

# Robert J. Henry

## List of Publications by Year in descending order

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526  
papers

24,071  
citations

13332

70  
h-index

14779

131  
g-index

566  
all docs

566  
docs citations

566  
times ranked

21160  
citing authors

#	ARTICLE	IF	CITATIONS
1	Systems seed biology to understand and manipulate rice grain quality and nutrition. <i>Critical Reviews in Biotechnology</i> , 2023, 43, 716-733.	5.1	1
2	Secondary gene pool of Australian <i>Cajanus</i> species contains sources of resistance to <i>Helicoverpa armigera</i> (H&A). <i>Annals of Applied Biology</i> , 2022, 180, 259-272.	1.3	3
3	<i>De novo</i> chromosome level assembly of a plant genome from long read sequence data. <i>Plant Journal</i> , 2022, 109, 727-736.	2.8	20
4	Cyanogenesis in the Sorghum Genus: From Genotype to Phenotype. <i>Genes</i> , 2022, 13, 140.	1.0	7
5	Exogenous putrescine attenuates the negative impact of drought stress by modulating physio-biochemical traits and gene expression in sugar beet ( <i>Beta vulgaris</i> L.). <i>PLoS ONE</i> , 2022, 17, e0262099.	1.1	24
6	A Comprehensive High-Quality DNA and RNA Extraction Protocol for a Range of Cultivars and Tissue Types of the Woody Crop Avocado. <i>Plants</i> , 2022, 11, 242.	1.6	9
7	New Hybrid Spikelet Sterility Gene Found in Interspecific Cross between <i>Oryza sativa</i> and <i>O. meridionalis</i> . <i>Plants</i> , 2022, 11, 378.	1.6	2
8	Transcript profiles of wild and domesticated sorghum under water-stressed conditions and the differential impact on dhurrin metabolism. <i>Planta</i> , 2022, 255, 51.	1.6	2
9	Starch Molecular Structural Features and Volatile Compounds Affecting the Sensory Properties of Polished Australian Wild Rice. <i>Foods</i> , 2022, 11, 511.	1.9	2
10	Comparison of the root, leaf and internode transcriptomes in sugarcane ( <i>Saccharum</i> spp. hybrids). <i>Current Research in Biotechnology</i> , 2022, 4, 167-178.	1.9	2
11	Transcriptome changes in the developing sugarcane culm associated with high yield and early-season high sugar content. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1619-1636.	1.8	1
12	Supporting in situ conservation of the genetic diversity of crop wild relatives using genomic technologies. <i>Molecular Ecology</i> , 2022, 31, 2207-2222.	2.0	20
13	<i>Applied Biosciences: Application of Biological Science and Technology.</i> , 2022, 1, 38-39.		1
14	Reticulate Evolution in AA-Genome Wild Rice in Australia. <i>Frontiers in Plant Science</i> , 2022, 13, 767635.	1.7	2
15	Tracking habitat or testing its suitability? Similar distributional patterns can hide very different histories of persistence versus nonequilibrium dynamics. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1209-1228.	1.1	3
16	Wild rice research: Advancing plant science and food security. <i>Molecular Plant</i> , 2022, 15, 563-565.	3.9	2
17	Unveiling the potential of water as a co-solvent in microwave-assisted delignification of sugarcane bagasse using ternary deep eutectic solvents. <i>Bioresource Technology</i> , 2022, 351, 127005.	4.8	28
18	Limited allele-specific gene expression in highly polyploid sugarcane. <i>Genome Research</i> , 2022, 32, 297-308.	2.4	8

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19	Potential of Genome Editing to Capture Diversity From Australian Wild Rice Relatives. <i>Frontiers in Genome Editing</i> , 2022, 4, 875243.	2.7	3
20	Allele expression biases in mixed-ploid sugarcane accessions. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
21	Testing the Linearity Assumption for Starch Structure-Property Relationships in Rices. <i>Frontiers in Nutrition</i> , 2022, 9, .	1.6	2
22	Evolution of an intermediate C4 photosynthesis in the non-foliar tissues of the Poaceae. <i>Photosynthesis Research</i> , 2022, 153, 125-134.	1.6	3
23	The Long Read Transcriptome of Rice ( <i>Oryza sativa</i> ssp. <i>japonica</i> var. <i>Nipponbare</i> ) Reveals Novel Transcripts. <i>Rice</i> , 2022, 15, .	1.7	2
24	Progress in Plant Genome Sequencing. , 2022, 1, 113-128.		10
25	RNA Extraction From Plant Seeds. , 2021, , 451-461.		1
26	Transcriptome of Sugarcane, a Highly Complex Polyploid. , 2021, , 614-626.		0
27	Development of Transcriptome Analysis Methods. , 2021, , 462-471.		2
28	Effect of sugar feedback regulation on major genes and proteins of photosynthesis in sugarcane leaves. <i>Plant Physiology and Biochemistry</i> , 2021, 158, 321-333.	2.8	14
29	Avocado Transcriptomic Resources. , 2021, , 544-557.		1
30	Iso-Seq Long Read Transcriptome Sequencing. , 2021, , 486-500.		2
31	RNA-Seq to Understand Transcriptomes and Application in Improving Crop Quality. , 2021, , 472-485.		1
32	Genetics and Genomics of African Rice ( <i>Oryza glaberrima</i> Steud) Domestication. <i>Rice</i> , 2021, 14, 6.	1.7	13
33	Coffee Bean Transcriptome. , 2021, , 627-639.		1
34	Isolation of genes/quantitative trait loci for drought stress tolerance in maize.. , 2021, , 267-281.		0
35	Wheat Grain Transcriptome. , 2021, , 501-512.		0
36	Association of gene expression with syringyl to guaiacyl ratio in sugarcane lignin. <i>Plant Molecular Biology</i> , 2021, 106, 173-192.	2.0	8

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37	Nitrogen availability and allocation in sorghum and its wild relatives: Divergent roles for cyanogenic glucosides. <i>Journal of Plant Physiology</i> , 2021, 258-259, 153393.	1.6	8
38	Improving rice salt tolerance by precision breeding in a new era. <i>Current Opinion in Plant Biology</i> , 2021, 60, 101996.	3.5	61
39	Variation in production of cyanogenic glucosides during early plant development: A comparison of wild and domesticated sorghum. <i>Phytochemistry</i> , 2021, 184, 112645.	1.4	16
40	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	2.0	21
41	Biochemical basis of resistance to pod borer ( <i>Helicoverpa armigera</i> ) in Australian wild relatives of pigeonpea. , 2021, 3, e101.		3
42	Access to biodiversity for food production: Reconciling open access digital sequence information with access and benefit sharing. <i>Molecular Plant</i> , 2021, 14, 701-704.	3.9	5
43	Genomic selection and genetic gain for nut yield in an Australian macadamia breeding population. <i>BMC Genomics</i> , 2021, 22, 370.	1.2	13
44	Fragrance in <i>Pandanus amaryllifolius</i> Roxb. Despite the Presence of a Betaine Aldehyde Dehydrogenase 2. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6968.	1.8	4
45	Phylogenetic relationships in the <i>Sorghum</i> genus based on sequencing of the chloroplast and nuclear genes. <i>Plant Genome</i> , 2021, 14, e20123.	1.6	13
46	Phenotypic Characterisation for Growth and Nut Characteristics Revealed the Extent of Genetic Diversity in Wild Macadamia Germplasm. <i>Agriculture (Switzerland)</i> , 2021, 11, 680.	1.4	11
47	Arsenic Accumulation in Rice Grain as Influenced by Water Management: Human Health Risk Assessment. <i>Agronomy</i> , 2021, 11, 1741.	1.3	9
48	Identification of genes associated with chapatti quality using transcriptome analysis. <i>Journal of Cereal Science</i> , 2021, 101, 103276.	1.8	0
49	The jojoba genome reveals wide divergence of the sex chromosomes in a dioecious plant. <i>Plant Journal</i> , 2021, 108, 1283-1294.	2.8	9
50	Improving enzymatic digestibility of sugarcane bagasse from different varieties of sugarcane using deep eutectic solvent pretreatment. <i>Bioresource Technology</i> , 2021, 337, 125480.	4.8	46
51	Starch structure-property relations in Australian wild rices compared to domesticated rices. <i>Carbohydrate Polymers</i> , 2021, 271, 118412.	5.1	15
52	Genomics of grain quality in cereals. <i>Crop Breeding and Applied Biotechnology</i> , 2021, 21, .	0.1	1
53	RNA Extraction for Transcriptome Analysis. , 2021, , 440-450.		0
54	Introduction to Transcriptomics. , 2021, , 439.		0

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55	Single kernel sorting of high and normal oleic acid peanuts using near infrared spectroscopy. <i>Journal of Near Infrared Spectroscopy</i> , 2021, 29, 366-370.	0.8	3
56	The genome of the endangered <i>Macadamia janseni</i> displays little diversity but represents an important genetic resource for plant breeding. <i>Plant Direct</i> , 2021, 5, e364.	0.8	7
57	Phylogenetic Relationship among <i>Macadamia integrifolia</i> and <i>Macadamia tetraphylla</i> Wild Accessions. <i>Proceedings (mdpi)</i> , 2020, 36, .	0.2	0
58	Isolation and Characterization of Full-Length Phenylalanine Ammonium Lyase and Cinnamyl Alcohol Dehydrogenase Genes Involved in Lignin Biosynthesis of <i>Erianthus Arundinaceus</i> . <i>Proceedings (mdpi)</i> , 2020, 36, .	0.2	0
59	Crop wild relatives as a genetic resource for generating low-cyanide, drought-tolerant Sorghum. <i>Environmental and Experimental Botany</i> , 2020, 169, 103884.	2.0	28
60	Transcriptome profiling of wheat genotypes under heat stress during grain-filling. <i>Journal of Cereal Science</i> , 2020, 91, 102895.	1.8	32
61	Innovations in plant genetics adapting agriculture to climate change. <i>Current Opinion in Plant Biology</i> , 2020, 56, 168-173.	3.5	57
62	Differential expression in leaves of <i>Saccharum</i> genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. <i>BMC Genomics</i> , 2020, 21, 673.	1.2	10
63	Wild Sorghum as a Promising Resource for Crop Improvement. <i>Frontiers in Plant Science</i> , 2020, 11, 1108.	1.7	87
64	Chromosome-Scale Assembly and Annotation of the <i>Macadamia</i> Genome ( <i>Macadamia integrifolia</i> ) Tj ETQq0.0.0 rgBT /Overlock 1	0.8	26
65	Metabolic changes in the developing sugarcane culm associated with high yield and early high sugar content. <i>Plant Direct</i> , 2020, 4, e00276.	0.8	12
66	Modelled distributions and conservation priorities of wild sorghums ( <i>Sorghum</i> Moench). <i>Diversity and Distributions</i> , 2020, 26, 1727-1740.	1.9	11
67	Innovations in Agriculture and Food Supply in Response to the COVID-19 Pandemic. <i>Molecular Plant</i> , 2020, 13, 1095-1097.	3.9	49
68	Two divergent chloroplast genome sequence clades captured in the domesticated rice gene pool may have significance for rice production. <i>BMC Plant Biology</i> , 2020, 20, 472.	1.6	18
69	Mobilizing Crop Biodiversity. <i>Molecular Plant</i> , 2020, 13, 1341-1344.	3.9	50
70	Variation in sugarcane biomass composition and enzymatic saccharification of leaves, internodes and roots. <i>Biotechnology for Biofuels</i> , 2020, 13, 201.	6.2	11
71	Sequence Variants Linked to Key Traits in Interspecific Crosses between African and Asian Rice. <i>Plants</i> , 2020, 9, 1653.	1.6	1
72	Pathways of Photosynthesis in Non-Leaf Tissues. <i>Biology</i> , 2020, 9, 438.	1.3	31

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73	Biotic exchange leaves detectable genomic patterns in the Australian rain forest flora. <i>Biotropica</i> , 2020, 52, 627-635.	0.8	6
74	The Nagoya Protocol and historical collections of plants. <i>Nature Plants</i> , 2020, 6, 430-432.	4.7	22
75	Genetic Structure of Wild Germplasm of Macadamia: Species Assignment, Diversity and Phylogeographic Relationships. <i>Plants</i> , 2020, 9, 714.	1.6	13
76	Slower development of lower canopy beans produces better coffee. <i>Journal of Experimental Botany</i> , 2020, 71, 4201-4214.	2.4	10
77	Genome-wide association studies for yield component traits in a macadamia breeding population. <i>BMC Genomics</i> , 2020, 21, 199.	1.2	25
78	Structural elements that modulate the substrate specificity of plant purple acid phosphatases: Avenues for improved phosphorus acquisition in crops. <i>Plant Science</i> , 2020, 294, 110445.	1.7	37
79	Molecular and Morphological Divergence of Australian Wild Rice. <i>Plants</i> , 2020, 9, 224.	1.6	4
80	Cereal Genomics Databases and Plant Genetic Resources in Crop Improvement. <i>Methods in Molecular Biology</i> , 2020, 2072, 9-14.	0.4	2
81	Comparison of long-read methods for sequencing and assembly of a plant genome. <i>GigaScience</i> , 2020, 9, .	3.3	62
82	Wild <i>Oryza</i> for Quality Improvement. , 2020, , 299-329.		0
83	Advances in Molecular Genetics and Genomics of African Rice ( <i>Oryza glaberrima</i> Steud). <i>Plants</i> , 2019, 8, 376.	1.6	10
84	Segregation Distortion Observed in the Progeny of Crosses Between <i>Oryza sativa</i> and <i>O. meridionalis</i> Caused by Abortion During Seed Development. <i>Plants</i> , 2019, 8, 398.	1.6	8
85	Relationship between sugarcane culm and leaf biomass composition and saccharification efficiency. <i>Biotechnology for Biofuels</i> , 2019, 12, 247.	6.2	17
86	Australian Wild Rice Populations: A Key Resource for Global Food Security. <i>Frontiers in Plant Science</i> , 2019, 10, 1354.	1.7	23
87	Phenotypic variation in Australian wild <i>Cajanus</i> and their interspecific hybrids. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1699-1712.	0.8	4
88	Target prediction of candidate miRNAs from <i>Oryza sativa</i> for silencing the RYMV genome. <i>Computational Biology and Chemistry</i> , 2019, 83, 107127.	1.1	14
89	Exploring and Exploiting Pan-genomics for Crop Improvement. <i>Molecular Plant</i> , 2019, 12, 156-169.	3.9	172
90	Midrib Sucrose Accumulation and Sugar Transporter Gene Expression in YCS-Affected Sugarcane Leaves. <i>Tropical Plant Biology</i> , 2019, 12, 186-205.	1.0	8

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91	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 654.	1.1	8
92	Evaluation of chloroplast genome annotation tools and application to analysis of the evolution of coffee species. <i>PLoS ONE</i> , 2019, 14, e0216347.	1.1	31
93	Genetic Modification of Biomass to Alter Lignin Content and Structure. <i>Industrial &amp; Engineering Chemistry Research</i> , 2019, 58, 16190-16203.	1.8	23
94	Analysis of the diversity and tissue specificity of sucrose synthase genes in the long read transcriptome of sugarcane. <i>BMC Plant Biology</i> , 2019, 19, 160.	1.6	36
95	Advances in understanding salt tolerance in rice. <i>Theoretical and Applied Genetics</i> , 2019, 132, 851-870.	1.8	148
96	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. <i>Proceedings (mdpi)</i> , 2019, 36, .	0.2	0
97	Analysis of Differences in Gene Expression Associated with Variation in Biomass Composition in Sugarcane. <i>Proceedings (mdpi)</i> , 2019, 36, 164.	0.2	0
98	Introgression of Large Grain Size from Australian Wild Rice and Its Agronomical Importance. <i>Proceedings (mdpi)</i> , 2019, 36, 121.	0.2	0
99	SNPs Linked to Key Traits in Hybrids between African and Asian Rice. <i>Proceedings (mdpi)</i> , 2019, 36, .	0.2	0
100	Transcriptomics Analysis for the Detection of Novel Drought Tolerance Genes in Jojoba ( <i>Simmondsia</i> ) Tj ETQq0 0 0 rBT /Overlock 10 Tf	0.2	0
101	Control of Sugar and Fibre: Insights from Sugarcane Transcriptome Analyses. <i>Proceedings (mdpi)</i> , 2019, 36, 204.	0.2	1
102	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. <i>Plants</i> , 2019, 8, 481.	1.6	5
103	Comparative Transcriptome Profiling of Resistant and Susceptible Sugarcane Cultivars in Response to Infection by <i>Xanthomonas albilineans</i> . <i>International Journal of Molecular Sciences</i> , 2019, 20, 6138.	1.8	26
104	Determination of Phylogenetic Relationships of the Genus <i>Sorghum</i> Using Nuclear and Chloroplast Genome Assembly. <i>Proceedings (mdpi)</i> , 2019, 36, 17.	0.2	1
105	DIFFERENTIAL RESPONSE OF WHEAT GENOTYPES TO HEAT STRESS DURING GRAIN FILLING. <i>Experimental Agriculture</i> , 2019, 55, 818-827.	0.4	6
106	Re-sequencing Resources to Improve Starch and Grain Quality in Rice. <i>Methods in Molecular Biology</i> , 2019, 1892, 201-240.	0.4	0
107	Analysis of the expression of transcription factors and other genes associated with aleurone layer development in wheat endosperm. <i>Journal of Cereal Science</i> , 2019, 85, 62-69.	1.8	3
108	Diversity of Domestication Loci in Wild Rice Populations. <i>Proceedings (mdpi)</i> , 2019, 36, .	0.2	0

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109	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.	4.1	48
110	<i>Oryza meridionalis</i> N.Q.Ng. <i>Compendium of Plant Genomes</i> , 2018, , 177-182.	0.3	5
111	Evolutionary Relationships Among the <i>Oryza</i> Species. <i>Compendium of Plant Genomes</i> , 2018, , 41-54.	0.3	7
112	<i>Oryza australiensis</i> Domin. <i>Compendium of Plant Genomes</i> , 2018, , 61-66.	0.3	2
113	<i>Oryza barthii</i> A. Chev. <i>Compendium of Plant Genomes</i> , 2018, , 67-74.	0.3	2
114	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
115	Phylogeny and Molecular Evolution of miR820 and miR396 microRNA Families in <i>Oryza</i> AA Genomes. <i>Tropical Plant Biology</i> , 2018, 11, 1-16.	1.0	6
116	Towards a genetic road map of wheat-processing quality. <i>Journal of Cereal Science</i> , 2018, 79, 516-517.	1.8	2
117	Filters of floristic exchange: How traits and climate shape the rain forest invasion of Sahul from Sunda. <i>Journal of Biogeography</i> , 2018, 45, 838-847.	1.4	34
118	Diversity and evolution of rice progenitors in Australia. <i>Ecology and Evolution</i> , 2018, 8, 4360-4366.	0.8	32
119	Role of genomics in promoting the utilization of plant genetic resources in genebanks. <i>Briefings in Functional Genomics</i> , 2018, 17, 198-206.	1.3	79
120	De novo assembly and characterizing of the culm-derived meta-transcriptome from the polyploid sugarcane genome based on coding transcripts. <i>Heliyon</i> , 2018, 4, e00583.	1.4	12
121	Annotation of the <i>Corymbia</i> terpene synthase gene family shows broad conservation but dynamic evolution of physical clusters relative to <i>Eucalyptus</i> . <i>Heredity</i> , 2018, 121, 87-104.	1.2	17
122	Sequencing of bulks of segregants allows dissection of genetic control of amylose content in rice. <i>Plant Biotechnology Journal</i> , 2018, 16, 100-110.	4.1	52
123	A Highly Efficient and Reproducible <i>Fusarium</i> spp. Inoculation Method for <i>Brachypodium distachyon</i> . <i>Methods in Molecular Biology</i> , 2018, 1667, 43-55.	0.4	1
124	Evaluating the sensory properties of unpolished Australian wild rice. <i>Food Research International</i> , 2018, 103, 406-414.	2.9	20
125	Origin and evolution of qingke barley in Tibet. <i>Nature Communications</i> , 2018, 9, 5433.	5.8	141
126	Breeding for improved blanchability in peanut: phenotyping, genotype × environment interaction and selection. <i>Crop and Pasture Science</i> , 2018, 69, 1237.	0.7	8



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127	Evidence of inter-sectional chloroplast capture in <i>Corymbia</i> among sections Torellianae and Maculatae. <i>Australian Journal of Botany</i> , 2018, 66, 369.	0.3	11
128	SNP in the <i>Coffea arabica</i> genome associated with coffee quality. <i>Tree Genetics and Genomes</i> , 2018, 14, 1.	0.6	19
129	Wheat seed transcriptome reveals genes controlling key traits for human preference and crop adaptation. <i>Current Opinion in Plant Biology</i> , 2018, 45, 231-236.	3.5	22
130	Chloroplast phylogeography of AA genome rice species. <i>Molecular Phylogenetics and Evolution</i> , 2018, 127, 475-487.	1.2	19
131	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.	1.6	91
132	The Challenge of Analyzing the Sugarcane Genome. <i>Frontiers in Plant Science</i> , 2018, 9, 616.	1.7	80
133	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. <i>Nature Communications</i> , 2018, 9, 2638.	5.8	299
134	The coffee bean transcriptome explains the accumulation of the major bean components through ripening. <i>Scientific Reports</i> , 2018, 8, 11414.	1.6	23
135	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.	1.4	52
136	Variation in bean morphology and biochemical composition measured in different genetic groups of arabica coffee ( <i>Coffea arabica</i> L.). <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	21
137	Grain physical characteristic of the Australian wild rices. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2017, 15, 409-420.	0.4	10
138	Comparison of Chapatti and Breadmaking Quality of Wheat Genotypes. <i>Cereal Chemistry</i> , 2017, 94, 409-416.	1.1	5
139	High-Throughput Profiling of the Fiber and Sugar Composition of Sugarcane Biomass. <i>Bioenergy Research</i> , 2017, 10, 400-416.	2.2	42
140	Molecular structures and properties of starches of Australian wild rice. <i>Carbohydrate Polymers</i> , 2017, 172, 213-222.	5.1	39
141	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.	1.2	180
142	Fasciclin-like arabinogalactan protein gene expression is associated with yield of flour in the milling of wheat. <i>Scientific Reports</i> , 2017, 7, 12539.	1.6	18
143	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.	1.6	76
144	Long-read sequencing of the coffee bean transcriptome reveals the diversity of full-length transcripts. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	90

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145	Does C <sub>4</sub> Photosynthesis Occur in Wheat Seeds?. <i>Plant Physiology</i> , 2017, 174, 1992-1995.	2.3	18
146	Transcriptome analysis of Brachypodium during fungal pathogen infection reveals both shared and distinct defense responses with wheat. <i>Scientific Reports</i> , 2017, 7, 17212.	1.6	27
147	The defence-associated transcriptome of hexaploid wheat displays homoeolog expression and induction bias. <i>Plant Biotechnology Journal</i> , 2017, 15, 533-543.	4.1	110
148	Thirty-three years of 2-acetyl-1-pyrroline, a principal basmati aroma compound in scented rice ( <i>Oryza sativa</i> L.): a status review. <i>Journal of the Science of Food and Agriculture</i> , 2017, 97, 384-395.	1.7	123
149	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. <i>Plant Biotechnology Journal</i> , 2017, 15, 765-774.	4.1	51
150	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.	1.2	46
151	Association of variation in the sugarcane transcriptome with sugar content. <i>BMC Genomics</i> , 2017, 18, 909.	1.2	41
152	<i>Plant Genetic Resources.</i> , 2017, , 15-29.		1
153	Association of gene expression with biomass content and composition in sugarcane. <i>PLoS ONE</i> , 2017, 12, e0183417.	1.1	26
154	Editorial: Biomass Modification, Characterization, and Process Monitoring Analytics to Support Biofuel and Biomaterial Production. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016, 4, 25.	2.0	1
155	Commentary: New evidence for grain specific C <sub>4</sub> photosynthesis in wheat. <i>Frontiers in Plant Science</i> , 2016, 7, 1537.	1.7	12
156	Evaluation of Relationships between Growth Rate, Tree Size, Lignocellulose Composition, and Enzymatic Saccharification in Interspecific <i>Corymbia</i> Hybrids and Parental Taxa. <i>Frontiers in Plant Science</i> , 2016, 7, 1705.	1.7	1
157	Advances in genomics for the improvement of quality in coffee. <i>Journal of the Science of Food and Agriculture</i> , 2016, 96, 3300-3312.	1.7	40
158	Effect of aging on lignin content, composition and enzymatic saccharification in <i>Corymbia</i> hybrids and parental taxa between years 9 and 12. <i>Biomass and Bioenergy</i> , 2016, 93, 50-59.	2.9	17
159	Characterization of fragrance in sorghum ( <i>Sorghum bicolor</i> (L.) Moench) grain and development of a gene-based marker for selection in breeding. <i>Molecular Breeding</i> , 2016, 36, 1.	1.0	18
160	Fungi associated with foliar diseases of wild and cultivated rice ( <i>Oryza</i> spp.) in northern Queensland. <i>Australasian Plant Pathology</i> , 2016, 45, 297-308.	0.5	16
161	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	4.1	221
162	Influence of genotype and environment on coffee quality. <i>Trends in Food Science and Technology</i> , 2016, 57, 20-30.	7.8	150

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346	Conserving genetic diversity in plants of environmental, social or economic importance.. , 2005, , 317-325.		1
347	Importance of plant diversity.. , 2005, , 1-5.		2
348	<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.	0.3	41
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