Guijun Yan

List of Publications by Year
in descending order

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175 papers	4,378 citations	109311 35 h-index	161844 54 g-index
179 all docs	179 docs citations	179 times ranked	4620 citing authors

#	Article	IF	Citations
1	The complex jujube genome provides insights into fruit tree biology. Nature Communications, 2014, 5, 5315.	12.8	251
2	Flower numbers, pod production, pollen viability, and pistil function are reduced and flower and pod abortion increased in chickpea (Cicer arietinum L.) under terminal drought. Journal of Experimental Botany, 2010, 61, 335-345.	4.8	193
3	Antioxidant activity and phenolics of an endophytic Xylaria sp. from Ginkgo biloba. Food Chemistry, 2007, 105, 548-554.	8.2	187
4	Production of viable male unreduced gametes in Brassica interspecific hybrids is genotype specific and stimulated by cold temperatures. BMC Plant Biology, 2011, 11, 103.	3.6	109
5	Sequencing consolidates molecular markers with plant breeding practice. Theoretical and Applied Genetics, 2015, 128, 779-795.	3.6	96
6	Transcriptomics Analyses Reveal Wheat Responses to Drought Stress during Reproductive Stages under Field Conditions. Frontiers in Plant Science, 2017, 8, 592.	3.6	93
7	Mapping a major gene for growth habit and QTLs for ascochyta blight resistance and flowering time in a population between chickpea and Cicer reticulatum. Euphytica, 2010, 173, 307-319.	1.2	90
8	Trigenomic Bridges forBrassicaImprovement. Critical Reviews in Plant Sciences, 2011, 30, 524-547.	5.7	83
9	Accelerated Generation of Selfed Pure Line Plants for Gene Identification and Crop Breeding. Frontiers in Plant Science, 2017, 8, 1786.	3.6	81
10	Identification of Putative Candidate Genes for Water Stress Tolerance in Canola (Brassica napus). Frontiers in Plant Science, 2015, 6, 1058.	3.6	73
11	Salicylic acid mediates antioxidant defense system and ABA pathway related gene expression in Oryza sativa against quinclorac toxicity. Ecotoxicology and Environmental Safety, 2016, 133, 146-156.	6.0	73
12	Changes in Î´15N in a soilâ€“plant system under different biochar feedstocks and application rates. Biology and Fertility of Soils, 2014, 50, 275-283.	4.3	70
13	Allelic Variations of a Light Harvesting Chlorophyll A/B-Binding Protein Gene (Lhcb1) Associated with Agronomic Traits in Barley. PLoS ONE, 2012, 7, e37573.	2.5	69
14	Genome structure affects the rate of autosyndesis and allosyndesis in AABC, BBAC and CCAB Brassica interspecific hybrids. Chromosome Research, 2010, 18, 655-666.	2.2	65
15	Both Male and Female Malfunction Contributes to Yield Reduction under Water Stress during Meiosis in Bread Wheat. Frontiers in Plant Science, 2016, 7, 2071.	3.6	65
16	Highâ€throughput genotyping for species identification and diversity assessment in germplasm collections. Molecular Ecology Resources, 2015, 15, 1091-1101.	4.8	64
17	Microspore culture preferentially selects unreduced (2n) gametes from an interspecific hybrid of Brassica napus L.ÂÂ—ÂBrassica carinata Braun. Theoretical and Applied Genetics, 2009, 119, 497-505.	3.6	63
18	Genetic analysis of pod and seed resistance to pea weevil in a Pisum sativumÃ—P. fulvum interspecific cross. Australian Journal of Agricultural Research, 2008, 59, 854.	1.5	59

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19	A novel fibrinolytic enzyme from Cordyceps militaris, a Chinese traditional medicinal mushroom. World Journal of Microbiology and Biotechnology, 2008, 24, 483-489.	3.6	49
20	Geographical patterns of genetic variation in the world collections of wild annual Cicer characterized by amplified fragment length polymorphisms. Theoretical and Applied Genetics, 2005, 110, 381-391.	3.6	48
21	A preliminary assessment of the potential of using an acaciaâ€"biochar system for spent mine site rehabilitation. Environmental Science and Pollution Research, 2015, 22, 2138-2144.	5.3	47
22	GmPAP4, a novel purple acid phosphatase gene isolated from soybean (Glycine max), enhanced extracellular phytate utilization in Arabidopsis thaliana. Plant Cell Reports, 2014, 33, 655-667.	5.6	45
23	Screening Wheat (Triticum spp.) Genotypes for Root Length under Contrasting Water Regimes: Potential Sources of Variability for Drought Resistance Breeding. Journal of Agronomy and Crop Science, 2015, 201, 189-194.	3.5	44
24	QTL Conferring Fusarium Crown Rot Resistance in the Elite Bread Wheat Variety EGA Wylie. PLoS ONE, 2014, 9, e96011.	2.5	43
25	Different Tolerance in Bread Wheat, Durum Wheat and Barley to Fusarium Crown Rot Disease Caused by Fusarium pseudograminearum. Journal of Phytopathology, 2012, 160, 412-417.	1.0	42
26	Genome-wide identification of MYB genes and expression analysis under different biotic and abiotic stresses in Helianthus annuus L.. Industrial Crops and Products, 2020, 143, 111924.	5.2	42
27	Transcriptome and Allele Specificity Associated with a 3BL Locus for Fusarium Crown Rot Resistance in Bread Wheat. PLoS ONE, 2014, 9, e113309.	2.5	42
28	Molecular Variation and Fingerprinting of Leucadendron Cultivars (Proteaceae) by ISSR Markers. Annals of Botany, 2005, 95, 1163-1170.	2.9	41
29	Fine mapping of a large-effect QTL conferring Fusarium crown rot resistance on the long arm of chromosome 3B in hexaploid wheat. BMC Genomics, 2015, 16, 850.	2.8	40
30	Mapping QTL for cotton fiber quality traits using simple sequence repeat markers, conserved intron-scanning primers, and transcript-derived fragments. Euphytica, 2015, 201, 215-230.	1.2	40
31	Genetic and signalling pathways of dry fruit size: targets for genome editingâ€based crop improvement. Plant Biotechnology Journal, 2020, 18, 1124-1140.	8.3	40
32	Karyotype evolution in the genus Boronia (Rutaceae). Botanical Journal of the Linnean Society, 2003, 142, 309-320.	1.6	39
33	Genotypic effects on the frequency of homoeologous and homologous recombination in Brassica napusÂÃ—Â B. carinata hybrids. Theoretical and Applied Genetics, 2011, 122, 543-553.	3.6	39
34	Genetic variations of HvP5CS1 and their association with drought tolerance related traits in barley (Hordeum vulgare L.). Scientific Reports, 2017, 7, 7870.	3.3	39
35	Categorization of wheat genotypes for phosphorus efficiency. PLoS ONE, 2018, 13, e0205471.	2.5	39
36	Application of RAPD and ISSR markers to analyse molecular relationships in Grevillea (Proteaceae). Australian Systematic Botany, 2004, 17, 49.	0.9	38

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37	Major genomic regions responsible for wheat yield and its components as revealed by meta-QTL and genotypeâ€“phenotype association analyses. Planta, 2020, 252, 65.	3.2	37
38	Successful induction of trigenomic hexaploid Brassica from a triploid hybrid of B. napus L. and B. nigra (L.) Koch. Euphytica, 2010, 176, 87-98.	1.2	36
39	Development of a sequence-specific PCR marker linked to the gene â€œpauperâ€•conferring low-alkaloids in white lupin (Lupinus albus L.) for marker assisted selection. Molecular Breeding, 2009, 23, 153-161.	2.1	35
40	Large-scale density-based screening for pea weevil resistance in advanced backcross lines derived from cultivated field pea (Pisum sativum) and Pisum fulvum. Crop and Pasture Science, 2012, 63, 612.	1.5	34
41	A fast generation cycling system for oat and triticale breeding. Plant Breeding, 2016, 135, 574-579.	1.9	34
42	Genome-Wide Association Mapping of Major Root Length QTLs Under PEG Induced Water Stress in Wheat. Frontiers in Plant Science, 2018, 9, 1759.	3.6	34
43	Biochar nutrient availability rather than its water holding capacity governs the growth of both C3 and C4 plants. Journal of Soils and Sediments, 2016, 16, 801-810.	3.0	33
44	Identification and validation of root length QTLs for water stress resistance in hexaploid wheat (Titicum aestivum L.). Euphytica, 2017, 213, 1.	1.2	33
45	Characteristics of membrane-bound fatty acid desaturase (FAD) genes in Brassica napus L. and their expressions under different cadmium and salinity stresses. Environmental and Experimental Botany, 2019, 162, 144-156.	4.2	33
46	A new method for producing allohexaploid Brassica through unreduced gametes. Euphytica, 2012, 186, 277-287.	1.2	32
47	Carrot browning on simulated market shelf and during cold storage. Journal of the Science of Food and Agriculture, 2005, 85, 16-20.	3.5	31
48	Numerically unreduced (2n) gametes and sexual polyploidization in Actinidia. Euphytica, 1997, 96, 267-272.	1.2	30
49	Fingerprinting of cauliflower cultivars using RAPD markers. Australian Journal of Agricultural Research, 2004, 55, 117.	1.5	30
50	Development of a DNA marker tightly linked to low-alkaloid gene iucundus in narrow-leafed lupin (Lupinus angustifolius L.) for marker-assisted selection. Crop and Pasture Science, 2011, 62, 218.	1.5	30
51	Identification and validation of a major chromosome region for high grain number per spike under meiotic stage water stress in wheat (Triticum aestivum L.). PLoS ONE, 2018, 13, e0194075.	2.5	30
52	New reports of chromosome numbers inActinidia(Actinidiaceae). New Zealand Journal of Botany, 1997, 35, 181-186.	1.1	28
53	Development of sequence-specific PCR markers associated with a polygenic controlled trait for marker-assisted selection using a modified selective genotyping strategy: a case study on anthracnose disease resistance in white lupin (Lupinus albus L.). Molecular Breeding, 2010, 25, 239-249.	2.1	28
54	Single Nucleotide Polymorphisms in HSP17.8 and Their Association with Agronomic Traits in Barley. PLoS ONE, 2013, 8, e56816.	2.5	27

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55	Responses of canola (Brassica napus L.) cultivars under contrasting temperature regimes during early seedling growth stage as revealed by multiple physiological criteria. Acta Physiologiae Plantarum, 2015, 37, 1.	2.1	27
56	Aluminium Effects on Pollen Germination and Tube Growth of Chamelaucium uncinatum. A Comparison with Other Ca2+Antagonists. Annals of Botany, 1999, 84, 559-564.	2.9	26
57	Use of variogram analysis to classify field peas with and without internal defects caused by weevil infestation. Journal of Food Engineering, 2014, 123, 17-22.	5.2	25
58	Identification of genome regions controlling cotyledon, pod wall/seed coat and pod wall resistance to pea weevil through QTL mapping. Theoretical and Applied Genetics, 2014, 127, 489-497.	3.6	25
59	Development of a co-dominant DNA marker tightly linked to gene tardus conferring reduced pod shattering in narrow-leafed lupin (Lupinus angustifolius L.). Euphytica, 2010, 176, 49-58.	1.2	24
60	Characterization of Brassica nigra collections using simple sequence repeat markers reveals distinct groups associated with geographical location, and frequent mislabelling of species identity. Genome, 2011, 54, 50-63.	2.0	24
61	A fully in vitro protocol towards large scale production of recombinant inbred lines in wheat (Triticum aestivum L.). Plant Cell, Tissue and Organ Culture, 2017, 128, 655-661.	2.3	24
62	Diploid female gametes induced by colchicine in Oriental lilies. Scientia Horticulturae, 2007, 114, 50-53.	3.6	23
63	Genetic diversity, seed traits and salinity tolerance of Millettia pinnata (L.) Panigrahi, a biodiesel tree. Genetic Resources and Crop Evolution, 2013, 60, 677-692.	1.6	23
64	In situ hybridization in Actinidia using repeat DNA and genomic probes. Theoretical and Applied Genetics, 1997, 94, 507-513.	3.6	22
65	A molecular marker linked to the mollis gene conferring soft-seediness for marker-assisted selection applicable to a wide range of crosses in lupin (Lupinus angustifolius L.) breeding. Molecular Breeding, 2012, 29, 361-370.	2.1	22
66	Cyto-evolution of Boronia genomes revealed by fluorescent in situ hybridization with rDNA probes. Genome, 2003, 46, 507-513.	2.0	21
67	Salsola tragus or S. australis (Chenopodiaceae) in Australiaâ€"untangling taxonomic confusion through molecular and cytological analyses. Australian Journal of Botany, 2008, 56, 600.	0.6	21
68	Putative interchromosomal rearrangements in the hexaploid wheat (Triticum aestivum L.) genotype â€˜Chinese Springâ€™ revealed by gene locations on homoeologous chromosomes. BMC Evolutionary Biology, 2015, 15, 37.	3.2	21
69	The first genetic map of a synthesized allohexaploid Brassica with A, B and C genomes based on simple sequence repeat markers. Theoretical and Applied Genetics, 2016, 129, 689-701.	3.6	21
70	Improvement of Soil Physical Properties and Aggregate-Associated C, N, and P After Cropland was Converted to Grassland in Semiarid Loess Plateau. Soil Science, 2010, 175, 99-104.	0.9	20
71	Enhancing Fusarium crown rot resistance by pyramiding large-effect QTL in common wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Ove	2.1	20
72	Multiple Near-Isogenic Lines Targeting a QTL Hotspot of Drought Tolerance Showed Contrasting Performance Under Post-anthesis Water Stress. Frontiers in Plant Science, 2019, 10, 271.	3.6	20

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73	Molecular characterization and phylogenetic analysis of active y-type high molecular weight glutenin subunit genes at Glu-A1 locus in wheat. Journal of Cereal Science, 2019, 86, 9-14.	3.7	20
74	Chromosome number and size variations in the Australian Salicornioideae (Chenopodiaceae)â€"evidence of polyploidisation. Australian Journal of Botany, 2003, 51, 441.	0.6	19
75	Diallel analyses reveal the genetic control of resistance to ascochyta blight in diverse chickpea and wild Cicer species. Euphytica, 2007, 154, 195-205.	1.2	19
76	Importance of Spatial and Spectral Data Reduction in the Detection of Internal Defects in Food Products. Applied Spectroscopy, 2015, 69, 473-480.	2.2	19
77	Characterization of Tomentosa cherry (Prunus tomentosa Thunb.) genotypes using SSR markers and morphological traits. Scientia Horticulturae, 2008, 118, 39-47.	3.6	18
78	Differential Recovery of Lupin Proteins from the Gluten Matrix in Lupinâ€"Wheat Bread As Revealed by Mass Spectrometry and Two-Dimensional Electrophoresis. Journal of Agricultural and Food Chemistry, 2011, 59, 6696-6704.	5.2	18
79	Identification and validation of QTL and their associated genes for pre-emergent metribuzin tolerance in hexaploid wheat (Triticum aestivum L.). BMC Genetics, 2018, 19, 102.	2.7	18
80	A High-Density Genetic Map of an Allohexaploid Brassica Doubled Haploid Population Reveals Quantitative Trait Loci for Pollen Viability and Fertility. Frontiers in Plant Science, 2018, 9, 1161.	3.6	18
81	Phenotypic and genotypic characterization of near-isogenic lines targeting a major 4BL QTL responsible for pre-harvest sprouting in wheat. BMC Plant Biology, 2019, 19, 348.	3.6	18
82	Genome-wide investigation and expression analysis of membrane-bound fatty acid desaturase genes under different biotic and abiotic stresses in sunflower (Helianthus annuus L.). International Journal of Biological Macromolecules, 2021, 175, 188-198.	7.5	18
83	Seed dormancy in barley is dictated by genetics, environments and their interactions. Euphytica, 2014, 197, 355-368.	1.2	17
84	Root transcriptome profiling of contrasting wheat genotypes provides an insight to their adaptive strategies to water deficit. Scientific Reports, 2020, 10, 4854.	3.3	17
85	Development of DNA fingerprinting keys for the identification of radish cultivars. Australian Journal of Experimental Agriculture, 2004, 44, 95.	1.0	16
86	Discovery of Novel Bmy1 Alleles Increasing Î²-Amylase Activity in Chinese Landraces and Tibetan Wild Barley for Improvement of Malting Quality via MAS. PLoS ONE, 2013, 8, e72875.	2.5	15
87	Morphological Features and Biomass Partitioning of Lucerne Plants (Medicago sativa L.) Subjected to Water Stress. Agronomy, 2020, 10, 322.	3.0	15
88	Genetic differentiation among morphological variants of Acacia saligna (Mimosaceae). Tree Genetics and Genomes, 2006, 2, 109-119.	1.6	14
89	Comparative analysis of genetic diversity between Qinghai-Tibetan wild and Chinese landrace barley. Genome, 2009, 52, 849-861.	2.0	14
90	Trigenomic hybrids from interspecific crosses between Brassica napus and B. nigra. Crop and Pasture Science, 2010, 61, 464.	1.5	14

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91	Comparative proteome analysis of seed storage and allergenic proteins among four narrow-leafed lupin cultivars. Food Chemistry, 2012, 135, 1230-1238.	8.2	14
92	Phenotypic and genotypic characterisation of root nodule bacteria nodulating Millettia pinnata (L.) Panigrahi, a biodiesel tree. Plant and Soil, 2013, 367, 363-377.	3.7	14
93	Enhancement of genetic diversity in canola-quality Brassica napus and B. juncea by interspecific hybridisation. Australian Journal of Agricultural Research, 2008, 59, 918.	1.5	14
94	Wheat Proteomics for Abiotic Stress Tolerance and Root System Architecture: Current Status and Future Prospects. Proteomes, 2022, 10, 17.	3.5	14
95	Genetic diversity of Indonesian cauliflower cultivars and their relationships with hybrid cultivars grown in Australia. Scientia Horticulturae, 2006, 108, 143-150.	3.6	13
96	Karyotypes in Leucadendron (Proteaceae): evidence of the primitiveness of the genus. Botanical Journal of the Linnean Society, 2006, 151, 387-394.	1.6	13
97	Development of a coâ€dominant DNA marker linked to the gene lentus conferring reduced pod shattering for markerâ€assisted selection in narrowâ€leafed lupin (Lupinus angustifolius) breeding. Plant Breeding, 2012, 131, 540-544.	1.9	13
98	Impact of increased temperature on spring wheat yield in northern China. Food and Energy Security, 2021, 10, 368-378.	4.3	13
99	First Report of Bituminaria Witches'-Broom in Australia Caused by a 16SrII Phytoplasma. Plant Disease, 2011, 95, 226-226.	1.4	13
100	Identification of new metribuzin-tolerant wheat (Triticum spp.) genotypes. Crop and Pasture Science, 2017, 68, 401.	1.5	12
101	Development of near-isogenic lines targeting a major QTL on 3AL for pre-harvest sprouting resistance in bread wheat. Crop and Pasture Science, 2018, 69, 864.	1.5	12
102	Inheritance of pre-emergent metribuzin tolerance and putative gene discovery through high-throughput SNP array in wheat (Triticum aestivum L.). BMC Plant Biology, 2019, 19, 457.	3.6	12
103	Roots of Lucerne Seedlings are More Resilient to a Water Deficit than Leaves or Stems. Agronomy, 2019, 9, 123.	3.0	12
104	Characterization of near-isogenic lines confirmed QTL and revealed candidate genes for plant height and yield-related traits in common wheat. Molecular Breeding, 2021, 41, 1.	2.1	12
105	Comparative transcriptome analyses for metribuzin tolerance provide insights into key genes and mechanisms restoring photosynthetic efficiency in bread wheat (Triticum aestivum L.). Genomics, 2021, 113, 910-918.	2.9	12
106	Interspecific Hybridisation of Boronias. Australian Journal of Botany, 1999, 47, 851.	0.6	11
107	New methods for comparison of chromosomes within and between species. Caryologia, 2003, 56, 227-231.	0.3	11
108	Successful stem cutting propagation of chickpea, its wild relatives and their interspecific hybrids. Australian Journal of Experimental Agriculture, 2006, 46, 1349.	1.0	11

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109	Performance of Ethiopian bread wheat (Tritium aestivum L.) genotypes under contrasting water regimes: potential sources of variability for drought resistance breeding. Australian Journal of Crop Science, 2016, 10, 370-376.	0.3	11
110	5-aminolevolinic acid enhances sunflower resistance to Orobanche cumana (Broomrape). Industrial Crops and Products, 2019, 140, 111467.	5.2	11
111	Wheat genotypes tolerant to heat at seedling stage tend to be also tolerant at adult stage: The possibility of early selection for heat tolerance breeding. Crop Journal, 2022, 10, 1006-1013.	5.2	11
112	Transcriptome Analyses of Near Isogenic Lines Reveal Putative Drought Tolerance Controlling Genes in Wheat. Frontiers in Plant Science, 2022, 13, 857829.	3.6	11
113	Diversity of seed protein among the Australian narrow-leafed lupin (Lupinus angustifolius L.) cultivars. Crop and Pasture Science, 2011, 62, 765.	1.5	10
114	Two complementary dominant genes control flowering time in albus lupin (Lupinus albus L.). Plant Breeding, 2011, 130, 496-499.	1.9	10
115	Interspecific introgression of male sterility from tetraploid oilseed Brassica napus to diploid vegetable B. rapa through hybridisation and backcrossing. Crop and Pasture Science, 2013, 64, 652.	1.5	10
116	QTL Mapping Using a High-Density Genetic Map to Identify Candidate Genes Associated With Metribuzin Tolerance in Hexaploid Wheat (Triticum aestivum L.). Frontiers in Plant Science, 2020, 11, 573439.	3.6	10
117	Identification of Candidate Genes for Root Traits Using Genotypeâ€“Phenotype Association Analysis of Near-Isogenic Lines in Hexaploid Wheat (Triticum aestivum L.). International Journal of Molecular Sciences, 2021, 22, 3579.	4.1	10
118	Chloroplast DNA inheritance and variation in Leucadendron species (Proteaceae) as revealed by PCR-RFLP. Theoretical and Applied Genetics, 2004, 109, 1694-1701.	3.6	9
119	Molecular mapping of major QTL conferring resistance to orange wheat blossom midge (Sitodiplosis) Tj ETQq1 1 0.784314 rgBT /Ove 2020, 133, 491-502.	3.6	9
120	Basic chromosome number in Boronia (Rutaceae)â€”competing hypotheses examined. Australian Journal of Botany, 2006, 54, 681.	0.6	8
121	Interspecific hybridization in the genus Leucadendron through embryo rescue. South African Journal of Botany, 2006, 72, 416-420.	2.5	8
122	Identification of duplicates and fingerprinting of primary and secondary wild annual Cicer gene pools using AFLP markers. Genetic Resources and Crop Evolution, 2007, 54, 519-527.	1.6	8
123	Differentially Expressed Genes and Enriched Pathways During Drought-Sensitive Period Under Field Conditions in Bread Wheat. Plant Molecular Biology Reporter, 2019, 37, 389-400.	1.8	8
124	RAMP based fingerprinting and assessment of relationships among Australian narrow-leafed lupin (Lupinus angustifolius L.) cultivars. Australian Journal of Agricultural Research, 2005, 56, 1339.	1.5	8
125	Characterisation of genetic diversity and DNA fingerprinting of Australian chickpea (Cicer arietinum) Tj ETQq1 1 0.784314 rgBT /Over	1.5	8
126	Genome-Wide Analysis of AP2/ERF Superfamily Genes in Contrasting Wheat Genotypes Reveals Heat Stress-Related Candidate Genes. Frontiers in Plant Science, 2022, 13, 853086.	3.6	8

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127	Development of DNA markers for hybrid identification in Leucadendron (proteaceae). Scientia Horticulturae, 2007, 113, 376-382.	3.6	7
128	Variability in feed quality between populations of Acacia saligna (Labill.) H. Wendl. (Mimosoideae)â€"implications for domestication. Animal Feed Science and Technology, 2007, 136, 109-127.	2.2	7
129	Quantitative analysis of gene actions controlling root length under water stress in spring wheat (Triticum aestivum L.) genotypes. Crop and Pasture Science, 2016, 67, 489.	1.5	7
130	Response of wheat to post-anthesis water stress, and the nature of gene action as revealed by combining ability analysis. Crop and Pasture Science, 2017, 68, 534.	1.5	7
131	Identification of Early Vigor QTLs and QTL by Environment Interactions in Wheat (Triticum eastivum) Tj ETQq1 1 0.784314 rgBT /Over	1.8	7
132	Development and Characterization of Near-Isogenic Lines Revealing Candidate Genes for a Major 7AL QTL Responsible for Heat Tolerance in Wheat. Frontiers in Plant Science, 2020, 11, 1316.	3.6	7
133	Mixed Mating With Preferential Outcrossing in Acacia saligna (Labill.) H. Wendl. (Leguminosae:) Tj ETQq1 1 0.784314 rgBT /Overlock	0.8	7
134	Heat Stress during Meiosis Has Lasting Impacts on Plant Growth and Reproduction in Wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10	3.0	7
135	NEW DEVELOPMENTS FROM THE CENTRE FOR AUSTRALIAN PLANTS. Acta Horticulturae, 2000, , 37-41.	0.2	6
136	INTERSPECIFIC HYBRIDISATION OF LEUCADENDRON. Acta Horticulturae, 2001, , 55-64.	0.2	6
137	IN VITRO CONSERVATION OF SYNAPHEA STENOLOBA (PROTEACEAE). Acta Horticulturae, 2010, , 143-156.	0.2	6
138	Identification of fast and slow germination accessions of Brassica napus L. for genetic studies and breeding for early vigour. Crop and Pasture Science, 2015, 66, 481.	1.5	6
139	Development of a simple and effective silver staining protocol for detection of DNA fragments. Electrophoresis, 2017, 38, 1175-1178.	2.4	6
140	Development of DNA fingerprinting keys for discrimination of Cicer echinospermum (P.H. Davis) accessions using AFLP markers. Australian Journal of Agricultural Research, 2004, 55, 947.	1.5	5
141	Identification of â€˜Sibâ€™ plants in hybrid cauliflowers using microsatellite markers. Euphytica, 2008, 164, 309-316.	1.2	5
142	MICROPROPAGATION OF LEUCADENDRON. Acta Horticulturae, 2006, , 25-34.	0.2	4
143	Leaf type is not associated with ascochyta blight disease in chickpea (Cicer arietinum L.). Euphytica, 2008, 162, 281-289.	1.2	4
144	Mass spectrometric fingerprints of seed protein for defining Lupinus spp. relationships. Genetic Resources and Crop Evolution, 2013, 60, 939-952.	1.6	4

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145	Molecular Markers for Genetics and Plant Breeding: The MFLP Marker System and Its Application in Narrow-Leafed Lupin (Lupinus angustifolius). Methods in Molecular Biology, 2013, 1069, 179-201.	0.9	4
146	Transcriptomic profiling of wheat near-isogenic lines reveals candidate genes on chromosome 3A for pre-harvest sprouting resistance. BMC Plant Biology, 2021, 21, 53.	3.6	4
147	Meiotic chromosome behaviour and Boronia (Rutaceae) genome reorganisation. Australian Journal of Botany, 2003, 51, 599.	0.6	3
148	Chloroplast DNA variation and inheritance in waxflowers (Myrtaceae). Australian Journal of Botany, 2004, 52, 55.	0.6	3
149	Identification of chromosome regions controlling seed storage proteins of narrow-leafed lupin (Lupinus angustifolius). Journal of Plant Research, 2013, 126, 395-401.	2.4	3
150	Genomic regions controlling yield-related traits in spring wheat: a mini review and a case study for rainfed environments in Australia and China. Genomics, 2022, 114, 110268.	2.9	3
151	WAXFLOWER SELECTION, BREEDING AND DEVELOPMENT - AN OVERVIEW. Acta Horticulturae, 2000, , 119-124.	0.2	2
152	Title is missing!. Plant Systematics and Evolution, 2002, 233, 147-161.	0.9	2
153	Correlation of morphological traits with molecular markers in radish (Raphanus sativus). Australian Journal of Experimental Agriculture, 2004, 44, 813.	1.0	2
154	GENETIC DIVERSITY OF OPEN POLLINATED CAULIFLOWER CULTIVARS IN INDONESIA. Acta Horticulturae, 2005, , 149-152.	0.2	2
155	Genotypic variation of metribuzin and carfentrazone-ethyl tolerance among yellow lupin (Lupinus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.3	2
156	Genetic and environment interactions of seed storage proteins in narrow-leafed lupin (Lupinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	1.5	2
157	Genomic Regions, Molecular Markers, and Flanking Genes of Metribuzin Tolerance in Wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Ov	3.6	2
158	INHERITANCE OF IMPORTANT TRAITS IN INTERSPECIFIC LEUCADENDRON HYBRIDS. Acta Horticulturae, 2003, , 23-28.	0.2	1
159	Correlation of important seedling traits in cauliflower varieties and potential association with RAPD markers. Australian Journal of Agricultural Research, 2007, 58, 1183.	1.5	1
160	Inheritance and QTL analysis of dough rheological parameters in wheat. Frontiers of Agriculture in China, 2011, 5, 15-21.	0.2	1
161	Novel approaches to modifying wheat flour processing characteristics and health attributes: from genetics to food technology. , 2012, , 259-295.		1
162	APPLICATION OF DNA TECHNOLOGY IN BREEDING PROTEACEOUS PLANTS. Acta Horticulturae, 2014, , 97-105.	0.2	1

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