

Robert J. Henry

List of Publications by Year in descending order

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526
papers

24,071
citations

11651
70
h-index

12946
131
g-index

566
all docs

566
docs citations

566
times ranked

19254
citing authors

#	ARTICLE	IF	CITATIONS
1	A simple and rapid preparation of alditol acetates for monosaccharide analysis. Carbohydrate Research, 1983, 113, 291-299.	2.3	1,846
2	Plant <scp>DNA</scp> barcoding: from gene to genome. Biological Reviews, 2015, 90, 157-166.	10.4	582
3	An improved procedure for the methylation analysis of oligosaccharides and polysaccharides. Carbohydrate Research, 1984, 127, 59-73.	2.3	571
4	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	12.6	520
5	Analysis of SSRs derived from grape ESTs. Theoretical and Applied Genetics, 2000, 100, 723-726.	3.6	486
6	Simultaneous Determination of Moisture, Organic Carbon, and Total Nitrogen by Near Infrared Reflectance Spectrophotometry. Soil Science Society of America Journal, 1986, 50, 120-123.	2.2	442
7	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	21.4	413
8	Microsatellite markers from sugarcane (Saccharum spp.) ESTs cross transferable to erianthus and sorghum. Plant Science, 2001, 160, 1115-1123.	3.6	384
9	The gene for fragrance in rice. Plant Biotechnology Journal, 2005, 3, 363-370.	8.3	371
10	Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. Plant Methods, 2014, 10, 21.	4.3	339
11	Identification of new volatile thiols in the aroma of Vitis vinifera L. var. Sauvignon blanc wines. Flavour and Fragrance Journal, 1998, 13, 159-162.	2.6	316
12	Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnology Journal, 2011, 9, 328-333.	8.3	316
13	Genomics of crop wild relatives: expanding the gene pool for crop improvement. Plant Biotechnology Journal, 2016, 14, 1070-1085.	8.3	303
14	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. Nature Communications, 2018, 9, 2638.	12.8	299
15	Recent innovations in analytical methods for the qualitative and quantitative assessment of lignin. Renewable and Sustainable Energy Reviews, 2015, 49, 871-906.	16.4	282
16	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. Frontiers in Plant Science, 2015, 6, 563.	3.6	243
17	Domestication to Crop Improvement: Genetic Resources for Sorghum and Saccharum (Andropogoneae). Annals of Botany, 2007, 100, 975-989.	2.9	227
18	Global agricultural intensification during climate change: a role for genomics. Plant Biotechnology Journal, 2016, 14, 1095-1098.	8.3	221

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19	Inactivation of an aminoaldehyde dehydrogenase is responsible for fragrance in rice. <i>Plant Molecular Biology</i> , 2008, 68, 439-449.	3.9	199
20	Characterisation of microsatellite markers from sugarcane (<i>Saccharum</i> sp.), a highly polyploid species. <i>Plant Science</i> , 2000, 155, 161-168.	3.6	184
21	Pentosan and (1 → 3),(1 → 4)- β -Glucan concentrations in endosperm and wholegrain of wheat, barley, oats and rye. <i>Journal of Cereal Science</i> , 1987, 6, 253-258.	3.7	180
22	A survey of the complex transcriptome from the highly polyploid sugarcane genome using full-length isoform sequencing and de novo assembly from short read sequencing. <i>BMC Genomics</i> , 2017, 18, 395.	2.8	180
23	A Perfect Marker for Fragrance Genotyping in Rice. <i>Molecular Breeding</i> , 2005, 16, 279-283.	2.1	177
24	Genome-wide DNA polymorphisms in elite <i>indica</i> rice inbreds discovered by whole-genome sequencing. <i>Plant Biotechnology Journal</i> , 2012, 10, 623-634.	8.3	175
25	Exploring and Exploiting Pan-genomics for Crop Improvement. <i>Molecular Plant</i> , 2019, 12, 156-169.	8.3	172
26	Gelatinization temperature of rice explained by polymorphisms in starch synthase. <i>Plant Biotechnology Journal</i> , 2006, 4, 115-122.	8.3	161
27	Influence of genotype and environment on coffee quality. <i>Trends in Food Science and Technology</i> , 2016, 57, 20-30.	15.1	150
28	Relationships of wild and domesticated rices (<i>Oryza</i> AA genome species) based upon whole chloroplast genome sequences. <i>Scientific Reports</i> , 2015, 5, 13957.	3.3	148
29	Advances in understanding salt tolerance in rice. <i>Theoretical and Applied Genetics</i> , 2019, 132, 851-870.	3.6	148
30	THE DISTRIBUTION OF FRUCTANS IN ONIONS. <i>New Phytologist</i> , 1978, 81, 29-34.	7.3	147
31	Molecular basis of barley quality. <i>Australian Journal of Agricultural Research</i> , 2003, 54, 1081.	1.5	146
32	A comparison of the non-starch carbohydrates in cereal grains. <i>Journal of the Science of Food and Agriculture</i> , 1985, 36, 1243-1253.	3.5	145
33	Identification of Volatile and Powerful Odorous Thiols in Bordeaux Red Wine Varieties. <i>Journal of Agricultural and Food Chemistry</i> , 1998, 46, 3095-3099.	5.2	144
34	Title is missing!. <i>Molecular Breeding</i> , 2002, 9, 63-71.	2.1	142
35	Origin and evolution of qingke barley in Tibet. <i>Nature Communications</i> , 2018, 9, 5433.	12.8	141
36	Targeted single nucleotide polymorphism (SNP) discovery in a highly polyploid plant species using 454 sequencing. <i>Plant Biotechnology Journal</i> , 2009, 7, 347-354.	8.3	134

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37	Variation in Amylose Fine Structure of Starches from Different Botanical Sources. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 4443-4453.	5.2	134
38	Sugarcane microsatellites for the assessment of genetic diversity in sugarcane germplasm. <i>Plant Science</i> , 2003, 165, 181-189.	3.6	133
39	Implementation of markers in Australian wheat breeding. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1349.	1.5	132
40	DIFFERENCES IN FRUCTAN CONTENT AND SYNTHESIS IN SOME ALLIUM SPECIES. <i>New Phytologist</i> , 1981, 87, 249-256.	7.3	130
41	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. <i>Scientific Reports</i> , 2013, 3, 3399.	3.3	129
42	A simplified method for the preparation of fungal genomic DNA for PCR and RAPD analysis. <i>BioTechniques</i> , 1994, 16, 48-50.	1.8	126
43	Microsatellite analysis of genetic structure in the mangrove species <i>Avicennia marina</i> (Forsk.) Vierh. (Avicenniaceae). <i>Molecular Ecology</i> , 2000, 9, 1853-1862.	3.9	124
44	Capturing chloroplast variation for molecular ecology studies: a simple next generation sequencing approach applied to a rainforest tree. <i>BMC Ecology</i> , 2013, 13, 8.	3.0	123
45	Thirty-three years of 2-acetyl-1-pyrroline, a principal basmati aroma compound in scented rice (<i>Oryza sativa</i>): a status review. <i>Journal of the Science of Food and Agriculture</i> , 2017, 97, 384-395.	3.5	123
46	Identification of Volatile Compounds with a "Toasty" Aroma in Heated Oak Used in Barrelmaking. <i>Journal of Agricultural and Food Chemistry</i> , 1997, 45, 2217-2224.	5.2	120
47	EST versus Genomic Derived Microsatellite Markers for Genotyping Wild and Cultivated Barley. <i>Genetic Resources and Crop Evolution</i> , 2005, 52, 903-909.	1.6	112
48	Assessment of Lignocellulosic Biomass Using Analytical Spectroscopy: an Evolution to High-Throughput Techniques. <i>Bioenergy Research</i> , 2014, 7, 1-23.	3.9	111
49	Impact Odorants Contributing to the Fungus Type Aroma from Grape Berries Contaminated by Powdery Mildew (<i>Uncinula necator</i>); Incidence of Enzymatic Activities of the Yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2002, 50, 3277-3282.	5.2	110
50	The defence-associated transcriptome of hexaploid wheat displays homoeolog expression and induction bias. <i>Plant Biotechnology Journal</i> , 2017, 15, 533-543.	8.3	110
51	cDNA microarray analysis of developing grape (<i>Vitis vinifera</i> cv. Shiraz) berry skin. <i>Functional and Integrative Genomics</i> , 2005, 5, 40-58.	3.5	109
52	Potential for Genetic Improvement of Sugarcane as a Source of Biomass for Biofuels. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 182.	4.1	109
53	Natural variation in the essential oil content of <i>Melaleuca alternifolia</i> Cheel (Myrtaceae). <i>Biochemical Systematics and Ecology</i> , 2000, 28, 367-382.	1.3	107
54	Betaine aldehyde dehydrogenase in plants. <i>Plant Biology</i> , 2009, 11, 119-130.	3.8	101

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55	Genetic and environmental variation in the diastatic power of australian barley. <i>Journal of Cereal Science</i> , 1995, 21, 63-70.	3.7	97
56	Evaluation of plant biomass resources available for replacement of fossil oil. <i>Plant Biotechnology Journal</i> , 2010, 8, 288-293.	8.3	95
57	Random amplified polymorphic DNA (RAPD) detection of dwarf off-types in micropropagated Cavendish (Musa spp. AAA) bananas. <i>Plant Cell Reports</i> , 1996, 16, 118-123.	5.6	94
58	SNP in starch biosynthesis genes associated with nutritional and functional properties of rice. <i>Scientific Reports</i> , 2012, 2, 557.	3.3	93
59	Genetic and environmental variation in the pentosan and β -glucan contents of barley, and their relation to malting quality. <i>Journal of Cereal Science</i> , 1986, 4, 269-277.	3.7	91
60	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.	1.9	91
61	Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content. <i>Scientific Reports</i> , 2018, 8, 11612.	3.3	91
62	Long-read sequencing of the coffee bean transcriptome reveals the diversity of full-length transcripts. <i>GigaScience</i> , 2017, 6, 1-13.	6.4	90
63	Sensitivity of random amplified polymorphic DNA analysis to detect genetic change in sugarcane during tissue culture. <i>Theoretical and Applied Genetics</i> , 1995, 90, 1169-1173.	3.6	89
64	Wild Sorghum as a Promising Resource for Crop Improvement. <i>Frontiers in Plant Science</i> , 2020, 11, 1108.	3.6	87
65	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. <i>BMC Genomics</i> , 2015, 16, 538.	2.8	86
66	Chloroplast genome sequence confirms distinctness of Australian and Asian wild rice. <i>Ecology and Evolution</i> , 2012, 2, 211-217.	1.9	84
67	Modifying plants for biofuel and biomaterial production. <i>Plant Biotechnology Journal</i> , 2014, 12, 1246-1258.	8.3	82
68	Evaluating the potential of SSR flanking regions for examining taxonomic relationships in the Vitaceae. <i>Theoretical and Applied Genetics</i> , 2002, 104, 61-66.	3.6	81
69	The Challenge of Analyzing the Sugarcane Genome. <i>Frontiers in Plant Science</i> , 2018, 9, 616.	3.6	80
70	Role of genomics in promoting the utilization of plant genetic resources in genebanks. <i>Briefings in Functional Genomics</i> , 2018, 17, 198-206.	2.7	79
71	A single nucleotide polymorphism (SNP) marker linked to the fragrance gene in rice (<i>Oryza sativa</i> L.). <i>Plant Science</i> , 2003, 165, 359-364.	3.6	78
72	Effects of genotype and temperature on accumulation of plant secondary metabolites in Canadian and Australian wheat grown under controlled environments. <i>Scientific Reports</i> , 2017, 7, 9133.	3.3	76

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73	Gene expression in the developing aleurone and starchy endosperm of wheat. <i>Plant Biotechnology Journal</i> , 2012, 10, 668-679.	8.3	75
74	The biosynthesis, structure and gelatinization properties of starches from wild and cultivated African rice species (<i>Oryza barthii</i> and <i>Oryza glaberrima</i>). <i>Carbohydrate Polymers</i> , 2015, 129, 92-100.	10.2	75
75	Marker-assisted selection for two rust resistance genes in sunflower. <i>Molecular Breeding</i> , 1998, 4, 227-234.	2.1	71
76	Title is missing!. <i>Molecular Breeding</i> , 2002, 9, 245-250.	2.1	71
77	The association of fructans with high percentage dry weight in onion cultivars suitable for dehydrating. <i>Journal of the Science of Food and Agriculture</i> , 1979, 30, 1035-1038.	3.5	68
78	Gas Chromatographic Determination of the Monosaccharide Composition of Plant Cell Wall Preparations. <i>Journal of the Association of Official Analytical Chemists</i> , 1988, 71, 272-275.	0.2	68
79	The application of SSRs characterized for grape (<i>Vitis vinifera</i>) to conservation studies in Vitaceae. <i>American Journal of Botany</i> , 2002, 89, 22-28.	1.7	68
80	Starch determination in horticultural plant material by an enzymic-colorimetric procedure. <i>Journal of the Science of Food and Agriculture</i> , 1990, 52, 159-170.	3.5	66
81	Discovery of polymorphisms in starch-related genes in rice germplasm by amplification of pooled DNA and deeply parallel sequencing ^{<sup>â€</sup>} . <i>Plant Biotechnology Journal</i> , 2011, 9, 1074-1085.	8.3	65
82	Detection of neutral and aminosugars from glycoproteins and polysaccharides as their alditol acetates. <i>Journal of Chromatography A</i> , 1983, 256, 419-427.	3.7	64
83	Analysis of grape ESTs: global gene expression patterns in leaf and berry. <i>Plant Science</i> , 2000, 159, 87-95.	3.6	64
84	Adaptive climatic molecular evolution in wild barley at the <i>Isa</i> defense locus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 2773-2778.	7.1	64
85	Fragrance in rice (<i>Oryza sativa</i>) is associated with reduced yield under salt treatment. <i>Environmental and Experimental Botany</i> , 2010, 68, 292-300.	4.2	64
86	Endosperm and starch granule morphology in wild cereal relatives. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2008, 6, 85-97.	0.8	62
87	Next-generation sequencing for understanding and accelerating crop domestication. <i>Briefings in Functional Genomics</i> , 2012, 11, 51-56.	2.7	62
88	New evidence for grain specific C4 photosynthesis in wheat. <i>Scientific Reports</i> , 2016, 6, 31721.	3.3	62
89	Comparison of long-read methods for sequencing and assembly of a plant genome. <i>GigaScience</i> , 2020, 9, .	6.4	62
90	Sucrose:sucrose fructosyltransferase and fructan:fructan fructosyltransferase from <i>allium cepa</i> . <i>Phytochemistry</i> , 1980, 19, 1017-1020.	2.9	61

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91	Comparison of promoters in transgenic rice. <i>Plant Biotechnology Journal</i> , 2008, 6, 679-693.	8.3	61
92	A comprehensive genetic map of sugarcane that provides enhanced map coverage and integrates high-throughput Diversity Array Technology (DART) markers. <i>BMC Genomics</i> , 2014, 15, 152.	2.8	61
93	Improving rice salt tolerance by precision breeding in a new era. <i>Current Opinion in Plant Biology</i> , 2021, 60, 101996.	7.1	61
94	Brachypodium as an emerging model for cereal-pathogen interactions. <i>Annals of Botany</i> , 2015, 115, 717-731.	2.9	60
95	Roles of GBSSI and SSIIa in determining amylose fine structure. <i>Carbohydrate Polymers</i> , 2015, 127, 264-274.	10.2	59
96	THE CARBOHYDRATES OF BARLEY GRAINS - A REVIEW. <i>Journal of the Institute of Brewing</i> , 1988, 94, 71-78.	2.3	58
97	Microsatellite variation and assessment of genetic structure in tea tree (<i>Melaleuca alternifolia</i> -) Tj ETQq1 1 0.784314rgBT /Overlock 10	3.9	58
98	Transpecific microsatellites for hard pines. <i>Theoretical and Applied Genetics</i> , 2002, 104, 819-827.	3.6	58
99	Characterisation of single nucleotide polymorphisms in sugarcane ESTs. <i>Theoretical and Applied Genetics</i> , 2006, 113, 331-343.	3.6	58
100	Analysis of promoters in transgenic barley and wheat. <i>Plant Biotechnology Journal</i> , 2009, 7, 240-253.	8.3	58
101	Complete chloroplast genome sequence of <i>Magnolia grandiflora</i> and comparative analysis with related species. <i>Science China Life Sciences</i> , 2013, 56, 189-198.	4.9	58
102	Exploring natural selection to guide breeding for agriculture. <i>Plant Biotechnology Journal</i> , 2014, 12, 655-662.	8.3	58
103	Australian <i>Oryza</i> : Utility and Conservation. <i>Rice</i> , 2010, 3, 235-241.	4.0	57
104	Innovations in plant genetics adapting agriculture to climate change. <i>Current Opinion in Plant Biology</i> , 2020, 56, 168-173.	7.1	57
105	PCR-based molecular markers for the fragrance gene in rice (<i>Oryza sativa</i> . L.). <i>Theoretical and Applied Genetics</i> , 2000, 101, 364-371.	3.6	56
106	Genes associated with the end of dormancy in grapes. <i>Functional and Integrative Genomics</i> , 2003, 3, 144-152.	3.5	56
107	Development of robust PCR-based DNA markers for each homoeo-allele of granule-bound starch synthase and their application in wheat breeding programs. <i>Australian Journal of Agricultural Research</i> , 2001, 52, 1409.	1.5	55
108	Title is missing!. <i>Euphytica</i> , 1999, 108, 53-63.	1.2	54

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109	The potential contribution of wild barley (<i>Hordeum vulgare</i> ssp. <i>spontaneum</i>) germplasm to drought tolerance of cultivated barley (<i>H. vulgare</i> ssp. <i>vulgare</i>). <i>Field Crops Research</i> , 2011, 120, 161-168.	5.1	54
110	Factors Influencing β -Glucan Synthesis by Particulate Enzymes from Suspension-Cultured <i>Lolium multiflorum</i> Endosperm Cells. <i>Plant Physiology</i> , 1982, 69, 632-636.	4.8	53
111	Prospects of breeding high-quality rice using post-genomic tools. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1449-1466.	3.6	53
112	The use of bulk segregant analysis to identify a RAPD marker linked to leaf rust resistance in barley. <i>Theoretical and Applied Genetics</i> , 1995, 91, 270-273.	3.6	52
113	The <i>Fusarium</i> crown rot pathogen <i>Fusarium pseudograminearum</i> triggers a suite of transcriptional and metabolic changes in bread wheat (<i>Triticum aestivum</i> L.). <i>Annals of Botany</i> , 2017, 119, mcw207.	2.9	52
114	Sequencing of bulks of segregants allows dissection of genetic control of amylose content in rice. <i>Plant Biotechnology Journal</i> , 2018, 16, 100-110.	8.3	52
115	Random amplified polymorphic DNA analysis of Australian rice (<i>Oryza sativa</i> L.) varieties. <i>Euphytica</i> , 1994, 80, 179-189.	1.2	51
116	Identifying New Volatile Compounds in Toasted Oak. <i>Journal of Agricultural and Food Chemistry</i> , 1999, 47, 1663-1667.	5.2	51
117	Characterisation and analysis of microsatellite loci in a mangrove species, <i>Avicennia marina</i> (Forsk.) Vierh. (Avicenniaceae). <i>Theoretical and Applied Genetics</i> , 2000, 101, 279-285.	3.6	51
118	Potential of SSR markers for plant breeding and variety identification in Australian barley germplasm. <i>Australian Journal of Agricultural Research</i> , 2003, 54, 1197.	1.5	51
119	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 765-774.	8.3	51
120	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	8.3	50
121	SAGE of the developing wheat caryopsis. <i>Plant Biotechnology Journal</i> , 2007, 5, 69-83.	8.3	49
122	Genomics strategies for germplasm characterization and the development of climate resilient crops. <i>Frontiers in Plant Science</i> , 2014, 5, 68.	3.6	49
123	Causal Relations Among Starch Biosynthesis, Structure, and Properties. <i>Springer Science Reviews</i> , 2014, 2, 15-33.	1.3	49
124	Innovations in Agriculture and Food Supply in Response to the COVID-19 Pandemic. <i>Molecular Plant</i> , 2020, 13, 1095-1097.	8.3	49
125	Practical Applications of Plant Molecular Biology. , 1997, , .		49
126	Use of a draft genome of coffee (<i>Coffea arabica</i>) to identify SNPs associated with caffeine content. <i>Plant Biotechnology Journal</i> , 2018, 16, 1756-1766.	8.3	48

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127	Nuclear ribosomal pseudogenes resolve a corroborated monophyly of the eucalypt genus <i>Corymbia</i> despite misleading hypotheses at functional ITS paralogs. <i>Molecular Phylogenetics and Evolution</i> , 2007, 44, 752-764.	2.7	47
128	RAPD and isozyme analysis of genetic relationships between <i>Carica papaya</i> and wild relatives. <i>Genetic Resources and Crop Evolution</i> , 1997, 44, 471-477.	1.6	46
129	Pollen flow in <i>Eucalyptus grandis</i> determined by paternity analysis using microsatellite markers. <i>Tree Genetics and Genomes</i> , 2007, 4, 37-47.	1.6	46
130	The transcriptome of the developing grain: a resource for understanding seed development and the molecular control of the functional and nutritional properties of wheat. <i>BMC Genomics</i> , 2017, 18, 766.	2.8	46
131	Improving enzymatic digestibility of sugarcane bagasse from different varieties of sugarcane using deep eutectic solvent pretreatment. <i>Bioresource Technology</i> , 2021, 337, 125480.	9.6	46
132	Molecular analysis of the DNA polymorphism of wild barley (<i>Hordeum spontaneum</i>) germplasm using the polymerase chain reaction. <i>Genetic Resources and Crop Evolution</i> , 1995, 42, 273-280.	1.6	45
133	Conservation and utilization of African <i>Oryza</i> genetic resources. <i>Rice</i> , 2013, 6, 29.	4.0	45
134	Genome and transcriptome sequencing characterises the gene space of <i>Macadamia integrifolia</i> (Proteaceae). <i>BMC Genomics</i> , 2016, 17, 937.	2.8	45
135	Measurement of genetic and environmental variation in barley (<i>Hordeum vulgare</i>) grain hardness. <i>Journal of Cereal Science</i> , 2007, 46, 82-92.	3.7	44
136	Enrichment of genomic DNA for polymorphism detection in a non-model highly polyploid crop plant. <i>Plant Biotechnology Journal</i> , 2012, 10, 657-667.	8.3	44
137	Quantitative Determination of Potent Flavor Compounds in Burgundy Pinot Noir Wines Using a Stable Isotope Dilution Assay. <i>Journal of Agricultural and Food Chemistry</i> , 1997, 45, 2120-2123.	5.2	43
138	Molecular relationships between Australian annual wild rice, <i>Oryza meridionalis</i> , and two related perennial forms. <i>Rice</i> , 2013, 6, 26.	4.0	43
139	High-Throughput Sequencing and Mutagenesis to Accelerate the Domestication of <i>Microlaena stipoides</i> as a New Food Crop. <i>PLoS ONE</i> , 2013, 8, e82641.	2.5	43
140	Chloroplast Genome of Novel Rice Germplasm Identified in Northern Australia. <i>Tropical Plant Biology</i> , 2014, 7, 111-120.	1.9	43
141	Polymorphisms in the β -amy1 gene of wild and cultivated barley revealed by the polymerase chain reaction. <i>Theoretical and Applied Genetics</i> , 1994, 89, 509-513.	3.6	42
142	Genetic analysis and phenotypic associations for drought tolerance in <i>Hordeum spontaneum</i> introgression lines using SSR and SNP markers. <i>Euphytica</i> , 2013, 189, 9-29.	1.2	42
143	High-Throughput Profiling of the Fiber and Sugar Composition of Sugarcane Biomass. <i>Bioenergy Research</i> , 2017, 10, 400-416.	3.9	42
144	Abundance and polymorphism of microsatellite markers in the tea tree (<i>Melaleuca alternifolia</i>). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62</i>	3.6	41

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145	<i>Sorghum laxiflorum</i> and <i>S. macrospermum</i> , the Australian native species most closely related to the cultivated <i>S. bicolor</i> based on ITS1 and <i>ndhF</i> sequence analysis of 25 <i>Sorghum</i> species. <i>Plant Systematics and Evolution</i> , 2004, 249, 233-246.	0.9	41
146	The effect of salt on betaine aldehyde dehydrogenase transcript levels and 2-acetyl-1-pyrroline concentration in fragrant and non-fragrant rice (<i>Oryza sativa</i>). <i>Plant Science</i> , 2008, 175, 539-546.	3.6	41
147	<i>Pectin Methylesterase</i> Genes Influence Solid Wood Properties of <i>Eucalyptus pilularis</i> . <i>Plant Physiology</i> , 2012, 158, 531-541.	4.8	41
148	Variation in sorghum starch synthesis genes associated with differences in starch phenotype. <i>Food Chemistry</i> , 2012, 131, 175-183.	8.2	41
149	High-throughput prediction of eucalypt lignin syringyl/guaiacyl content using multivariate analysis: a comparison between mid-infrared, near-infrared, and Raman spectroscopies for model development. <i>Biotechnology for Biofuels</i> , 2014, 7, 93.	6.2	41
150	Association of variation in the sugarcane transcriptome with sugar content. <i>BMC Genomics</i> , 2017, 18, 909.	2.8	41
151	Genetic diversity in sunflower (<i>Helianthus annuus</i> L.) as revealed by random amplified polymorphic DNA analysis. <i>Australian Journal of Agricultural Research</i> , 1994, 45, 1319.	1.5	40
152	Single nucleotide polymorphism, haplotype diversity and recombination in the <i>Isa</i> gene of barley. <i>Theoretical and Applied Genetics</i> , 2004, 109, 543-551.	3.6	40
153	The wheat <i>Em</i> promoter drives reporter gene expression in embryo and aleurone tissue of transgenic barley and rice. <i>Plant Biotechnology Journal</i> , 2005, 3, 421-434.	8.3	40
154	Eucalypts as a biofuel feedstock. <i>Biofuels</i> , 2011, 2, 639-657.	2.4	40
155	Advances in genomics for the improvement of quality in coffee. <i>Journal of the Science of Food and Agriculture</i> , 2016, 96, 3300-3312.	3.5	40
156	Cultivation Effects on Carbohydrate Contents of Soil and Soil Fractions. <i>Soil Science Society of America Journal</i> , 1988, 52, 1361-1365.	2.2	39
157	The identification and characterisation of alleles of sucrose phosphate synthase gene family III in sugarcane. <i>Molecular Breeding</i> , 2006, 18, 39-50.	2.1	39
158	Molecular structures and properties of starches of Australian wild rice. <i>Carbohydrate Polymers</i> , 2017, 172, 213-222.	10.2	39
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