models for self-incompatibility in autotetraploid perennial ryegrass using high resolution melting-based markers. <i>Plant Breeding</i> , 2014, 133, 765-770.	1.9	5
100	Analysis of Maize ( <i>Zea mays</i> L.) Seedling Roots with the High-Throughput Image Analysis Tool ARIA (Automatic Root Image Analysis). <i>PLoS ONE</i> , 2014, 9, e108255.	2.5	104
101	Genetic and Morphometric Analysis of Cob Architecture and Biomass-Related Traits in the Intermated B73-Mo17 Recombinant Inbred Lines of Maize. <i>Bioenergy Research</i> , 2013, 6, 903-916.	3.9	8
102	Combined linkage and association mapping reveals candidates for Scmv1, a major locus involved in resistance to sugarcane mosaic virus (SCMV) in maize. <i>BMC Plant Biology</i> , 2013, 13, 162.	3.6	68
103	Accelerating plant breeding. <i>Trends in Plant Science</i> , 2013, 18, 667-672.	8.8	73
104	Genotypic variation and relationships between seedling and adult plant traits in maize ( <i>Zea mays</i> L.) inbred lines grown under contrasting nitrogen levels. <i>Euphytica</i> , 2013, 189, 123-133.	1.2	85
105	The Genetic and Molecular Basis of Plant Resistance to Pathogens. <i>Journal of Genetics and Genomics</i> , 2013, 40, 23-35.	3.9	100
106	Identification of genomic loci associated with crown rust resistance in perennial ryegrass ( <i>Lolium</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	3.6	7
107	Prospects and Limitations for Development and Application of Functional Markers in Plants. , 2013, , 329-346.		5
108	Parent Selection - Usefulness and Prediction of Hybrid Performance. , 2013, , 349-368.		1

#	ARTICLE	IF	CITATIONS
109	Estimation of Temporal Allele Frequency Changes in Ryegrass Populations Selected for Axillary Tiller Development. , 2013, , 81-87.		0
110	The Perennial Ryegrass GenomeZipper: Targeted Use of Genome Resources for Comparative Grass Genomics Å Å. Plant Physiology, 2013, 161, 571-582.	4.8	75
111	Mapping a New Source of Self-fertility in Perennial Ryegrass ( <i>Lolium perenne</i> L.). Plant Breeding and Biotechnology, 2013, 1, 385-395.	0.9	9
112	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
113	Genetic and physical fine mapping of the novel brown midrib gene <i>bm6</i> in maize ( <i>Zea mays</i> L.) to a 180Åkb region on chromosome 2. Theoretical and Applied Genetics, 2012, 125, 1223-1235.	3.6	17
114	Genotypic and phenotypic characterization of isogenic doubled haploid exotic introgression lines in maize. Molecular Breeding, 2012, 30, 1001-1016.	2.1	19
115	Marker-assisted introgression of <i>qHSR1</i> to improve maize resistance to head smut. Molecular Breeding, 2012, 30, 1077-1088.	2.1	59
116	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
117	PollenCALC: Software for estimation of pollen compatibility of self-incompatible allo- and autotetraploid species. BMC Bioinformatics, 2012, 13, 125.	2.6	1
118	A transcriptome map of perennial ryegrass ( <i>Lolium perenne</i> L.). BMC Genomics, 2012, 13, 140.	2.8	60
119	Application of doubled haploids for target gene fixation in backcross programmes of maize. Plant Breeding, 2012, 131, 449-452.	1.9	30
120	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
121	Turning Maize Cobs into a Valuable Feedstock. Bioenergy Research, 2012, 5, 20-31.	3.9	19
122	Prospects for Hybrid Breeding in Bioenergy Grasses. Bioenergy Research, 2012, 5, 10-19.	3.9	22
123	Nucleotide diversity and linkage disequilibrium of nine genes with putative effects on flowering time in perennial ryegrass ( <i>Lolium perenne</i> L.). Plant Science, 2011, 180, 228-237.	3.6	41
124	Genetic variation, population structure, and linkage disequilibrium in European elite germplasm of perennial ryegrass. Plant Science, 2011, 181, 412-420.	3.6	51
125	Comparative sequence analysis of <i>VRN1</i> alleles of <i>Lolium perenne</i> with the co-linear regions in barley, wheat, and rice. Molecular Genetics and Genomics, 2011, 286, 433-447.	2.1	25
126	Variation in the Vernalization Response of a Geographically Diverse Collection of Timothy Genotypes. Crop Science, 2011, 51, 2689-2697.	1.8	7



#	ARTICLE	IF	CITATIONS
127	Genetic and physical fine mapping of Scmv2, a potyvirus resistance gene in maize. Theoretical and Applied Genetics, 2010, 120, 1621-1634.	3.6	35
128	Polymorphisms in monolignol biosynthetic genes are associated with biomass yield and agronomic traits in European maize ( <i>Zea mays</i> L.). BMC Plant Biology, 2010, 10, 12.	3.6	30
129	EST-derived SSR markers used as anchor loci for the construction of a consensus linkage map in ryegrass ( <i>Lolium</i> spp.). BMC Plant Biology, 2010, 10, 177.	3.6	42
130	Polymorphisms in O-methyltransferase genes are associated with stover cell wall digestibility in European maize ( <i>Zea mays</i> L.). BMC Plant Biology, 2010, 10, 27.	3.6	32
131	Mapping of quantitative trait loci/locus conferring resistance to foxtail mosaic virus in maize using the intermated B73×Mo17 population. Plant Breeding, 2010, 129, 721-723.	1.9	5
132	Identification of novel <i>brown midrib</i> genes in maize by tests of allelism. Plant Breeding, 2010, 129, 724-726.	1.9	23
133	Nucleotide diversity and linkage disequilibrium in five <i>Lolium perenne</i> genes with putative role in shoot morphology. Plant Science, 2010, 179, 194-201.	3.6	20
134	Molecular basis of trait correlations. Trends in Plant Science, 2010, 15, 454-461.	8.8	135
135	Application of Genomics to Plant Breeding. , 2010, , 494-527.		0
136	Development and mapping of DArT markers within the Festuca - Lolium complex. BMC Genomics, 2009, 10, 473.	2.8	49
137	Validation of candidate genes putatively associated with resistance to SCMV and MDMV in maize ( <i>Zea</i> ) Tj ETQq1 1.0,784314,rgBT/Over	3.6	56
138	From dwarves to giants? Plant height manipulation for biomass yield. Trends in Plant Science, 2009, 14, 454-461.	8.8	195
139	"PolyMin": software for identification of the minimum number of polymorphisms required for haplotype and genotype differentiation. BMC Bioinformatics, 2009, 10, 176.	2.6	4
140	Expressed sequence tag-derived microsatellite markers of perennial ryegrass ( <i>Lolium perenne</i> L.). Molecular Breeding, 2008, 21, 533-548.	2.1	31
141	Functional markers in wheat: technical and economic aspects. Molecular Breeding, 2008, 22, 319-328.	2.1	29
142	Genetic characterisation of seed yield and fertility traits in perennial ryegrass ( <i>Lolium perenne</i> L.). Theoretical and Applied Genetics, 2008, 117, 781-791.	3.6	67
143	Mapping of QTL for resistance to powdery mildew and resistance gene analogues in perennial ryegrass. Plant Breeding, 2008, 127, 368-375.	1.9	16
144	Characterization of phenylpropanoid pathway genes within European maize ( <i>Zea mays</i> L.) inbreds. BMC Plant Biology, 2008, 8, 2.	3.6	51

#	ARTICLE	IF	CITATIONS
145	Functional Markers in Resistance Breeding. Progress in Botany Fortschritte Der Botanik, 2008, , 61-87.	0.3	18
146	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
147	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
148	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
149	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
150	Nucleotide diversity and linkage disequilibrium in 11 expressed resistance candidate genes in Lolium perenne. BMC Plant Biology, 2007, 7, 43.	3.6	62
151	Identification of candidate genes associated with cell wall digestibility and eQTL (expression) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Genomics, 2007, 8, 22.	2.8	77
152	Functional markers in wheat. Current Opinion in Plant Biology, 2007, 10, 211-216.	7.1	92
153	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
154	Application Of Genomics To Forage CROP Breeding For Quality Traits. , 2007, , 281-306.		0
155	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
156	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
157	Two chromosome segments confer multiple potyvirus resistance in maize. Plant Breeding, 2006, 125, 352-356.	1.9	25
158	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
159	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
160	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
161	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
162	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

#	ARTICLE	IF	CITATIONS
163	Function of genetic material: From genomics to functional markers in maize. , 2006, , 53-74.		1
164	Development and mapping of a public reference set of SSR markers in <i>Lolium perenne</i> L.. <i>Molecular Ecology Notes</i> , 2005, 5, 951-957.	1.7	52
165	Need for multidisciplinary research towards a second green revolution. <i>Current Opinion in Plant Biology</i> , 2005, 8, 337-341.	7.1	97
166	QTL mapping of vernalization response in perennial ryegrass ( <i>Lolium perenne</i> L.) reveals co-location with an orthologue of wheat VRN1. <i>Theoretical and Applied Genetics</i> , 2005, 110, 527-536.	3.6	147
167	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.	3.6	115
168	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.	2.1	36
169	Development and application of functional markers in maize. <i>Euphytica</i> , 2005, 146, 101-108.	1.2	46
170	Association between SCMV Resistance and Macroarray-based Expression Patterns in Maize Inbreds. <i>Molecular Breeding</i> , 2005, 16, 173-184.	2.1	5
171	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.	0.8	9
172	Targeted BSA mapping of <i>Scmv1</i> and <i>Scmv2</i> conferring resistance to SCMV using <i>PstI/MseI</i> compared with <i>EcoRI/MseI</i> AFLP markers. <i>Plant Breeding</i> , 2004, 123, 434-437.	1.9	10
173	Genetic diversity in cornsalad ( <i>Valerianella locusta</i> ) and related species as determined by AFLP markers. <i>Plant Breeding</i> , 2004, 123, 460-466.	1.9	26
174	Duplicate marker loci can result in incorrect locus orders on linkage maps. <i>Theoretical and Applied Genetics</i> , 2004, 109, 305-316.	3.6	9
175	Identification of genetically linked RGAs by BAC screening in maize and implications for gene cloning, mapping and MAS. <i>Theoretical and Applied Genetics</i> , 2003, 106, 1171-1177.	3.6	25
176	Saturation of two chromosome regions conferring resistance to SCMV with SSR and AFLP markers by targeted BSA. <i>Theoretical and Applied Genetics</i> , 2003, 106, 485-493.	3.6	46
177	Functional markers in plants. <i>Trends in Plant Science</i> , 2003, 8, 554-560.	8.8	640
178	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.	3.6	41
179	Conversion of AFLP fragments tightly linked to SCMV resistance genes <i>Scmv1</i> and <i>Scmv2</i> into simple PCR-based markers. <i>Theoretical and Applied Genetics</i> , 2002, 105, 1190-1195.	3.6	28
180	Function of Genetic Material: Genes Involved in Quantitative and Qualitative Resistance. <i>Progress in Botany Fortschritte Der Botanik</i> , 2002, , 80-105.	0.3	7

#	ARTICLE	IF	CITATIONS
181	QTL Mapping of Forage Traits. , 2002, , 585-600.		0
182	Influence of genetic background and heterozygosity on meiotic recombination in <i>Arabidopsis thaliana</i> . <i>Genome</i> , 2001, 44, 971-978.	2.0	28
183	Influence of genetic background and heterozygosity on meiotic recombination in <i>Arabidopsis thaliana</i> . <i>Genome</i> , 2001, 44, 971-978.	2.0	5
184	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.	1.9	51
185	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.	3.6	19
186	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.	3.5	19
187	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.	1.8	79
188	QTL mapping of resistance to <i>Sporisorium reilianum</i> in maize. <i>Theoretical and Applied Genetics</i> , 1999, 99, 593-598.	3.6	40
189	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.	3.6	39
190	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.	3.6	217
191	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
192	Quantitative Trait Loci Mapping of Resistance to Sugarcane Mosaic Virus in Maize. <i>Phytopathology</i> , 1999, 89, 660-667.	2.2	84
193	Species-Specific Detection of the Maize Pathogens <i>Sporisorium reilianum</i> and <i>Ustilago maydis</i> by Dot Blot Hybridization and PCR-Based Assays. <i>Plant Disease</i> , 1999, 83, 390-395.	1.4	34
194	Application of microsatellites from maize to teosinte and other relatives of maize. <i>Plant Breeding</i> , 1998, 117, 447-450.	1.9	29
195	Genetic basis of resistance to sugarcane mosaic virus in European maize germplasm. <i>Theoretical and Applied Genetics</i> , 1998, 96, 1151-1161.	3.6	63
196	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.	3.6	43
197	Molecular characterization of the spinach G-box binding protein family. <i>Physiologia Plantarum</i> , 1998, 103, 415-425.	5.2	0
198	Comparative Quantitative Trait Loci Mapping of Partial Resistance to <i>Puccinia sorghi</i> Across Four Populations of European Flint Maize. <i>Phytopathology</i> , 1998, 88, 1324-1329.	2.2	28

#	ARTICLE	IF	CITATIONS
199	QTL Mapping in Testcrosses of Flint Lines of Maize: III. Comparison across Populations for Forage Traits. <i>Crop Science</i> , 1998, 38, 1278-1289.	1.8	76
200	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.	1.8	66
201	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.	1.8	113
202	Evidence that the plastid signal and light operate via the same cis-acting elements in the promoters of nuclear genes for plastid proteins. <i>Molecular Genetics and Genomics</i> , 1996, 252, 631-639.	2.4	42
203	Evidence that the plastid signal and light operate via the same. <i>Molecular Genetics and Genomics</i> , 1996, 252, 631.	2.4	7
204	The Role of Plastids in the Expression of Nuclear Genes for Thylakoid Proteins Studied with Chimeric [beta]-Glucuronidase Gene Fusions. <i>Plant Physiology</i> , 1994, 105, 1355-1364.	4.8	47
205	Promoters from Genes for Plastid Proteins Possess Regions with Different Sensitivities toward Red and Blue Light. <i>Plant Physiology</i> , 1994, 104, 997-1006.	4.8	31
206	Interacting cis elements in the plastocyanin promoter from spinach ensure regulated high-level expression. <i>Molecular Genetics and Genomics</i> , 1994, 242, 602-613.	2.4	27
207	Segments encoding 5'-untranslated leaders of genes for thylakoid proteins contain cis-elements essential for transcription. <i>Plant Journal</i> , 1994, 6, 513-523.	5.7	56
208	The role of cysteine residues of spinach ferredoxin-NADP+ reductase as assessed by site-directed mutagenesis. <i>Biochemistry</i> , 1993, 32, 6374-6380.	2.5	67
209	Probing the role of lysine 116 and lysine 244 in the spinach ferredoxin-NADP+ reductase by site-directed mutagenesis. <i>Journal of Biological Chemistry</i> , 1991, 266, 17760-17763.	3.4	36
210	Maize Doubled Haploids. , 0, , 123-166.		25
211	Combining data sets for maize root seedling traits increases the power of GWAS and genomic prediction accuracies. <i>Journal of Experimental Botany</i> , 0, , .	4.8	2