

Roberto Tuberosa

List of Publications by Year in descending order

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162
papers

16,865
citations

23500

58
h-index

16127

124
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175
all docs

175
docs citations

175
times ranked

11657
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Wide Association Study Uncovers the QTLome for Osmotic Adjustment and Related Drought Adaptive Traits in Durum Wheat. <i>Genes</i> , 2022, 13, 293.	1.0	12
2	Cloning the barley <i>nec3</i> disease lesion mimic mutant using complementation by sequencing. <i>Plant Genome</i> , 2022, , e20187.	1.6	0
3	Sequence-Based Marker Assisted Selection in Wheat. , 2022, , 513-538.		3
4	Editorial: Proceedings of FSTP3 Congressâ€œA Sustainable Durum Wheat Chain for Food Security and Healthy Lives. <i>Frontiers in Plant Science</i> , 2021, 12, 675510.	1.7	0
5	Wheat root systems as a breeding target for climate resilience. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1645-1662.	1.8	74
6	High-throughput field phenotyping reveals genetic variation in photosynthetic traits in durum wheat under drought. <i>Plant, Cell and Environment</i> , 2021, 44, 2858-2878.	2.8	12
7	<i>ENHANCED GRAVITROPISM 2</i> encodes a STERILE ALPHA MOTIF-containing protein that controls root growth angle in barley and wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
8	Back Cover Image. <i>Plant, Cell and Environment</i> , 2021, 44, .	2.8	0
9	Breeding custom-designed crops for improved drought adaptation. <i>Genetics & Genomics Next</i> , 2021, 2, e202100017.	0.8	48
10	Genome-wide association analysis unveils novel QTLs for seminal root system architecture traits in Ethiopian durum wheat. <i>BMC Genomics</i> , 2021, 22, 20.	1.2	33
11	Resequencing of 145 Landmark Cultivars Reveals Asymmetric Sub-genome Selection and Strong Founder Genotype Effects on Wheat Breeding in China. <i>Molecular Plant</i> , 2020, 13, 1733-1751.	3.9	129
12	Genomic Regions Associated with the Control of Flowering Time in Durum Wheat. <i>Plants</i> , 2020, 9, 1628.	1.6	15
13	The Global Durum Wheat Panel (GDP): An International Platform to Identify and Exchange Beneficial Alleles. <i>Frontiers in Plant Science</i> , 2020, 11, 569905.	1.7	44
14	Carbon Isotope Composition and the NDVI as Phenotyping Approaches for Drought Adaptation in Durum Wheat: Beyond Trait Selection. <i>Agronomy</i> , 2020, 10, 1679.	1.3	4
15	Quantitative trait loci for agronomic traits in tetraploid wheat for enhancing grain yield in Kazakhstan environments. <i>PLoS ONE</i> , 2020, 15, e0234863.	1.1	19
16	Genome-wide association mapping for grain shape and color traits in Ethiopian durum wheat (<i>Triticum</i>) Tj ETQq0 0.0,rgBT /Overlock 10	2.3	38
17	Carotenoid Pigment Content in Durum Wheat (<i>Triticum turgidum</i> L. var <i>durum</i>): An Overview of Quantitative Trait Loci and Candidate Genes. <i>Frontiers in Plant Science</i> , 2019, 10, 1347.	1.7	59
18	Multi-Trait, Multi-Environment Genomic Prediction of Durum Wheat With Genomic Best Linear Unbiased Predictor and Deep Learning Methods. <i>Frontiers in Plant Science</i> , 2019, 10, 1311.	1.7	47

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19	Reduced response diversity does not negatively impact wheat climate resilience. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10623-10624.	3.3	11
20	Marker-Assisted Breeding in Crops. , 2019, , 453-475.		0
21	Durum wheat genome highlights past domestication signatures and future improvement targets. Nature Genetics, 2019, 51, 885-895.	9.4	576
22	Genomic tools for durum wheat breeding: de novo assembly of Svevo transcriptome and SNP discovery in elite germplasm. BMC Genomics, 2019, 20, 278.	1.2	7
23	Exploring and exploiting the genetic variation of Fusarium head blight resistance for genomic-assisted breeding in the elite durum wheat gene pool. Theoretical and Applied Genetics, 2019, 132, 969-988.	1.8	57
24	Asparagine synthetase genes (AsnS1 and AsnS2) in durum wheat: structural analysis and expression under nitrogen stress. Euphytica, 2018, 214, 1.	0.6	21
25	Dehydration survival of crop plants and its measurement. Journal of Experimental Botany, 2018, 69, 975-981.	2.4	43
26	Yield of chromosomally engineered durum wheat-Thinopyrum ponticum recombinant lines in a range of contrasting rain-fed environments. Field Crops Research, 2018, 228, 147-157.	2.3	11
27	Comparative Aerial and Ground Based High Throughput Phenotyping for the Genetic Dissection of NDVI as a Proxy for Drought Adaptive Traits in Durum Wheat. Frontiers in Plant Science, 2018, 9, 893.	1.7	117
28	Progress in understanding drought tolerance: from alleles to cropping systems. Journal of Experimental Botany, 2018, 69, 3175-3179.	2.4	40
29	Marker-Assisted Breeding in Crops. , 2018, , 1-24.		0
30	Identification of Early Represented Gluten Proteins during Durum Wheat Grain Development. Journal of Agricultural and Food Chemistry, 2017, 65, 3242-3250.	2.4	28
31	Genome-wide association mapping for seedling and field resistance to Puccinia striiformis f. sp. tritici in elite durum wheat. Theoretical and Applied Genetics, 2017, 130, 649-667.	1.8	71
32	Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. Science, 2017, 357, 93-97.	6.0	781
33	Leveraging plant genomics for better and healthier food. Current Opinion in Food Science, 2017, 16, 100-105.	4.1	5
34	<i>In vitro</i> physical mutagenesis of giant reed (<i>Arundo donax</i> L.). GCB Bioenergy, 2017, 9, 1380-1389.	2.5	12
35	Genome-wide association mapping reveals a rich genetic architecture of stripe rust resistance loci in emmer wheat (<i>Triticum turgidum</i> ssp. <i>dicoccum</i>). Theoretical and Applied Genetics, 2017, 130, 2249-2270.	1.8	80
36	Improving crop performance under drought – cross-fertilization of disciplines. Journal of Experimental Botany, 2017, 68, 1393-1398.	2.4	8

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37	Novel Sources of Stripe Rust Resistance Identified by Genome-Wide Association Mapping in Ethiopian Durum Wheat (<i>Triticum turgidum</i> ssp. <i>durum</i>). <i>Frontiers in Plant Science</i> , 2017, 8, 774.	1.7	66
38	Extending the Marker × Environment Interaction Model for Genomic-Enabled Prediction and Genome-Wide Association Analysis in Durum Wheat. <i>Crop Science</i> , 2016, 56, 2193-2209.	0.8	101
39	A multiparental cross population for mapping <i>QTL</i> for agronomic traits in durum wheat (<i>Triticum turgidum</i> ssp. <i>durum</i>). <i>Plant Biotechnology Journal</i> , 2016, 14, 735-748.	4.1	121
40	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	4.1	221
41	Genome-wide analysis of yield in Europe: allelic effects as functions of drought and heat scenarios. <i>Plant Physiology</i> , 2016, 172, pp.00621.2016.	2.3	140
42	Two major quantitative trait loci controlling the number of seminal roots in maize co-map with the root developmental genes <i>rtcs</i> and <i>rum1</i> . <i>Journal of Experimental Botany</i> , 2016, 67, 1149-1159.	2.4	40
43	Prioritizing quantitative trait loci for root system architecture in tetraploid wheat. <i>Journal of Experimental Botany</i> , 2016, 67, 1161-1178.	2.4	206
44	Genetic variation for aerenchyma and other root anatomical traits in durum wheat (<i>Triticum durum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.8	5
45	Yield QTLome distribution correlates with gene density in maize. <i>Plant Science</i> , 2016, 242, 300-309.	1.7	61
46	The Genetic Basis of Composite Spike Form in Barley and "Miracle-Wheat"™. <i>Genetics</i> , 2015, 201, 155-165.	1.2	109
47	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	1.7	243
48	The crop QTLome comes of age. <i>Current Opinion in Biotechnology</i> , 2015, 32, 179-185.	3.3	122
49	A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. <i>Plant Biotechnology Journal</i> , 2015, 13, 648-663.	4.1	386
50	Genomics Approaches to Dissect the Genetic Basis of Drought Resistance in Durum Wheat. , 2015, , 213-223.		2
51	Association Mapping Reveals Novel Stem Rust Resistance Loci in Durum Wheat at the Seedling Stage. <i>Plant Genome</i> , 2014, 7, plantgenome2013.08.0026.	1.6	67
52	Two decades of InterDrought conferences: are we bridging the genotype-to-phenotype gap?. <i>Journal of Experimental Botany</i> , 2014, 65, 6137-6139.	2.4	13
53	A MITE Transposon Insertion Is Associated with Differential Methylation at the Maize Flowering Time QTL <i>Vgt1</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 805-812.	0.8	93
54	Association mapping for root architectural traits in durum wheat seedlings as related to agronomic performance. <i>Molecular Breeding</i> , 2014, 34, 1629-1645.	1.0	115

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55	Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. <i>Plant Biotechnology Journal</i> , 2014, 12, 787-796.	4.1	1,828
56	QTL dissection of yield components and morpho-physiological traits in a durum wheat elite population tested in contrasting thermo-pluviometric conditions. <i>Crop and Pasture Science</i> , 2014, 65, 80.	0.7	79
57	Genomics of plant genetic resources: a gateway to a new era of global food security. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S2-S5.	0.4	4
58	Durum wheat genomics comes of age. <i>Molecular Breeding</i> , 2014, 34, 1527-1530.	1.0	23
59	A consensus framework map of durum wheat (<i>Triticum durum</i> Desf.) suitable for linkage disequilibrium analysis and genome-wide association mapping. <i>BMC Genomics</i> , 2014, 15, 873.	1.2	85
60	Strategies to increase the yield and yield stability of crops under drought – are we making progress?. <i>Functional Plant Biology</i> , 2014, 41, 1199.	1.1	32
61	New Starch Phenotypes Produced by TILLING in Barley. <i>PLoS ONE</i> , 2014, 9, e107779.	1.1	59
62	Systems Responses to Progressive Water Stress in Durum Wheat. <i>PLoS ONE</i> , 2014, 9, e108431.	1.1	52
63	Development of COS-SNP and HRM markers for high-throughput and reliable haplotype-based detection of Lr14a in durum wheat (<i>Triticum durum</i> Desf.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1077-1101.	1.8	43
64	Searching for novel sources of field resistance to Ug99 and Ethiopian stem rust races in durum wheat via association mapping. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1237-1256.	1.8	116
65	Sequence-based SNP genotyping in durum wheat. <i>Plant Biotechnology Journal</i> , 2013, 11, 809-817.	4.1	63
66	Marker-Assisted breeding/breed, see also animal breeding marker-assisted Breeding breeding/breed, see also animal breeding in <i>Crops</i> . , 2013, , 1158-1181.		1
67	Phenotyping for drought tolerance of crops in the genomics era. <i>Frontiers in Physiology</i> , 2012, 3, 347.	1.3	448
68	Biotechnology for enhancing plant production and food quality: IBS 2010 part III. <i>Journal of Biotechnology</i> , 2012, 159, 249-250.	1.9	0
69	Can genomics boost productivity of orphan crops?. <i>Nature Biotechnology</i> , 2012, 30, 1172-1176.	9.4	248
70	Biotechnology for a more sustainable world. <i>Biotechnology Advances</i> , 2012, 30, 931-932.	6.0	12
71	Genetic analysis of Soil-Borne Cereal Mosaic Virus response in durum wheat: evidence for the role of the major quantitative trait locus QSbm.ubo-2BS and of minor quantitative trait loci. <i>Molecular Breeding</i> , 2012, 29, 973-988.	1.0	11
72	Genomics of Root Architecture and Functions in Maize. , 2011, , 179-204.		14

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73	Resistance to Soil-borne cereal mosaic virus in durum wheat is controlled by a major QTL on chromosome arm 2BS and minor loci. <i>Theoretical and Applied Genetics</i> , 2011, 123, 527-544.	1.8	25
74	High-throughput SNP discovery and genotyping in durum wheat (<i>Triticum durum</i> Desf.). <i>Theoretical and Applied Genetics</i> , 2011, 123, 555-569.	1.8	120
75	Genetic dissection of maize phenology using an intraspecific introgression library. <i>BMC Plant Biology</i> , 2011, 11, 4.	1.6	63
76	Genomics of plant genetic resources: an introduction. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 151-154.	0.4	18
77	Starch metabolism mutants in barley: A TILLING approach. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 170-173.	0.4	7
78	Association mapping in durum wheat grown across a broad range of water regimes. <i>Journal of Experimental Botany</i> , 2011, 62, 409-438.	2.4	270
79	Identification of root morphology mutants in barley. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2011, 9, 357-360.	0.4	6
80	Association mapping of leaf rust response in durum wheat. <i>Molecular Breeding</i> , 2010, 26, 189-228.	1.0	86
81	Dissection and modelling of abiotic stress tolerance in plants. <i>Current Opinion in Plant Biology</i> , 2010, 13, 206-212.	3.5	281
82	TILLMore: a Forward- and a Reverse-Genetics Resource for the Identification of Root Morphology-Related Mutants. <i>Journal of Biotechnology</i> , 2010, 150, 497-497.	1.9	0
83	Starch Metabolism Mutants in Barley: a TILLING Approach. <i>Journal of Biotechnology</i> , 2010, 150, 497-498.	1.9	0
84	Fine mapping approaches of two major QTLs for yield in durum wheat. <i>Journal of Biotechnology</i> , 2010, 150, 501-502.	1.9	1
85	1 out of 27 "European politicians score poorly in agbiotech. <i>Nature Biotechnology</i> , 2010, 28, 551-552.	9.4	1
86	Understanding the relationships between genetic and phenotypic structures of a collection of elite durum wheat accessions. <i>Field Crops Research</i> , 2010, 119, 91-105.	2.3	54
87	Virulence Phenotypes and Molecular Genotypes in Collections of <i>Puccinia triticina</i> from Italy. <i>Plant Disease</i> , 2010, 94, 420-424.	0.7	26
88	Characterization of root-yield-1.06, a major constitutive QTL for root and agronomic traits in maize across water regimes. <i>Journal of Experimental Botany</i> , 2010, 61, 3553-3562.	2.4	79
89	Genetic and genomic dissection of maize root development and architecture. <i>Current Opinion in Plant Biology</i> , 2009, 12, 172-177.	3.5	230
90	Genome studies and molecular genetics "from sequence to crops: genomics comes of age. <i>Current Opinion in Plant Biology</i> , 2009, 12, 103-106.	3.5	23

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91	Genomics of Tolerance to Abiotic Stress in the Triticeae. , 2009, , 481-558.		8
92	QTL for Agronomic Traits in Maize Production. , 2009, , 501-541.		28
93	An integrated DArT-SSR linkage map of durum wheat. <i>Molecular Breeding</i> , 2008, 22, 629-648.	1.0	97
94	A major QTL for durable leaf rust resistance widely exploited in durum wheat breeding programs maps on the distal region of chromosome arm 7BL. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1225-1240.	1.8	59
95	Vivipary as a tool to analyze late embryogenic events in maize. <i>Heredity</i> , 2008, 101, 465-470.	1.2	23
96	TILLMore, a resource for the discovery of chemically induced mutants in barley. <i>Plant Biotechnology Journal</i> , 2008, 6, 477-485.	4.1	177
97	Translational research impacting on crop productivity in drought-prone environments. <i>Current Opinion in Plant Biology</i> , 2008, 11, 171-179.	3.5	324
98	Principles and practices of plant genomics. Volume 1. Genome mapping. <i>Annals of Botany</i> , 2008, 102, 879-880.	1.4	0
99	Quantitative Trait Loci and Crop Performance under Abiotic Stress: Where Do We Stand?: Table I.. <i>Plant Physiology</i> , 2008, 147, 469-486.	2.3	518
100	Quantitative Trait Loci for Grain Yield and Adaptation of Durum Wheat (<i>Triticum durum</i> Desf.) Across a Wide Range of Water Availability. <i>Genetics</i> , 2008, 178, 489-511.	1.2	397
101	Conserved noncoding genomic sequences associated with a flowering-time quantitative trait locus in maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 11376-11381.	3.3	536
102	Genome-wide Approaches to Investigate and Improve Maize Response to Drought. <i>Crop Science</i> , 2007, 47, S-120.	0.8	48
103	Root system architecture: opportunities and constraints for genetic improvement of crops. <i>Trends in Plant Science</i> , 2007, 12, 474-481.	4.3	608
104	Cloning Qtls in Plants. , 2007, , 207-225.		33
105	Relationships among durum wheat accessions. II. A comparison of molecular and pedigree information. <i>Genome</i> , 2007, 50, 385-399.	0.9	18
106	Relationships among durum wheat accessions. I. Comparative analysis of SSR, AFLP, and phenotypic data. <i>Genome</i> , 2007, 50, 373-384.	0.9	37
107	Improving water use efficiency in Mediterranean agriculture: what limits the adoption of new technologies?. <i>Annals of Applied Biology</i> , 2007, 150, 157-162.	1.3	49
108	Genetic dissection of seminal root architecture in elite durum wheat germplasm. <i>Annals of Applied Biology</i> , 2007, 151, 291-305.	1.3	115

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109	Dissecting Qtls For Tolerance to Drought and Salinity. , 2007, , 381-411.		9
110	Genomics-Assisted Crop Improvement: An Overview. , 2007, , 1-12.		18
111	Nucleotide-binding site (NBS) profiling of genetic diversity in durum wheat. <i>Genome</i> , 2006, 49, 1473-1480.	0.9	26
112	A panel of elite accessions of durum wheat (<i>Triticum durum</i> Desf.) suitable for association mapping studies. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2006, 4, 79-85.	0.4	54
113	Genomics-based approaches to improve drought tolerance of crops. <i>Trends in Plant Science</i> , 2006, 11, 405-412.	4.3	478
114	Validation of Quantitative Trait Loci for Multiple Disease Resistance in Barley Using Advanced Backcross Lines Developed with a Wild Barley. <i>Crop Science</i> , 2006, 46, 1179-1186.	0.8	47
115	Distribution of β -amylase I haplotypes among European cultivated barleys. <i>Molecular Breeding</i> , 2006, 18, 341-354.	1.0	20
116	Barley transcript profiles under dehydration shock and drought stress treatments: a comparative analysis. <i>Journal of Experimental Botany</i> , 2006, 58, 229-240.	2.4	201
117	Root-ABA1 QTL affects root lodging, grain yield, and other agronomic traits in maize grown under well-watered and water-stressed conditions. <i>Journal of Experimental Botany</i> , 2006, 58, 319-326.	2.4	89
118	Genetic evaluation of root complexity in maize. <i>Acta Agronomica Hungarica: an International Multidisciplinary Journal in Agricultural Science</i> , 2006, 54, 291-303.	0.2	25
119	A high-density genetic map of hexaploid wheat (<i>Triticum aestivum</i> L.) from the cross Chinese Spring \times SQ1 and its use to compare QTLs for grain yield across a range of environments. <i>Theoretical and Applied Genetics</i> , 2005, 110, 865-880.	1.8	437
120	Population structure and long-range linkage disequilibrium in a durum wheat elite collection. <i>Molecular Breeding</i> , 2005, 15, 271-290.	1.0	212
121	Validation and characterization of a major QTL affecting leaf ABA concentration in maize. <i>Molecular Breeding</i> , 2005, 15, 291-303.	1.0	59
122	Root-ABA1, a major constitutive QTL, affects maize root architecture and leaf ABA concentration at different water regimes. <i>Journal of Experimental Botany</i> , 2005, 56, 3061-3070.	2.4	165
123	To clone or not to clone plant QTLs: present and future challenges. <i>Trends in Plant Science</i> , 2005, 10, 297-304.	4.3	487
124	Genotype and phenotype associations with drought tolerance in barley tested in North Africa. <i>Annals of Applied Biology</i> , 2004, 144, 157-168.	1.3	108
125	Identification of <i>Hordeum spontaneum</i> QTL alleles improving field performance of barley grown under rainfed conditions. <i>Annals of Applied Biology</i> , 2004, 144, 309-319.	1.3	101
126	QTLs and Genes for Tolerance to Abiotic Stress in Cereals. , 2004, , 253-315.		9

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127	Extension of the Messapia x dicoccoides linkage map of Triticum turgidum (L.) Thell. Cellular and Molecular Biology Letters, 2004, 9, 529-41.	2.7	18
128	Searching for quantitative trait loci controlling root traits in maize: a critical appraisal. Plant and Soil, 2003, 255, 35-54.	1.8	104
129	Microsatellite analysis reveals a progressive widening of the genetic basis in the elite durum wheat germplasm. Theoretical and Applied Genetics, 2003, 107, 783-797.	1.8	104
130	Searching for quantitative trait loci controlling root traits in maize: a critical appraisal. , 2003, , 35-54.		14
131	Unravelling the Genetic Basis of Drought Tolerance in Crops. , 2003, , 71-122.		11
132	Mapping QTLs Regulating Morpho-physiological Traits and Yield: Case Studies, Shortcomings and Perspectives in Drought-stressed Maize. Annals of Botany, 2002, 89, 941-963.	1.4	331
133	Genetic diversity in cultivars and landraces of Oryza sativa subsp. indica as revealed by AFLP markers. Genome, 2002, 45, 451-459.	0.9	34
134	Cereal genomics: ushering in a brave new world. Plant Molecular Biology, 2002, 48, 445-449.	2.0	37
135	Toward positional cloning of Vgt1, a QTL controlling the transition from the vegetative to the reproductive phase in maize. Plant Molecular Biology, 2002, 48, 601-613.	2.0	116
136	Monitoring large-scale changes in transcript abundance in drought- and salt-stressed barley. Plant Molecular Biology, 2002, 48, 551-573.	2.0	503
137	Comparative genomic mapping between a 754 kb region flanking DREB1A in Arabidopsis thaliana and maize. Plant Molecular Biology, 2002, 48, 741-750.	2.0	19
138	Identification of QTLs for root characteristics in maize grown in hydroponics and analysis of their overlap with QTLs for grain yield in the field at two water regimes. Plant Molecular Biology, 2002, 48, 697-712.	2.0	285
139	Direct and Correlated Responses to Divergent Selection for Leaf Abscisic Acid Concentration in Two Maize Populations. Crop Science, 2001, 41, 335-344.	0.8	32
140	Title is missing!. Molecular Breeding, 2001, 8, 169-176.	1.0	24
141	Genetic Diversity of Japanese Barley Cultivars Based on SSR Analysis.. Breeding Science, 2001, 51, 215-218.	0.9	7
142	Comparative Analyses of the Genetic Diversity among European Spelt and Wheat Accessions with AFLP, RFLP and SSR Markers. Developments in Plant Breeding, 2001, , 733-738.	0.2	1
143	Integration of AFLP markers into an RFLP-based map of durum wheat. Plant Breeding, 2000, 119, 393-401.	1.0	31
144	The development and application of molecular markers for abiotic stress tolerance in barley. Journal of Experimental Botany, 2000, 51, 19-27.	2.4	117

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145	The development and application of molecular markers for abiotic stress tolerance in barley. <i>Journal of Experimental Botany</i> , 2000, 51, 19-27.	2.4	29
146	QTL analysis of drought-related traits and grain yield in relation to genetic variation for leaf abscisic acid concentration in field-grown maize. <i>Journal of Experimental Botany</i> , 1999, 50, 1289-1297.	2.4	86
147	RFLP mapping of quantitative trait loci controlling abscisic acid concentration in leaves of drought-stressed maize (<i>Zea mays</i> L.). <i>Theoretical and Applied Genetics</i> , 1998, 97, 744-755.	1.8	105
148	Comparative analysis of genetic relationships in barley based on RFLP and RAPD markers. <i>Genome</i> , 1997, 40, 607-616.	0.9	29
149	Genetic and environmental effects on abscisic acid accumulation in leaves of field-grown maize. <i>Euphytica</i> , 1994, 78, 81-89.	0.6	11
150	Recurrent Selection for Regeneration Capacity from Immature Embryo-Derived Calli in Maize. <i>Crop Science</i> , 1994, 34, 343-347.	0.8	13
151	Abscisic Acid Concentration in Leaf and Xylem Sap, Leaf Water Potential, and Stomatal Conductance in Maize. <i>Crop Science</i> , 1994, 34, 1557-1563.	0.8	20
152	Involvement of Chromosomes 5A and 5D in Cold-Induced Abscisic Acid Accumulation in and Frost Tolerance of Wheat Calli. <i>Plant Breeding</i> , 1993, 110, 237-242.	1.0	35
153	Effect of Abscisic Acid on Pollen Germination and Tube Growth of Maize Genotypes1. <i>Plant Breeding</i> , 1993, 110, 250-254.	1.0	22
154	Number of endosperm cells and endosperm abscisic acid content in relation to kernel weight in four barley genotypes. <i>European Journal of Agronomy</i> , 1992, 1, 125-132.	1.9	14
155	Chlorsulfuron Tolerance and Acetolactate Synthase Activity in Corn (<i>Zea mays</i> L.) Inbred Lines. <i>Weed Science</i> , 1991, 39, 553-557.	0.8	20
156	Comparison between responses to gametophytic and sporophytic recurrent selection in maize (<i>Zea</i>)	1.8	22
157	Abscisic acid in developing grains of wheat and barley genotypes differing in grain weight. <i>Plant Growth Regulation</i> , 1988, 7, 3-17.	1.8	26
158	Direct and Correlated Responses to Four Cycles of Divergent Selection for Heading Date in Barley*. <i>Plant Breeding</i> , 1988, 101, 313-320.	1.0	0
159	Divergent Selection for Heading Date in Barley. <i>Plant Breeding</i> , 1986, 97, 345-351.	1.0	5
160	Registration of GaspÃ© Flint 1.1.1, a small-size early-flowering maize inbred line. <i>Journal of Plant Registrations</i> , 0, , .	0.4	1
161	From QTLs to Genes Controlling Root Traits in Maize. , 0, , 15-24.		16
162	Molecular Bases of Plant Adaptation to Abiotic Stress and Approaches to Enhance Tolerance to Hostile Environments. , 0, , .		1