Robert J. Henry

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4339729/publications.pdf

Version: 2024-02-01

526	24,071	11651	12946
papers	citations	70 h-index	131 g-index

566	566	566	19254
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Systems seed biology to understand and manipulate rice grain quality and nutrition. Critical Reviews in Biotechnology, 2023, 43, 716-733.	9.0	1
2	Secondary genepool of Australian Cajanus species contains sources of resistance to Helicoverpa armigera (HÃ¼bner). Annals of Applied Biology, 2022, 180, 259-272.	2.5	3
3	Deâ€‰novo chromosome level assembly of a plant genome from long read sequence data. Plant Journal, 2022, 109, 727-736.	5.7	20
4	Cyanogenesis in the Sorghum Genus: From Genotype to Phenotype. Genes, 2022, 13, 140.	2.4	7
5	Exogenous putrescine attenuates the negative impact of drought stress by modulating physio-biochemical traits and gene expression in sugar beet (Beta vulgaris L.). PLoS ONE, 2022, 17, e0262099.	2.5	24
6	A Comprehensive High-Quality DNA and RNA Extraction Protocol for a Range of Cultivars and Tissue Types of the Woody Crop Avocado. Plants, 2022, 11, 242.	3.5	9
7	New Hybrid Spikelet Sterility Gene Found in Interspecific Cross between Oryza sativa and O. meridionalis. Plants, 2022, 11, 378.	3.5	2
8	Transcript profiles of wild and domesticated sorghum under water-stressed conditions and the differential impact on dhurrin metabolism. Planta, 2022, 255, 51.	3.2	2
9	Starch Molecular Structural Features and Volatile Compounds Affecting the Sensory Properties of Polished Australian Wild Rice. Foods, 2022, 11, 511.	4.3	2
10	Comparison of the root, leaf and internode transcriptomes in sugarcane (Saccharum spp. hybrids). Current Research in Biotechnology, 2022, 4, 167-178.	3.7	2
11	Transcriptome changes in the developing sugarcane culm associated with high yield and early-season high sugar content. Theoretical and Applied Genetics, 2022, 135, 1619-1636.	3.6	1
12	Supporting in situ conservation of the genetic diversity of crop wild relatives using genomic technologies. Molecular Ecology, 2022, 31, 2207-2222.	3.9	20
13	Applied Biosciences: Application of Biological Science and Technology. , 2022, 1, 38-39.		1
14	Reticulate Evolution in AA-Genome Wild Rice in Australia. Frontiers in Plant Science, 2022, 13, 767635.	3.6	2
15	Tracking habitat or testing its suitability? Similar distributional patterns can hide very different histories of persistence versus nonequilibrium dynamics. Evolution; International Journal of Organic Evolution, 2022, 76, 1209-1228.	2.3	3
16	Wild rice research: Advancing plant science and food security. Molecular Plant, 2022, 15, 563-565.	8.3	2
17	Unveiling the potential of water as a co-solvent in microwave-assisted delignification of sugarcane bagasse using ternary deep eutectic solvents. Bioresource Technology, 2022, 351, 127005.	9.6	28
18	Limited allele-specific gene expression in highly polyploid sugarcane. Genome Research, 2022, 32, 297-308.	5.5	8

#	Article	IF	Citations
19	Potential of Genome Editing to Capture Diversity From Australian Wild Rice Relatives. Frontiers in Genome Editing, 2022, 4, 875243.	5.2	3
20	Allele expression biases in mixed-ploid sugarcane accessions. Scientific Reports, 2022, 12, .	3.3	1
21	Testing the Linearity Assumption for Starch Structure-Property Relationships in Rices. Frontiers in Nutrition, 2022, 9, .	3.7	2
22	Evolution of an intermediate C4 photosynthesis in the non-foliar tissues of the Poaceae. Photosynthesis Research, 2022, 153, 125-134.	2.9	3
23	The Long Read Transcriptome of Rice (Oryza sativa ssp. japonica var. Nipponbare) Reveals Novel Transcripts. Rice, 2022, 15, .	4.0	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. Plant Physiology and Biochemistry, 2021, 158, 321-333.	5.8	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 (Oryza glaberrima Steud) Domestication. Rice, 2021, 14, 6.	4.0	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. Plant Molecular Biology, 2021, 106, 173-192.	3.9	8

#	Article	IF	Citations
37	Nitrogen availability and allocation in sorghum and its wild relatives: Divergent roles for cyanogenic glucosides. Journal of Plant Physiology, 2021, 258-259, 153393.	3.5	8
38	Improving rice salt tolerance by precision breeding in a new era. Current Opinion in Plant Biology, 2021, 60, 101996.	7.1	61
39	Variation in production of cyanogenic glucosides during early plant development: A comparison of wild and domesticated sorghum. Phytochemistry, 2021, 184, 112645.	2.9	16
40	Pests, diseases, and aridity have shaped the genome of Corymbia citriodora. Communications Biology, 2021, 4, 537.	4.4	21
41	Biochemical basis of resistance to pod borer (Helicoverpa armigera) 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. Molecular Plant, 2021, 14, 701-704.	8.3	5
43	Genomic selection and genetic gain for nut yield in an Australian macadamia breeding population. BMC Genomics, 2021, 22, 370.	2.8	13
44	Fragrance in Pandanus amaryllifolius Roxb. Despite the Presence of a Betaine Aldehyde Dehydrogenase 2. International Journal of Molecular Sciences, 2021, 22, 6968.	4.1	4
45	Phylogenetic relationships in the Sorghum genus based on sequencing of the chloroplast and nuclear genes. Plant Genome, 2021, 14, e20123.	2.8	13
46	Phenotypic Characterisation for Growth and Nut Characteristics Revealed the Extent of Genetic Diversity in Wild Macadamia Germplasm. Agriculture (Switzerland), 2021, 11, 680.	3.1	11
47	Arsenic Accumulation in Rice Grain as Influenced by Water Management: Human Health Risk Assessment. Agronomy, 2021, 11, 1741.	3.0	9
48	Identification of genes associated with chapatti quality using transcriptome analysis. Journal of Cereal Science, 2021, 101, 103276.	3.7	0
49	The jojoba genome reveals wide divergence of the sex chromosomes in a dioecious plant. Plant Journal, 2021, 108, 1283-1294.	5.7	9
50	Improving enzymatic digestibility of sugarcane bagasse from different varieties of sugarcane using deep eutectic solvent pretreatment. Bioresource Technology, 2021, 337, 125480.	9.6	46
51	Starch structure-property relations in Australian wild rices compared to domesticated rices. Carbohydrate Polymers, 2021, 271, 118412.	10.2	15
52	Genomics of grain quality in cereals. Crop Breeding and Applied Biotechnology, 2021, 21, .	0.4	1
53	RNA Extraction for Transcriptome Analysis. , 2021, , 440-450.		0
54	Introduction to Transcriptomics. , 2021, , 439.		0

#	Article	IF	Citations
55	Single kernel sorting of high and normal oleic acid peanuts using near infrared spectroscopy. Journal of Near Infrared Spectroscopy, 2021, 29, 366-370.	1.5	3
56	The genome of the endangered Macadamia jansenii displays little diversity but represents an important genetic resource for plant breeding. Plant Direct, 2021, 5, e364.	1.9	7
57	Phylogenetic Relationship among Macadamia integrifolia and Macadamia tetraphylla Wild Accessions. Proceedings (mdpi), 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 Erianthus Arundinaceus. Proceedings (mdpi), 2020, 36, .	0.2	0
59	Crop wild relatives as a genetic resource for generating low-cyanide, drought-tolerant Sorghum. Environmental and Experimental Botany, 2020, 169, 103884.	4.2	28
60	Transcriptome profiling of wheat genotypes under heat stress during grain-filling. Journal of Cereal Science, 2020, 91, 102895.	3.7	32
61	Innovations in plant genetics adapting agriculture to climate change. Current Opinion in Plant Biology, 2020, 56, 168-173.	7.1	57
62	Differential expression in leaves of Saccharum genotypes contrasting in biomass production provides evidence of genes involved in carbon partitioning. BMC Genomics, 2020, 21, 673.	2.8	10
63	Wild Sorghum as a Promising Resource for Crop Improvement. Frontiers in Plant Science, 2020, 11, 1108.	3.6	87
64	Chromosome-Scale Assembly and Annotation of the Macadamia Genome (Macadamia integrifolia) Tj ETQq0 0 0 rgBT /Overlock 1	1.8	26
65	Metabolic changes in the developing sugarcane culm associated with high yield and early high sugar content. Plant Direct, 2020, 4, e00276.	1.9	12
66	Modelled distributions and conservation priorities of wild sorghums (Sorghum Moench). Diversity and Distributions, 2020, 26, 1727-1740.	4.1	11
67	Innovations in Agriculture and Food Supply in Response to the COVID-19 Pandemic. Molecular Plant, 2020, 13, 1095-1097.	8.3	49
68	Two divergent chloroplast genome sequence clades captured in the domesticated rice gene pool may have significance for rice production. BMC Plant Biology, 2020, 20, 472.	3.6	18
69	Mobilizing Crop Biodiversity. Molecular Plant, 2020, 13, 1341-1344.	8.3	50
70	Variation in sugarcane biomass composition and enzymatic saccharification of leaves, internodes and roots. Biotechnology for Biofuels, 2020, 13, 201.	6.2	11
71	Sequence Variants Linked to Key Traits in Interspecific Crosses between African and Asian Rice. Plants, 2020, 9, 1653.	3.5	1
72	Pathways of Photosynthesis in Non-Leaf Tissues. Biology, 2020, 9, 438.	2.8	31

#	Article	IF	Citations
73	Biotic exchange leaves detectable genomic patterns in the Australian rain forest flora. Biotropica, 2020, 52, 627-635.	1.6	6
74	The Nagoya Protocol and historical collections of plants. Nature Plants, 2020, 6, 430-432.	9.3	22
75	Genetic Structure of Wild Germplasm of Macadamia: Species Assignment, Diversity and Phylogeographic Relationships. Plants, 2020, 9, 714.	3.5	13
76	Slower development of lower canopy beans produces better coffee. Journal of Experimental Botany, 2020, 71, 4201-4214.	4.8	10
77	Genome-wide association studies for yield component traits in a macadamia breeding population. BMC Genomics, 2020, 21, 199.	2.8	25
78	Structural elements that modulate the substrate specificity of plant purple acid phosphatases: Avenues for improved phosphorus acquisition in crops. Plant Science, 2020, 294, 110445.	3.6	37
79	Molecular and Morphological Divergence of Australian Wild Rice. Plants, 2020, 9, 224.	3.5	4
80	Cereal Genomics Databases and Plant Genetic Resources in Crop Improvement. Methods in Molecular Biology, 2020, 2072, 9-14.	0.9	2
81	Comparison of long-read methods for sequencing and assembly of a plant genome. GigaScience, 2020, 9, .	6.4	62
82	Wild Oryza for Quality Improvement. , 2020, , 299-329.		0
83	Advances in Molecular Genetics and Genomics of African Rice (Oryza glaberrima Steud). Plants, 2019, 8, 376.	3.5	10
84	Segregation Distortion Observed in the Progeny of Crosses Between Oryza sativa and O. meridionalis Caused by Abortion During Seed Development. Plants, 2019, 8, 398.	3.5	8
85	Relationship between sugarcane culm and leaf biomass composition and saccharification efficiency. Biotechnology for Biofuels, 2019, 12, 247.	6.2	17
86	Australian Wild Rice Populations: A Key Resource for Global Food Security. Frontiers in Plant Science, 2019, 10, 1354.	3.6	23
87	Phenotypic variation in Australian wild Cajanus and their interspecific hybrids. Genetic Resources and Crop Evolution, 2019, 66, 1699-1712.	1.6	4
88	Target prediction of candidate miRNAs from Oryza sativa for silencing the RYMV genome. Computational Biology and Chemistry, 2019, 83, 107127.	2.3	14
89	Exploring and Exploiting Pan-genomics for Crop Improvement. Molecular Plant, 2019, 12, 156-169.	8.3	172
90	Midrib Sucrose Accumulation and Sugar Transporter Gene Expression in YCS-Affected Sugarcane Leaves. Tropical Plant Biology, 2019, 12, 186-205.	1.9	8

#	Article	IF	Citations
91	The Impact of cDNA Normalization on Long-Read Sequencing of a Complex Transcriptome. Frontiers in Genetics, 2019, 10, 654.	2.3	8
92	Evaluation of chloroplast genome annotation tools and application to analysis of the evolution of coffee species. PLoS ONE, 2019, 14, e0216347.	2.5	31
93	Genetic Modification of Biomass to Alter Lignin Content and Structure. Industrial & Engineering Chemistry Research, 2019, 58, 16190-16203.	3.7	23
94	Analysis of the diversity and tissue specificity of sucrose synthase genes in the long read transcriptome of sugarcane. BMC Plant Biology, 2019, 19, 160.	3.6	36
95	Advances in understanding salt tolerance in rice. Theoretical and Applied Genetics, 2019, 132, 851-870.	3.6	148
96	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. Proceedings (mdpi), 2019, 36, .	0.2	0
97	Analysis of Differences in Gene Expression Associated with Variation in Biomass Composition in Sugarcane. Proceedings (mdpi), 2019, 36, 164.	0.2	0
98	Introgression of Large Grain Size from Australian Wild Rice and Its Agronomical Importance. Proceedings (mdpi), 2019, 36, 121.	0.2	0
99	SNPs Linked to Key Traits in Hybrids between African and Asian Rice. Proceedings (mdpi), 2019, 36, .	0.2	0
100	Transcriptomics Analysis for the Detection of Novel Drought Tolerance Genes in Jojoba (Simmondsia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.2	0
101	Control of Sugar and Fibre: Insights from Sugarcane Transcriptome Analyses. Proceedings (mdpi), 2019, 36, 204.	0.2	1
102	Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. Plants, 2019, 8, 481.	3.5	5
103	Comparative Transcriptome Profiling of Resistant and Susceptible Sugarcane Cultivars in Response to Infection by Xanthomonas albilineans. International Journal of Molecular Sciences, 2019, 20, 6138.	4.1	26
104	Determination of Phylogenetic Relationships of the Genus Sorghum Using Nuclear and Chloroplast Genome Assembly. Proceedings (mdpi), 2019, 36, 17.	0.2	1
105	DIFFERENTIAL RESPONSE OF WHEAT GENOTYPES TO HEAT STRESS DURING GRAIN FILLING. Experimental Agriculture, 2019, 55, 818-827.	0.9	6
106	Re-sequencing Resources to Improve Starch and Grain Quality in Rice. Methods in Molecular Biology, 2019, 1892, 201-240.	0.9	0
107	Analysis of the expression of transcription factors and other genes associated with aleurone layer development in wheat endosperm. Journal of Cereal Science, 2019, 85, 62-69.	3.7	3
108	Diversity of Domestication Loci in Wild Rice Populations. Proceedings (mdpi), 2019, 36, .	0.2	0

#	Article	IF	Citations
109	Use of a draft genome of coffee (Coffea arabica) to identify <scp>SNP</scp>s associated with caffeine content. Plant Biotechnology Journal, 2018, 16, 1756-1766.	8.3	48
110	Oryza meridionalis N.Q.Ng. Compendium of Plant Genomes, 2018, , 177-182.	0.5	5
111	Evolutionary Relationships Among the Oryza Species. Compendium of Plant Genomes, 2018, , 41-54.	0.5	7
112	Oryza australiensis Domin. Compendium of Plant Genomes, 2018, , 61-66.	0.5	2
113	Oryza barthii A. Chev. Compendium of Plant Genomes, 2018, , 67-74.	0.5	2
114	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
115	Phylogeny and Molecular Evolution of miR820 and miR396 microRNA Families in Oryza AA Genomes. Tropical Plant Biology, 2018, 11, 1-16.	1.9	6
116	Towards a genetic road map of wheat-processing quality. Journal of Cereal Science, 2018, 79, 516-517.	3.7	2
117	Filters of floristic exchange: How traits and climate shape the rain forest invasion of Sahul from Sunda. Journal of Biogeography, 2018, 45, 838-847.	3.0	34
118	Diversity and evolution of rice progenitors in Australia. Ecology and Evolution, 2018, 8, 4360-4366.	1.9	32
119	Role of genomics in promoting the utilization of plant genetic resources in genebanks. Briefings in Functional Genomics, 2018, 17, 198-206.	2.7	79
120	De novo assembly and characterizing of the culm-derived meta-transcriptome from the polyploid sugarcane genome based on coding transcripts. Heliyon, 2018, 4, e00583.	3.2	12
121	Annotation of the Corymbia terpene synthase gene family shows broad conservation but dynamic evolution of physical clusters relative to Eucalyptus. Heredity, 2018, 121, 87-104.	2.6	17
122	Sequencing of bulks of segregants allows dissection of genetic control of amylose content in rice. Plant Biotechnology Journal, 2018, 16, 100-110.	8.3	52
123	A Highly Efficient and Reproducible Fusarium spp. Inoculation Method for Brachypodium distachyon. Methods in Molecular Biology, 2018, 1667, 43-55.	0.9	1
124	Evaluating the sensory properties of unpolished Australian wild rice. Food Research International, 2018, 103, 406-414.	6.2	20
125	Origin and evolution of qingke barley in Tibet. Nature Communications, 2018, 9, 5433.	12.8	141
126	Breeding for improved blanchability in peanut: phenotyping, genotype Ã— environment interaction and selection. Crop and Pasture Science, 2018, 69, 1237.	1.5	8

#	Article	IF	Citations
127	Evidence of inter-sectional chloroplast capture in Corymbia among sections Torellianae and Maculatae. Australian Journal of Botany, 2018, 66, 369.	0.6	11
128	SNP in the Coffea arabica genome associated with coffee quality. Tree Genetics and Genomes, 2018, 14, 1.	1.6	19
129	Wheat seed transcriptome reveals genes controlling key traits for human preference and crop adaptation. Current Opinion in Plant Biology, 2018, 45, 231-236.	7.1	22
130	Chloroplast phylogeography of AA genome rice species. Molecular Phylogenetics and Evolution, 2018, 127, 475-487.	2.7	19
131	Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content. Scientific Reports, 2018, 8, 11612.	3.3	91
132	The Challenge of Analyzing the Sugarcane Genome. Frontiers in Plant Science, 2018, 9, 616.	3.6	80
133	A mosaic monoploid reference sequence for the highly complex genome of sugarcane. Nature Communications, 2018, 9, 2638.	12.8	299
134	The coffee bean transcriptome explains the accumulation of the major bean components through ripening. Scientific Reports, 2018, 8, 11414.	3.3	23
135	The Fusarium crown rot pathogenFusarium pseudograminearumtriggers a suite of transcriptional and metabolic changes in bread wheat (Triticum aestivumL.). Annals of Botany, 2017, 119, mcw207.	2.9	52
136	Variation in bean morphology and biochemical composition measured in different genetic groups of arabica coffee (Coffea arabica L.). Tree Genetics and Genomes, 2017, 13, 1.	1.6	21
137	Grain physical characteristic of the Australian wild rices. Plant Genetic Resources: Characterisation and Utilisation, 2017, 15, 409-420.	0.8	10
138	Comparison of Chapatti and Breadmaking Quality of Wheat Genotypes. Cereal Chemistry, 2017, 94, 409-416.	2.2	5
139	High-Throughput Profiling of the Fiber and Sugar Composition of Sugarcane Biomass. Bioenergy Research, 2017, 10, 400-416.	3.9	42
140	Molecular structures and properties of starches of Australian wild rice. Carbohydrate Polymers, 2017, 172, 213-222.	10.2	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. BMC Genomics, 2017, 18, 395.	2.8	180
142	Fasciclin-like arabinogalactan protein gene expression is associated with yield of flour in the milling of wheat. Scientific Reports, 2017, 7, 12539.	3.3	18
143	Effects of genotype and temperature on accumulation of plant secondary metabolites in Canadian and Australian wheat grown under controlled environments. Scientific Reports, 2017, 7, 9133.	3.3	76
144	Long-read sequencing of the coffee bean transcriptome reveals the diversity of full-length transcripts. GigaScience, 2017, 6, 1-13.	6.4	90

#	Article	IF	Citations
145	Does C₄ Photosynthesis Occur in Wheat Seeds?. Plant Physiology, 2017, 174, 1992-1995.	4.8	18
146	Transcriptome analysis of Brachypodium during fungal pathogen infection reveals both shared and distinct defense responses with wheat. Scientific Reports, 2017, 7, 17212.	3.3	27
147	The defenceâ€associated transcriptome of hexaploid wheat displays homoeolog expression and induction bias. Plant Biotechnology Journal, 2017, 15, 533-543.	8.3	110
148	Thirty-three years of 2-acetyl-1-pyrroline, a principal basmati aroma compound in scented rice (Oryza sativaL.): a status review. Journal of the Science of Food and Agriculture, 2017, 97, 384-395.	3.5	123
149	Sequencing of Australian wild rice genomes reveals ancestral relationships with domesticated rice. Plant Biotechnology Journal, 2017, 15, 765-774.	8.3	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. BMC Genomics, 2017, 18, 766.	2.8	46
151	Association of variation in the sugarcane transcriptome with sugar content. BMC Genomics, 2017, 18, 909.	2.8	41
152	Plant Genetic Resources. , 2017, , 15-29.		1
153	Association of gene expression with biomass content and composition in sugarcane. PLoS ONE, 2017, 12, e0183417.	2.5	26
154	Editorial: Biomass Modification, Characterization, and Process Monitoring Analytics to Support Biofuel and Biomaterial Production. Frontiers in Bioengineering and Biotechnology, 2016, 4, 25.	4.1	1
155	Commentary: New evidence for grain specific C4 photosynthesis in wheat. Frontiers in Plant Science, 2016, 7, 1537.	3.6	12
156	Evaluation of Relationships between Growth Rate, Tree Size, Lignocellulose Composition, and Enzymatic Saccharification in Interspecific Corymbia Hybrids and Parental Taxa. Frontiers in Plant Science, 2016, 7, 1705.	3.6	1
157	Advances in genomics for the improvement of quality in coffee. Journal of the Science of Food and Agriculture, 2016, 96, 3300-3312.	3.5	40
158	Effect of aging on lignin content, composition and enzymatic saccharification in Corymbia hybrids and parental taxa between years 9 and 12. Biomass and Bioenergy, 2016, 93, 50-59.	5.7	17
159	Characterization of fragrance in sorghum (Sorghum bicolor (L.) Moench) grain and development of a gene-based marker for selection in breeding. Molecular Breeding, 2016, 36, 1.	2.1	18
160	Fungi associated with foliar diseases of wild and cultivated rice (Oryza spp.) in northern Queensland. Australasian Plant Pathology, 2016, 45, 297-308.	1.0	16
161	Global agricultural intensification during climate change: a role for genomics. Plant Biotechnology Journal, 2016, 14, 1095-1098.	8.3	221
162	Influence of genotype and environment on coffee quality. Trends in Food Science and Technology, 2016, 57, 20-30.	15.1	150

#	Article	IF	Citations
163	New evidence for grain specific C4 photosynthesis in wheat. Scientific Reports, 2016, 6, 31721.	3.3	62
164	Genome and transcriptome sequencing characterises the gene space of Macadamia integrifolia (Proteaceae). BMC Genomics, 2016, 17, 937.	2.8	45
165	Functional cereals for production in new and variable climates. Current Opinion in Plant Biology, 2016, 30, 11-18.	7.1	33
166	Molecular cloning and characterization of a novel bi-functional Î±-amylase/subtilisin inhibitor from Hevea brasiliensis. Plant Physiology and Biochemistry, 2016, 101, 76-87.	5.8	26
167	Genomics of crop wild relatives: expanding the gene pool for crop improvement. Plant Biotechnology Journal, 2016, 14, 1070-1085.	8.3	303
168	Genomics Strategies for Germplasm Characterization and the Development of Climate Resilient Crops. , 2016, , 3-10.		2
169	Influence of Gene Expression on Hardness in Wheat. PLoS ONE, 2016, 11, e0164746.	2.5	24
170	Implications of Advances in Molecular Genetic Technology for Food Security and Ownership. , 2016, , 11-20.		0
171	Developing Cereals Acceptable to Consumers for Production in New and Variable Climates. Procedia Environmental Sciences, 2015, 29, 9-10.	1.4	0
172	Next generation sequencing of total DNA from sugarcane provides no evidence for chloroplast heteroplasmy. New Negatives in Plant Science, 2015, 1-2, 33-45.	0.9	23
173	Relationships of wild and domesticated rices (Oryza AA genome species) based upon whole chloroplast genome sequences. Scientific Reports, 2015, 5, 13957.	3.3	148
174	Analysis of the chloroplast genome of a coffee relative from northern Australia. Acta Horticulturae, 2015, , 177-182.	0.2	0
175	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. Frontiers in Plant Science, 2015, 6, 563.	3.6	243
176	Potential for Genetic Improvement of Sugarcane as a Source of Biomass for Biofuels. Frontiers in Bioengineering and Biotechnology, 2015, 3, 182.	4.1	109
177	Efficient Eucalypt Cell Wall Deconstruction and Conversion for Sustainable Lignocellulosic Biofuels. Frontiers in Bioengineering and Biotechnology, 2015, 3, 190.	4.1	18
178	Sustainable Utilization of TCM Resources. Evidence-based Complementary and Alternative Medicine, 2015, 2015, 1-2.	1.2	4
179	A novel highly differentially expressed gene in wheat endosperm associated with bread quality. Scientific Reports, 2015, 5, 10446.	3.3	37
180	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

#	Article	IF	Citations
181	Prospects of breeding high-quality rice using post-genomic tools. Theoretical and Applied Genetics, 2015, 128, 1449-1466.	3.6	53
182	High-Throughput Prediction of Acacia and Eucalypt Lignin Syringyl/Guaiacyl Content Using FT-Raman Spectroscopy and Partial Least Squares Modeling. Bioenergy Research, 2015, 8, 953-963.	3.9	9
183	The biosynthesis, structure and gelatinization properties of starches from wild and cultivated African rice species (Oryza barthii and Oryza glaberrima). Carbohydrate Polymers, 2015, 129, 92-100.	10.2	75
184	Roles of GBSSI and SSIIa in determining amylose fine structure. Carbohydrate Polymers, 2015, 127, 264-274.	10.2	59
185	Characterisation of alleles of the sucrose phosphate synthase gene family in sugarcane and their association with sugar-related traits. Molecular Breeding, 2015, 35, 1.	2.1	12
186	Brachypodium as an emerging model for cerealâ€“pathogen interactions. Annals of Botany, 2015, 115, 717-731.	2.9	60
187	RiTE database: a resource database for genus-wide rice genomics and evolutionary biology. BMC Genomics, 2015, 16, 538.	2.8	86
188	Localization of polyhydroxybutyrate in sugarcane using Fourier-transform infrared microspectroscopy and multivariate imaging. Biotechnology for Biofuels, 2015, 8, 98.	6.2	10
189	Genome wide polymorphisms and yield heterosis in rice (Oryza sativa subsp. indica). Tropical Plant Biology, 2015, 8, 117-125.	1.9	2
190	Plant <scp>DNA</scp> barcoding: from gene to genome. Biological Reviews, 2015, 90, 157-166.	10.4	582
191	Direct Chloroplast Sequencing: Comparison of Sequencing Platforms and Analysis Tools for Whole Chloroplast Barcoding. PLoS ONE, 2014, 9, e110387.	2.5	22
192	Chloroplast Genome of Novel Rice Germplasm Identified in Northern Australia. Tropical Plant Biology, 2014, 7, 111-120.	1.9	43
193	Next-Generation Technologies to Determine Plastid Genome Sequences. Methods in Molecular Biology, 2014, 1132, 39-46.	0.9	5
194	Genomics strategies for germplasm characterization and the development of climate resilient crops. Frontiers in Plant Science, 2014, 5, 68.	3.6	49
195	A comprehensive genetic map of sugarcane that provides enhanced map coverage and integrates high-throughput Diversity Array Technology (DArT) markers. BMC Genomics, 2014, 15, 152.	2.8	61
196	Exploring natural selection to guide breeding for agriculture. Plant Biotechnology Journal, 2014, 12, 655-662.	8.3	58
197	Adaptive evolution of Î±â€amylase genes in wild barley (Hordeum spontaneum) on micro and macro scales. Journal of Systematics and Evolution, 2014, 52, 765-778.	3.1	3
198	Sequencing of wild crop relatives to support the conservation and utilization of plant genetic resources. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, S9-S11.	0.8	25

#	Article	IF	Citations
199	A Method for Discovery of Genome-Wide SNP Between Any Two Genotypes from Whole-Genome Re-sequencing Data. Methods in Molecular Biology, 2014, 1099, 287-294.	0.9	1
200	Modifying plants for biofuel and biomaterial production. Plant Biotechnology Journal, 2014, 12, 1246-1258.	8.3	82
201	Assessment of Lignocellulosic Biomass Using Analytical Spectroscopy: an Evolution to High-Throughput Techniques. Bioenergy Research, 2014, 7, 1-23.	3.9	111
202	Wild Oryza Grain Physico-Chemical Properties. Tropical Plant Biology, 2014, 7, 13-18.	1.9	9
203	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	12.6	520
204	Variation in Amylose Fine Structure of Starches from Different Botanical Sources. Journal of Agricultural and Food Chemistry, 2014, 62, 4443-4453.	5.2	134
205	Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. Plant Methods, 2014, 10, 21.	4.3	339
206	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. Biotechnology for Biofuels, 2014, 7, 93.	6.2	41
207	Escape from the laboratory: new horizons for plant genetics. Trends in Plant Science, 2014, 19, 554-555.	8.8	17
208	A Survey Sequence Comparison of Saccharum Genotypes Reveals Allelic Diversity Differences. Tropical Plant Biology, 2014, 7, 71-83.	1.9	14
209	Causal Relations Among Starch Biosynthesis, Structure, and Properties. Springer Science Reviews, 2014, 2, 15-33.	1.3	49
210	Wheat Genomics for Grain Quality Improvement. Cereal Foods World, 2014, 59, 22-24.	0.2	11
211	Contrasting breeding systems revealed in the rainforest genus Davidsonia (Cunoniaceae): can polyembryony turn the tables on rarity?. Australian Journal of Botany, 2014, 62, 451.	0.6	5
212	Australian Wild Rice Reveals Pre-Domestication Origin of Polymorphism Deserts in Rice Genome. PLoS ONE, 2014, 9, e98843.	2.5	36
213	Novel microsatellite markers for the endangered Australian rainforest tree Davidsonia jerseyana (Cunoniaceae) and cross-species amplification in the Davidsonia genus. Conservation Genetics Resources, 2013, 5, 161-164.	0.8	5
214	Capturing chloroplast variation for molecular ecology studies: a simple next generation sequencing approach applied to a rainforest tree. BMC Ecology, 2013, 13, 8.	3.0	123
215	Complete chloroplast genome sequence of Magnolia grandiflora and comparative analysis with related species. Science China Life Sciences, 2013, 56, 189-198.	4.9	58
216	SSR analysis of introgression of drought tolerance from the genome of Hordeum spontaneum into cultivated barley (Hordeum vulgare ssp vulgare). Euphytica, 2013, 191, 231-243.	1.2	18

#	Article	IF	Citations
217	Independent target region amplification polymorphism and singleâ€nucleotide polymorphism marker utility in genetic evaluation of sugarcane genotypes. Plant Breeding, 2013, 132, 736-747.	1.9	13
218	Genetic analysis and phenotypic associations for drought tolerance in Hordeum spontaneum introgression lines using SSR and SNP markers. Euphytica, 2013, 189, 9-29.	1.2	42
219	Comparative genomics analysis in <scp>P</scp>runoideae to identify biologically relevant polymorphisms. Plant Biotechnology Journal, 2013, 11, 883-893.	8.3	20
220	SNP genotyping allows an in-depth characterisation of the genome of sugarcane and other complex autopolyploids. Scientific Reports, 2013, 3, 3399.	3.3	129
221	Microsatellite markers for Eucalyptus pilularis (Subgenus Eucalyptus); sourcing genetic markers outside the subgenus. Silvae Genetica, 2013, 62, 246-255.	0.8	1
222	Conservation and utilization of African Oryza genetic resources. Rice, 2013, 6, 29.	4.0	45
223	Molecular relationships between Australian annual wild rice, Oryza meridionalis, and two related perennial forms. Rice, 2013, 6, 26.	4.0	43
224	High-Throughput Sequencing and Mutagenesis to Accelerate the Domestication of Microlaena stipoides as a New Food Crop. PLoS ONE, 2013, 8, e82641.	2.5	43
225	Facilitation of Future Research and Extension Through Funding and Networking Support. , 2013, , 415-432.		4
226	Analysis of adaptive ribosomal gene diversity in wild plant populations from contrasting climatic environments. Plant Signaling and Behavior, 2012, 7, 602-604.	2.4	15
227	SNP in starch biosynthesis genes associated with nutritional and functional properties of rice. Scientific Reports, 2012, 2, 557.	3.3	93
228	Pectin Methylesterase Genes Influence Solid Wood Properties of Eucalyptus pilularis Â Â Â Â. Plant Physiology, 2012, 158, 531-541.	4.8	41
229	Next-generation sequencing for understanding and accelerating crop domestication. Briefings in Functional Genomics, 2012, 11, 51-56.	2.7	62
230	Advances in DNA sequencing enabling more rapid development of improved biomass and biofuel conversion technologies. Biofuels, 2012, 3, 507-509.	2.4	4
231	Application of large-scale sequencing to marker discovery in plants. Journal of Biosciences, 2012, 37, 829-841.	1.1	35
232	Analysis of Starch Gene Diversity in the Wild Relatives of Oryza sativa. Tropical Plant Biology, 2012, 5, 286-308.	1.9	17
233	Structural and Chemical Characterization of Hardwood from Tree Species with Applications as Bioenergy Feedstocks. PLoS ONE, 2012, 7, e52820.	2.5	32
234	Chloroplast genome sequence confirms distinctness of Australian and Asian wild rice. Ecology and Evolution, 2012, 2, 211-217.	1.9	84

#	Article	IF	Citations
235	Variation in sorghum starch synthesis genes associated with differences in starch phenotype. Food Chemistry, 2012, 131, 175-183.	8.2	41
236	Genomeâ€wide DNA polymorphisms in elite indica rice inbreds discovered by wholeâ€genome sequencing. Plant Biotechnology Journal, 2012, 10, 623-634.	8.3	175
237	Gene expression in the developing aleurone and starchy endosperm of wheat. Plant Biotechnology Journal, 2012, 10, 668-679.	8.3	75
238	Enrichment of genomic DNA for polymorphism detection in a nonâ€model highly polyploid crop plant. Plant Biotechnology Journal, 2012, 10, 657-667.	8.3	44
239	Preface: advances in DNA sequencing accelerating plant biotechnology. Plant Biotechnology Journal, 2012, 10, 621-622.	8.3	16
240	Genomics for Bioenergy Production. , 2012, , 21-29.		2
241	Sorghum. , 2011, , 397-406.		4
242	Saccharum. , 2011, , 165-177.		15
243	Miscanthus. , 2011, , 157-164.		11
244	Erianthus. , 2011, , 97-107.		32
245	Eucalyptus. , 2011, , 65-75.		2
246	The potential contribution of wild barley (Hordeum vulgare ssp. spontaneum) germplasm to drought tolerance of cultivated barley (H. vulgare ssp. vulgare). Field Crops Research, 2011, 120, 161-168.	5.1	54
247	Chloroplast genome sequences from total DNA for plant identification. Plant Biotechnology Journal, 2011, 9, 328-333.	8.3	316
248	Discovery of polymorphisms in starchâ€related genes in rice germplasm by amplification of pooled DNA and deeply parallel sequencing^{â€}. Plant Biotechnology Journal, 2011, 9, 1074-1085.	8.3	65
249	Characterizing homologues of crop domestication genes in poorly described wild relatives by highâ€throughput sequencing of whole genomes. Plant Biotechnology Journal, 2011, 9, 1131-1140.	8.3	28
250	DNA sequencing methods contributing to new directions in cereal research. Journal of Cereal Science, 2011, 54, 395-400.	3.7	21
251	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. Tropical Plant Biology, 2011, 4, 145-156.	1.9	91
252	The Endosperm Morphology of Rice and its Wild Relatives as Observed by Scanning Electron Microscopy. Rice, 2011, 4, 12-20.	4.0	27

#	Article	IF	Citations
253	SNP discovery and association mapping in Eucalyptus pilularis (blackbutt). BMC Proceedings, 2011, 5, .	1.6	3
254	Genome diversity in wild grasses under environmental stress. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21140-21145.	7.1	38
255	Eucalypts as a biofuel feedstock. Biofuels, 2011, 2, 639-657.	2.4	40
256	Australian Oryza: Utility and Conservation. Rice, 2010, 3, 235-241.	4.0	57
257	Two sympatric spotted gum species are molecularly homogeneous. Conservation Genetics, 2010, 11, 45-56.	1.5	20
258	Capture of assay template by multiplex PCR of long amplicons for genotyping SNPs and InDels with MALDI-TOF mass spectrometry. Molecular Breeding, 2010, 25, 471-480.	2.1	15
259	Puroindoline genotype, starch granule size distribution and milling quality of wheat. Journal of Cereal Science, 2010, 52, 314-320.	3.7	23
260	Cereal variety identification using MALDI-TOF mass spectrometry SNP genotyping. Journal of Cereal Science, 2010, 52, 356-361.	3.7	14
261	Fragrance in rice (Oryza sativa) is associated with reduced yield under salt treatment. Environmental and Experimental Botany, 2010, 68, 292-300.	4.2	64
262	Evaluation of plant biomass resources available for replacement of fossil oil. Plant Biotechnology Journal, 2010, 8, 288-293.	8.3	95
263	The role of plant biotechnology in bio-energy production. Plant Biotechnology Journal, 2010, 8, 243-243.	8.3	5
264	Whole grain morphology of Australian rice species. Plant Genetic Resources: Characterisation and Utilisation, 2010, 8, 74-81.	0.8	12
265	Geographical and historical determinants of microsatellite variation in Eucalyptus pilularis. Canadian Journal of Forest Research, 2010, 40, 1051-1063.	1.7	16
266	Genetic association studies inEucalyptus pilularisSmith (blackbutt). Australian Forestry, 2010, 73, 254-258.	0.9	13
267	An Overview of Advances in Plant Genomics in the New Millennium. , 2010, , 1-23.		0
268	Aleurone and subaleurone morphology in native Australian wild cereal relatives. Australian Journal of Botany, 2009, 57, 688.	0.6	9
269	Variation in Granule Bound Starch Synthase I (GBSSI) loci amongst Australian wild cereal relatives (Poaceae). Journal of Cereal Science, 2009, 49, 4-11.	3.7	23
270	Analysis of promoters in transgenic barley and wheat. Plant Biotechnology Journal, 2009, 7, 240-253.	8.3	58

#	Article	IF	Citations
271	Targeted single nucleotide polymorphism (SNP) discovery in a highly polyploid plant species using 454 sequencing. Plant Biotechnology Journal, 2009, 7, 347-354.	8.3	134
272	A highâ€throughput assay for rapid and simultaneous analysis of perfect markers for important quality and agronomic traits in rice using multiplexed MALDIâ€TOF mass spectrometry. Plant Biotechnology Journal, 2009, 7, 355-363.	8.3	36
273	New tools for single nucleotide polymorphism (SNP) discovery and analysis accelerating plant biotechnology. Plant Biotechnology Journal, 2009, 7, 311-311.	8.3	22
274	Betaine aldehyde dehydrogenase in plants. Plant Biology, 2009, 11, 119-130.	3.8	101
275	Is Malting Barley Better Feed for Cattle than Feed Barley?. Journal of the Institute of Brewing, 2009, 115, 95-104.	2.3	15
276	CHAPTER 11: Enzymes and Enzyme Inhibitors Endogenous to Wheat. , 2009, , 401-435.		14
277	THE GENOMICS OF FRUIT QUALITY. Acta Horticulturae, 2009, , 421-426.	0.2	1
278	Inactivation of an aminoaldehyde dehydrogenase is responsible for fragrance in rice. Plant Molecular Biology, 2008, 68, 439-449.	3.9	199
279	Mapping species differences for adventitious rooting in a Corymbia torelliana Ã— Corymbia citriodora subspecies variegata hybrid. Tree Genetics and Genomes, 2008, 4, 715-725.	1.6	28
280	Assessing for genetic and environmental effects on ruminant feed quality in barley (Hordeum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382	1.2	15
281	Genetic diversity of ICARDAâ€™s worldwide barley landrace collection. Genetic Resources and Crop Evolution, 2008, 55, 1221-1230.	1.6	24
282	Endonucleolytic mutation analysis by internal labeling (EMAIL). Electrophoresis, 2008, 29, 1291-1301.	2.4	26
283	Comparison of promoters in transgenic rice. Plant Biotechnology Journal, 2008, 6, 679-693.	8.3	61
284	Effect of endosperm starch granule size distribution on milling yield in hard wheat. Journal of Cereal Science, 2008, 48, 180-192.	3.7	34
285	GTP cyclohydrolase 1 expression and folate accumulation in the developing wheat seed. Journal of Cereal Science, 2008, 48, 503-512.	3.7	19
286	Genes of folate biosynthesis in wheat. Journal of Cereal Science, 2008, 48, 632-638.	3.7	15
287	The effect of salt on betaine aldehyde dehydrogenase transcript levels and 2-acetyl-1-pyrroline concentration in fragrant and non-fragrant rice (Oryza sativa). Plant Science, 2008, 175, 539-546.	3.6	41
288	Differential LongSAGE tag abundance analysis in a barley seed germination time course and validation with relative real-time RT-PCR. Plant Science, 2008, 175, 858-867.	3.6	8

#	Article	IF	Citations
289	Endosperm and starch granule morphology in wild cereal relatives. Plant Genetic Resources: Characterisation and Utilisation, 2008, 6, 85-97.	0.8	62
290	SNP discovery in plants.. , 2008, , 1-29.		8
291	Snp discovery by ecotilling using capillary electrophoresis.. , 2008, , 78-87.		3
292	Nanotechnology: the future of cost-effective plant genotyping.. , 2008, , 133-153.		1
293	Genotyping for rice eating qualities.. , 2008, , 187-194.		1
294	DNA extraction from plant tissue.. , 2008, , 219-271.		9
295	Future prospects for plant genotyping.. , 2008, , 272-280.		3
296	Genetic Variation Within Two Sympatric Spotted Gum Eucalypts Exceeds Between Taxa Variation. Silvae Genetica, 2008, 57, 249-256.	0.8	17
297	Rare SNP discovery with endonucleases.. , 2008, , 44-67.		0
298	Sequence polymorphisms in the flanking regions of microsatellite markers.. , 2008, , 68-77.		0
299	Towards universal loci for plant genotyping.. , 2008, , 195-206.		0
300	Mutation screening.. , 2008, , 114-132.		0
301	Genotyping by allele-specific PCR.. , 2008, , 88-97.		0
302	DNA banks as a resource for SNP genotyping.. , 2008, , 207-218.		0
303	Domestication to Crop Improvement: Genetic Resources for Sorghum and Saccharum (Andropogoneae). Annals of Botany, 2007, 100, 975-989.	2.9	227
304	Genetic Manipulation of Starch Properties in Plants: Patents 2001-2006. Recent Patents on Biotechnology, 2007, 1, 252-259.	0.8	5
305	Genomics as a Tool for Cereal Chemistry. Cereal Chemistry, 2007, 84, 365-369.	2.2	6
306	Assessment of commercial milling potential of hard wheat by measurement of the rheological properties of whole grain. Journal of Cereal Science, 2007, 45, 122-127.	3.7	30

#	Article	IF	Citations
307	Adaptive climatic molecular evolution in wild barley at the Isa defense locus. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2773-2778.	7.1	64
308	Grape. , 2007, , 63-101.		2
309	Microsatellites retain phylogenetic signals across genera in eucalypts (Myrtaceae). Genetics and Molecular Biology, 2007, 30, 1125-1134.	1.3	34
310	Nuclear ribosomal pseudogenes resolve a corroborated monophyly of the eucalypt genus Corymbia despite misleading hypotheses at functional ITS paralogs. Molecular Phylogenetics and Evolution, 2007, 44, 752-764.	2.7	47
311	SAGE of the developing wheat caryopsis. Plant Biotechnology Journal, 2007, 5, 69-83.	8.3	49
312	A quinolizidine alkaloid O-tigloyltransferase gene in wild and domesticated white lupin (Lupinus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 5	2.5	5
313	Investigation of the effect of conditioning on the fracture of hard and soft wheat grain by the single-kernel characterization system: A comparison with roller milling. Journal of Cereal Science, 2007, 46, 64-74.	3.7	17
314	Measurement of genetic and environmental variation in barley (Hordeum vulgare) grain hardness. Journal of Cereal Science, 2007, 46, 82-92.	3.7	44
315	Relationship Between Hardness Genes and Quality in Barley (Hordeum vulgare). Journal of the Institute of Brewing, 2007, 113, 87-95.	2.3	26
316	Measurement of Barley Grain Rheology for the Quality Selection of Breeding Material. Journal of the Institute of Brewing, 2007, 113, 135-141.	2.3	11
317	Pollen flow in Eucalyptus grandis determined by paternity analysis using microsatellite markers. Tree Genetics and Genomes, 2007, 4, 37-47.	1.6	46
318	Sorghum resolved as a distinct genus based on combined ITS1, ndhF and Adh1 analyses. Plant Systematics and Evolution, 2007, 268, 29-43.	0.9	32
319	The ripening wine grape berry skin transcriptome. Plant Science, 2006, 171, 132-138.	3.6	26
320	The process for implementation of a Quality Management System within a multi-functional cereal laboratory. Quality Assurance Journal, 2006, 10, 262-269.	0.1	1
321	Gelatinization temperature of rice explained by polymorphisms in starch synthase. Plant Biotechnology Journal, 2006, 4, 115-122.	8.3	161
322	Abundant transcripts of malting barley identified by serial analysis of gene expression (SAGE). Plant Biotechnology Journal, 2006, 4, 289-301.	8.3	37
323	Locked nucleic acids for optimizing displacement probes for quantitative real-time PCR. Analytical Biochemistry, 2006, 348, 294-299.	2.4	16
324	An optimized ecotilling protocol for polyploids or pooled samples using a capillary electrophoresis system. Analytical Biochemistry, 2006, 355, 145-147.	2.4	22

#	Article	IF	Citations
325	Genetic Impacts of the Hull on Barley Grain Quality. Journal of the Institute of Brewing, 2006, 112, 101-107.	2.3	12
326	Chloroplast DNA variation and population structure in the widespread forest tree, Eucalyptus grandis. Conservation Genetics, 2006, 7, 691-703.	1.5	31
327	Sequence Polymorphism Discovery in Wheat Microsatellite Flanking Regions using Pyrophosphate Sequencing. Molecular Breeding, 2006, 17, 281-289.	2.1	23
328	Congruence in QTL for adventitious rooting in Pinus elliottiiâ€‰Ã—â€‰Pinus caribaea hybrids resolves between and within-species effects. Molecular Breeding, 2006, 18, 11-28.	2.1	16
329	The identification and characterisation of alleles of sucrose phosphate synthase gene family III in sugarcane. Molecular Breeding, 2006, 18, 39-50.	2.1	39
330	Screening for the rice blast resistance gene Pi-ta using LNA displacement probes and real-time PCR. Molecular Breeding, 2006, 18, 185-193.	2.1	8
331	Robust allele-specific polymerase chain reaction markers developed for single nucleotide polymorphisms in expressed barley sequences. Theoretical and Applied Genetics, 2006, 112, 358-365.	3.6	37
332	Characterisation of single nucleotide polymorphisms in sugarcane ESTs. Theoretical and Applied Genetics, 2006, 113, 331-343.	3.6	58
333	Selecting for increased barley grain size. Journal of Cereal Science, 2006, 43, 198-208.	3.7	34
334	DNA banks and their role in facilitating the application of genomics to plant germplasm. Plant Genetic Resources: Characterisation and Utilisation, 2006, 4, 64-70.	0.8	11
335	Construction of Microsatellite Linkage Maps for Corymbia. Silvae Genetica, 2006, 55, 228-238.	0.8	35
336	The new use of Sorghum bicolor-derived SSR markers to evaluate genetic diversity in 17 Australian Sorghum species. Plant Genetic Resources: Characterisation and Utilisation, 2005, 3, 19-28.	0.8	15
337	The gene for fragrance in rice. Plant Biotechnology Journal, 2005, 3, 363-370.	8.3	371
338	The wheat Em promoter drives reporter gene expression in embryo and aleurone tissue of transgenic barley and rice. Plant Biotechnology Journal, 2005, 3, 421-434.	8.3	40
339	A universal protocol for identification of cereals. Journal of Cereal Science, 2005, 41, 37-46.	3.7	13
340	cDNA microarray analysis of developing grape (Vitis vinifera cv. Shiraz) berry skin. Functional and Integrative Genomics, 2005, 5, 40-58.	3.5	109
341	Microarray analysis of gene expression in germinating barley embryos (Hordeum vulgare L.). Functional and Integrative Genomics, 2005, 5, 155-162.	3.5	32
342	Consistent production of cost-effective longSAGE libraries. Plant Molecular Biology Reporter, 2005, 23, 139-143.	1.8	4

#	Article	IF	Citations
343	Low efficiency of pseudotestcross mapping design was consistent with limited genetic diversity and low heterozygosity in hoop pine (Araucaria cunninghamii, Araucariaceae). Tree Genetics and Genomes, 2005, 1, 124-134.	1.6	8
344	EST versus Genomic Derived Microsatellite Markers for Genotyping Wild and Cultivated Barley. Genetic Resources and Crop Evolution, 2005, 52, 903-909.	1.6	112
345	A Perfect Marker for Fragrance Genotyping in Rice. Molecular Breeding, 2005, 16, 279-283.	2.1	177
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	Sorghum laxiflorum and S. macrospermum, the Australian native species most closely related to the cultivated S. bicolor based on ITS1 and ndhF sequence analysis of 25 Sorghum species. Plant Systematics and Evolution, 2004, 249, 233-246.	0.9	41
349	Single nucleotide polymorphism, haplotype diversity and recombination in the Isa gene of barley. Theoretical and Applied Genetics, 2004, 109, 543-551.	3.6	40
350	Isolation and partial characterisation of a putative monoterpene synthase from Melaleuca alternifolia. Plant Physiology and Biochemistry, 2004, 42, 875-882.	5.8	16
351	Isopentenyl pyrophosphate isomerases fromMelaleuca alternifolia(Cheel) and their role in isoprenoid biosynthesis. Journal of Horticultural Science and Biotechnology, 2004, 79, 289-292.	1.9	9
352	New Saccharum hybrids in S. spontaneum cytoplasm developed through a combination of conventional and molecular breeding approaches. Plant Genetic Resources: Characterisation and Utilisation, 2004, 2, 131-139.	0.8	10
353	The promoter of the asi gene directs expression in the maternal tissues of the seed in transgenic barley. Plant Molecular Biology, 2003, 52, 787-800.	3.9	26
354	Single nucleotide polymorphisms in cytochrome P450 genes from barley. Theoretical and Applied Genetics, 2003, 106, 676-682.	3.6	26
355	Genetic maps for Pinus elliottii var. elliottii and P. caribaea var. hondurensis using AFLP and microsatellite markers. Theoretical and Applied Genetics, 2003, 106, 1409-1419.	3.6	37
356	Genes associated with the end of dormancy in grapes. Functional and Integrative Genomics, 2003, 3, 144-152.	3.5	56
357	Characterization of highly conserved microsatellite loci in Araucaria cunninghamii and related species. Plant Systematics and Evolution, 2003, 236, 115-123.	0.9	22
358	Single-nucleotide polymorphism detection in plants using a single-stranded pyrosequencing protocol with a universal biotinylated primer. Analytical Biochemistry, 2003, 317, 166-170.	2.4	38
359	Potential of SSR markers for plant breeding and variety identification in Australian barley germplasm. Australian Journal of Agricultural Research, 2003, 54, 1197.	1.5	51
360	Sugarcane microsatellites for the assessment of genetic diversity in sugarcane germplasm. Plant Science, 2003, 165, 181-189.	3.6	133

#	Article	IF	Citations
361	A single nucleotide polymorphism (SNP) marker linked to the fragrance gene in rice (Oryza sativa L.). Plant Science, 2003, 165, 359-364.	3.6	78
362	Genetics of physical wood properties and early growth in a tropical pine hybrid. Canadian Journal of Forest Research, 2003, 33, 1923-1932.	1.7	6
363	Molecular basis of barley quality. Australian Journal of Agricultural Research, 2003, 54, 1081.	1.5	146
364	Application of SSR markers in the construction of Australian barley genetic maps. Australian Journal of Agricultural Research, 2003, 54, 1187.	1.5	10
365	Branch architecture QTL for Pinus elliottii var. elliottii ï¿½ Pinus caribaea var. hondurensis hybrids. Annals of Forest Science, 2002, 59, 617-625.	2.0	21
366	Impact Odorants Contributing to the Fungus Type Aroma from Grape Berries Contaminated by Powdery Mildew (Uncinula necator); Incidence of Enzymatic Activities of the Yeast Saccharomyces cerevisiae. Journal of Agricultural and Food Chemistry, 2002, 50, 3277-3282.	5.2	110
367	The application of SSRs characterized for grape (Vitis vinifera) to conservation studies in Vitaceae. American Journal of Botany, 2002, 89, 22-28.	1.7	68
368	Isolation of genes involved in secondary metabolism from Melaleuca alternifolia (Cheel) using expressed sequence tags (ESTs). Plant Science, 2002, 162, 9-15.	3.6	21
369	Geographic variation in the essential oils and morphology of natural populations of Melaleuca alternifolia (Myrtaceae). Biochemical Systematics and Ecology, 2002, 30, 343-360.	1.3	24
370	Transpecific microsatellites for hard pines. Theoretical and Applied Genetics, 2002, 104, 819-827.	3.6	58
371	Genetic control of monoterpene composition in the essential oil of Melaleuca alternifolia (Cheel). Theoretical and Applied Genetics, 2002, 105, 377-383.	3.6	20
372	Evaluating the potential of SSR flanking regions for examining taxonomic relationships in the Vitaceae. Theoretical and Applied Genetics, 2002, 104, 61-66.	3.6	81
373	Measurement of green fluorescent protein concentration in single cells by image analysis. Analytical Biochemistry, 2002, 310, 84-92.	2.4	35
374	Title is missing!. Molecular Breeding, 2002, 9, 245-250.	2.1	71
375	Title is missing!. Molecular Breeding, 2002, 9, 63-71.	2.1	142
376	Implementation of markers in Australian wheat breeding. Australian Journal of Agricultural Research, 2001, 52, 1349.	1.5	132
377	Natural Inter-subgeneric Hybridization Between Eucalyptus acmenoides Schauer and Eucalyptus cloeziana F. Muell (Myrtaceae) in Southeast Queensland. Annals of Botany, 2001, 88, 563-570.	2.9	24
378	Microsatellite markers from sugarcane (Saccharum spp.) ESTs cross transferable to erianthus and sorghum. Plant Science, 2001, 160, 1115-1123.	3.6	384

#	Article	IF	Citations
379	The use of ribosomal ITS to determine phylogenetic relationships within Sorghum. Plant Systematics and Evolution, 2001, 230, 97-110.	0.9	19
380	Intergeneric relationships in the Australian Vitaceae: new evidence from cpDNA analysis. Genetic Resources and Crop Evolution, 2001, 48, 307-314.	1.6	37
381	The reproductive biology and genetic diversity of Potamophila parviflora R. Br.. Genetic Resources and Crop Evolution, 2001, 48, 483-497.	1.6	4
382	Development of robust PCR-based DNA markers for each homoeo-allele of granule-bound starch synthase and their application in wheat breeding programs. Australian Journal of Agricultural Research, 2001, 52, 1409.	1.5	55
383	Exploiting cereal genetic resources. Advances in Botanical Research, 2001, 34, 23-57.	1.1	1
384	Microsatellites as markers for Australian wheat improvement. Australian Journal of Agricultural Research, 2001, 52, 1121.	1.5	29
385	Microsatellite analysis in cultivated hexaploid wheat and wild wheat relatives.. , 2001, , 147-159.		9
386	Plant DNA extraction.. , 2001, , 239-249.		7
387	Commercial applications of plant genotyping.. , 2001, , 265-273.		5
388	Molecular analysis of wild plant germplasm: the case of tea tree (Melaleuca alternifolia).. , 2001, , 95-107.		0
389	Interspecific amplification of tea tree (Melaleuca alternifolia-Myrtaceae) microsatellite loci-potential implications for conservation studies. Australian Journal of Botany, 2000, 48, 367.	0.6	22
390	Microsatellite analysis of genetic structure in the mangrove speciesAvicennia marina(Forsk.) Vierh. (Avicenniaceae). Molecular Ecology, 2000, 9, 1853-1862.	3.9	124
391	Natural variation in the essential oil content of Melaleuca alternifolia Cheel (Myrtaceae). Biochemical Systematics and Ecology, 2000, 28, 367-382.	1.3	107
392	Title is missing!. Conservation Genetics, 2000, 1, 217-229.	1.5	12
393	Analysis of SSRs derived from grape ESTs. Theoretical and Applied Genetics, 2000, 100, 723-726.	3.6	486
394	Characterisation and analysis of microsatellite loci in a mangrove species, Avicennia marina (Forsk.) Vierh. (Avicenniaceae). Theoretical and Applied Genetics, 2000, 101, 279-285.	3.6	51
395	PCR-based molecular markers for the fragrance gene in rice (Oryza sativa. L.). Theoretical and Applied Genetics, 2000, 101, 364-371.	3.6	56
396	Accessing genes in the tertiary gene pool of rice by direct introduction of total DNA fromZizania palustris (wild rice). Plant Molecular Biology Reporter, 2000, 18, 133-138.	1.8	18

#	Article	IF	Citations
397	Characterisation of microsatellite markers from sugarcane (Saccharum sp.), a highly polyploid species. Plant Science, 2000, 155, 161-168.	3.6	184
398	Analysis of grape ESTs: global gene expression patterns in leaf and berry. Plant Science, 2000, 159, 87-95.	3.6	64
399	Microsatellite variation and assessment of genetic structure in tea tree (Melaleuca alternifolia-) Tj ETQq1 1 0.784314 rgBT /Overlock 10	3.9	58
400	Improved Regeneration Efficiency from Mature Embryos of Barley Cultivars. Biologia Plantarum, 1999, 42, 505-513.	1.9	19
401	Title is missing!. Euphytica, 1999, 108, 53-63.	1.2	54
402	Detection of Transgenes in Crop Plants Using Molecular Beacon Assays. Plant Molecular Biology Reporter, 1999, 17, 363-370.	1.8	13
403	Optimisation of a Microsatellite Enrichment Technique in Saccharum spp.. Plant Molecular Biology Reporter, 1999, 17, 225-229.	1.8	28
404	Title is missing!. Plant Molecular Biology Reporter, 1999, 17, 351-354.	1.8	6
405	Microwave Extraction of Total Genomic DNA From Barley Grains for use in PCR. Journal of the Institute of Brewing, 1999, 105, 185-190.	2.3	21
406	Abundance and polymorphism of microsatellite markers in the tea tree (Melaleuca alternifolia,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382	3.6	41
407	Identifying New Volatile Compounds in Toasted Oak. Journal of Agricultural and Food Chemistry, 1999, 47, 1663-1667.	5.2	51
408	Title is missing!. , 1998, 4, 509-517.		6
409	Marker-assisted selection for two rust resistance genes in sunflower. Molecular Breeding, 1998, 4, 227-234.	2.1	71
410	Title is missing!. Genetic Resources and Crop Evolution, 1998, 45, 399-406.	1.6	9
411	Identification of the creatine binding domain of creatine kinase by photoaffinity labeling. BBA - Proteins and Proteomics, 1998, 1387, 80-88.	2.1	9
412	Identification of new volatile thiols in the aroma ofVitis vinifera L. var. Sauvignon blanc wines. Flavour and Fragrance Journal, 1998, 13, 159-162.	2.6	316
413	Identification of Volatile and Powerful Odorous Thiols in Bordeaux Red Wine Varieties. Journal of Agricultural and Food Chemistry, 1998, 46, 3095-3099.	5.2	144
414	Molecular and Biochemical Characterization of Somaclonal Variation. Current Plant Science and Biotechnology in Agriculture, 1998, , 485-499.	0.0	18

#	Article	IF	Citations
415	BACTERIAL EXPRESSION OF THE BIFUNCTIONAL Î±-AMYLASE/SUBTILISIN INHIBITOR FROM BARLEY. Journal of the Institute of Brewing, 1997, 103, 31-33.	2.3	2
416	Identification of Volatile Compounds with a â€œToastyâ€•Aroma in Heated Oak Used in Barrelmaking. Journal of Agricultural and Food Chemistry, 1997, 45, 2217-2224.	5.2	120
417	Quantitative Determination of Potent Flavor Compounds in Burgundy Pinot Noir Wines Using a Stable Isotope Dilution Assayâ€. Journal of Agricultural and Food Chemistry, 1997, 45, 2120-2123.	5.2	43
418	Alpha-amylase/subtilisin Inhibitor Levels in Australian Barleys. Journal of Cereal Science, 1997, 25, 261-266.	3.7	11
419	The defensive secretion of Eurycotis floridana (Dictyoptera, Blattidae, Polyzosteriinae): Chemical identification and evidence of an alarm function. Insect Biochemistry and Molecular Biology, 1997, 27, 577-586.	2.7	14
420	Dichloroaromatic phosphoguanidines are potent inhibitors but very poor substrates for cytosolic creatine kinase. Biochimica Et Biophysica Acta - Molecular Cell Research, 1997, 1357, 49-56.	4.1	2
421	N-Dibenzylphospho-Nâ€²-3-(2,6-dichlorophenyl)propyl-guanidine is a bisubstrate-analog for creatine kinase. BBA - Proteins and Proteomics, 1997, 1342, 83-89.	2.1	5
422	Molecular Distinction between Monocotyledons and Dicotyledons: more than a simple dichotomy. Plant Molecular Biology Reporter, 1997, 15, 216-218.	1.8	16
423	RAPD and isozyme analysis of genetic relationships between Carica papaya and wild relatives. Genetic Resources and Crop Evolution, 1997, 44, 471-477.	1.6	46
424	Practical Applications of Plant Molecular Biology. , 1997, , .		49
425	Preparation of Fungal Genomic DNA for PCR and RAPD Analysis. , 1997, , 29-34.		5
426	An Efficient Transformation System for the Australian Rice Cultivar, Jarrah. Functional Plant Biology, 1997, 24, 133.	2.1	13
427	Estimation of genetic variation in plants using molecular techniques. , 1997, , 57-98.		1
428	Useful routine protocols in plant molecular biology. , 1997, , 175-220.		0
429	Plant transformation. , 1997, , 135-173.		0
430	Identification of plants using molecular techniques. , 1997, , 1-55.		1
431	Random amplified polymorphic DNA (RAPD) detection of dwarf off-types in micropropagated Cavendish (Musa spp. AAA) bananas. Plant Cell Reports, 1996, 16, 118-123.	5.6	94
432	Genetic diversity of Kensington mango in Australia. Australian Journal of Experimental Agriculture, 1996, 36, 243.	1.0	20

#	Article	IF	Citations
433	Fast resolution of identification problems in seed production and plant breeding using molecular markers. Australian Journal of Experimental Agriculture, 1996, 36, 571.	1.0	6
434	Phylogenetic position of hoop pine (Araucaria cunninghamii). Australian Systematic Botany, 1996, 9, 893.	0.9	11
435	RAPD markers for a sunflower rust resistance gene. Australian Journal of Agricultural Research, 1996, 47, 395.	1.5	13
436	Specific 5S ribosomal RNA primers for plant species i dentification in admixtures 3. Plant Molecular Biology Reporter, 1996, 14, 33-43.	1.8	15
437	A protocol for the efficient screening of putatively transformed plants forbar, the selectable marker gene, using the polymerase chain reaction. Plant Molecular Biology Reporter, 1996, 14, 363-368.	1.8	15
438	Synthesis and Differential Properties of Creatine Analogues as Inhibitors for Human Creatine Kinase Isoenzymes. FEBS Journal, 1996, 238, 446-452.	0.2	8
439	ASSESSMENT OFBACILLUS LICHENIFORMISÎ±-AMYLASE AS A CANDIDATE ENZYME FOR GENETIC ENGINEERING OF MALTING BARLEY1. Journal of the Institute of Brewing, 1996, 102, 75-78.	2.3	7
440	Random amplified polymorphic DNA (RAPD) detection of dwarf off-types in micropropagated Cavendish (Musa spp. AAA) bananas. Plant Cell Reports, 1996, 16, 118-123.	5.6	1
441	Optimisation of Tissue Culture Conditions for Transformation Studies Using Immature Embryos of Australian Barley Cultivars. Australian Journal of Botany, 1995, 43, 499.	0.6	8
442	Molecular analysis of the DNA polymorphism of wild barley (Hordeum spontaneum) germplasm using the polymerase chain reaction. Genetic Resources and Crop Evolution, 1995, 42, 273-280.	1.6	45
443	The use of bulk segregant analysis to identify a RAPD marker linked to leaf rust resistance in barley. Theoretical and Applied Genetics, 1995, 91, 270-273.	3.6	52
444	Sensitivity of random amplified polymorphic DNA analysis to detect genetic change in sugarcane during tissue culture. Theoretical and Applied Genetics, 1995, 90, 1169-1173.	3.6	89
445	ANALYSIS OF WATER-SOLUBLE PROTEINS FROM BARLEY BY ION-EXCHANGE HIGH PERFORMANCE LIQUID CHROMATOGRAPHY. Journal of the Institute of Brewing, 1995, 101, 181-185.	2.3	2
446	Influence of bile salt molecular species on cholesterol crystallization from supersaturated model biles. Lipids and Lipid Metabolism, 1995, 1254, 89-97.	2.6	15
447	Control of Gene Expression for the Genetic Engineering of Cereal Quality. Journal of Cereal Science, 1995, 22, 203-210.	3.7	6
448	Genetic and environmental variation in the diastatic power of australian barley. Journal of Cereal Science, 1995, 21, 63-70.	3.7	97
449	RAPD Analysis of Sugarcane During Tissue Culture. Current Plant Science and Biotechnology in Agriculture, 1995, , 241-246.	0.0	28
450	Polymorphisms in the Î±-amy1 gene of wild and cultivated barley revealed by the polymerase chain reaction. Theoretical and Applied Genetics, 1994, 89, 509-513.	3.6	42

#	Article	IF	Citations
451	Random amplified polymorphic DNA analysis of Australian rice (Oryza sativa L.) varieties. Euphytica, 1994, 80, 179-189.	1.2	51
452	Identification of Cereals using the Polymerase Chain Reaction. Journal of Cereal Science, 1994, 19, 101-106.	3.7	34
453	Genetic diversity in sunflower (Helianthus annuus L.) as revealed by random amplified polymorphic DNA analysis. Australian Journal of Agricultural Research, 1994, 45, 1319.	1.5	40
454	IDENTIFICATION OF BARLEY VARIETIES USING THE POLYMERASE CHAIN REACTION. Journal of the Institute of Brewing, 1994, 100, 405-407.	2.3	12
455	Identification of navy bean varieties using a random amplification of polymorphic DNA. Australian Journal of Experimental Agriculture, 1994, 34, 1173.	1.0	8
456	Genetic Engineering of Resistance to Starch Hydrolysis Caused by Pre-Harvest Sprouting. , 1994, , 129-132.		1
457	Rapid Cereal Genotype Analysis. , 1994, , 153-157.		1
458	A simplified method for the preparation of fungal genomic DNA for PCR and RAPD analysis. BioTechniques, 1994, 16, 48-50.	1.8	126
459	Use of DNA from dry leaves for PCR and RAPD analysis. Plant Molecular Biology Reporter, 1993, 11, 202-206.	1.8	20
460	A RAPID SMALL SCALE METHOD FOR THE DETERMINATION OF MALT EXTRACT. Journal of the Institute of Brewing, 1993, 99, 73-75.	2.3	7
461	AN INTER-LABORATORY STUDY OF STARCH DEGRADING ENZYME ASSAYS. Journal of the Institute of Brewing, 1992, 98, 25-26.	2.3	2
462	Enantiomeric ratios of pantolactone, solerone, 4-carboethoxy-4-hydroxy-butyrolactone and of sotolon, a flavour impact compound of flor-sherry and botrytized wines. Zeitschrift Fur Lebensmittel-Untersuchung Und -Forschung, 1992, 195, 540-544.	0.6	27
463	Control of wheat Î±-amylase using inhibitors from cereals. Journal of the Science of Food and Agriculture, 1992, 58, 281-284.	3.5	22
464	Gas chromatographyâ€"mass spectrometry and gas chromatographyâ€"tandem mass spectrometry of cyclic fatty acid monomers isolated from heated fats. Biomedical Applications, 1991, 562, 659-672.	1.7	19
465	Ion-pair high-performance liquid chromatography of bile salt conjugates: Application to pig bile. Lipids, 1991, 26, 578-583.	1.7	37
466	Amplification of a GC-rich sequence from barley by a two-step polymerase chain reaction in glycerol. Plant Molecular Biology Reporter, 1991, 9, 139-144.	1.8	10
467	Chiral ?-lactones from Fusarium poae. Zeitschrift Fur Lebensmittel-Untersuchung Und -Forschung, 1991, 193, 26-31.	0.6	19
468	Rapid determination of shoot nitrogen status in rice using near infrared reflectance spectroscopy. Journal of the Science of Food and Agriculture, 1991, 54, 191-197.	3.5	34

#	Article	IF	Citations
469	FACTORS INFLUENCING THE HARDNESS (MILLING ENERGY) AND MALTING QUALITY OF BARLEY. Journal of the Institute of Brewing, 1990, 96, 135-136.	2.3	33
470	Enzymic Determination of Starch in Samples with High Sugar Content. Starch/Staerke, 1990, 42, 468-470.	2.1	6
471	Starch determination in horticultural plant material by an enzymic-colorimetric procedure. Journal of the Science of Food and Agriculture, 1990, 52, 159-170.	3.5	66
472	High-performance liquid chromatography of Î±-amylases from germinating wheat and complexes with the Î±-amylase inhibitor from barley. Journal of Cereal Science, 1990, 12, 73-81.	3.7	19
473	Quantitative analysis of barley (1 â†' 3), (1 â†' 4)-Î²-glucanase isoenzymes by high-performance liquid chromatography. Journal of Cereal Science, 1990, 12, 187-192.	3.7	2
474	RapidÎ±-amylase assays for assessment of pre-harvest sprouting damage in wheat. Journal of the Science of Food and Agriculture, 1989, 49, 15-23.	3.5	8
475	Rapid separation of Î±-amylases from barley by ion-exchange high-performance liquid chromatography on non-porous columns. Journal of Chromatography A, 1989, 481, 397-402.	3.7	5
476	Cell-wall polysaccharides of rye-derived wheats: Investigations of the biochemical causes of dough stickiness. Food Chemistry, 1989, 34, 309-316.	8.2	19
477	Factors influencing the rate of modification of barleys during malting. Journal of Cereal Science, 1989, 10, 51-59.	3.7	21
478	Changes in Î²-glucan and other carbohydrate components of barley during malting. Journal of the Science of Food and Agriculture, 1988, 42, 333-341.	3.5	33
479	Evaluation of a general method for measurement of (1â†'3), (1â†'4)-Î²-Glucans. Journal of the Science of Food and Agriculture, 1988, 44, 75-87.	3.5	23
480	Dormancy breaking procedures and the breeding of white-grained wheat with resistance to pre-harvest sprouting. Euphytica, 1988, 39, 161-166.	1.2	4
481	Cultivation Effects on Carbohydrate Contents of Soil and Soil Fractions. Soil Science Society of America Journal, 1988, 52, 1361-1365.	2.2	39
482	Hydrolysis of barley endosperm storage proteins during malting. II. Quantification by enzyme- and radio-immunoassay. Journal of Cereal Science, 1988, 7, 265-281.	3.7	13
483	THE CARBOHYDRATES OF BARLEY GRAINS - A REVIEW. Journal of the Institute of Brewing, 1988, 94, 71-78.	2.3	58
484	Gas Chromatographic Determination of the Monosaccharide Composition of Plant Cell Wall Preparations. Journal of the Association of Official Analytical Chemists, 1988, 71, 272-275.	0.2	68
485	A SIMPLE AND RAPID TEST FOR ASSESSMENT OF ENDOSPERM PROTEIN MODIFICATION DURING MALTING*. Journal of the Institute of Brewing, 1987, 93, 413-419.	2.3	7
486	Pentosan and (1 â†' 3),(1 â†' 4)-Î²-Glucan concentrations in endosperm and wholegrain of wheat, barley, oats and rye. Journal of Cereal Science, 1987, 6, 253-258.	3.7	180

#	Article	IF	Citations
487	Reduction of the Î±-amylase content of sprouted wheat by pearling and milling. Journal of Cereal Science, 1987, 5, 155-166.	3.7	25
488	Variation in the Carbohydrate Composition of Wild Barley (Hordeum spontaneum) Grain. Plant Breeding, 1987, 98, 97-103.	1.9	17
489	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
490	Genetic and environmental variation in the pentosan and Î²-glucan contents of barley, and their relation to malting quality. Journal of Cereal Science, 1986, 4, 269-277.	3.7	91
491	Re-evaluation of fluorescein dibutyrate staining as a method for assessment of pre-harvest sprouting in wheat and barley. Journal of Cereal Science, 1986, 4, 51-56.	3.7	2
492	DETERMINATION OF TOTAL Î²-GLUCAN IN MALT. Journal of the Institute of Brewing, 1986, 92, 354-356.	2.3	24
493	EVALUATION OF BARLEY AND MALT QUALITY USING NEAR-INFRARED REFLECTANCE TECHNIQUES. Journal of the Institute of Brewing, 1985, 91, 393-396.	2.3	18
494	RATES OF ENDOSPERM MODIFICATION DURING MICRO-MALTING OF SOME AUSTRALIAN BARLEYS. Journal of the Institute of Brewing, 1985, 91, 318-320.	2.3	6
495	Evaluation of methods for the assessment of malting quality in barley breeding. Euphytica, 1985, 34, 135-145.	1.2	12
496	Near-infrared reflectance analysis of carbohydrates and its application to the determination of (1â†'3),(1â†'4)-Î²-d-glucan in barley. Carbohydrate Research, 1985, 141, 13-19.	2.3	20
497	Extent of Î²-glucan chain elongation by ryegrass (Lolium multiflorum) enzymes. Carbohydrate Polymers, 1985, 5, 1-12.	10.2	11
498	Use of a scanning near-infrared reflectance spectrophotometer for assessment of the malting potential of barley. Journal of the Science of Food and Agriculture, 1985, 36, 249-254.	3.5	13
499	A comparison of the non-starch carbohydrates in cereal grains. Journal of the Science of Food and Agriculture, 1985, 36, 1243-1253.	3.5	145
500	A comparative study of the total Î²-glucan contents of some Australian barleys. Australian Journal of Experimental Agriculture, 1985, 25, 424.	1.0	21
501	Effect of sample size on the micro-malting of barley. Journal of the Science of Food and Agriculture, 1984, 35, 767-772.	3.5	21
502	An improved procedure for the methylation analysis of oligosaccharides and polysaccharides. Carbohydrate Research, 1984, 127, 59-73.	2.3	571
503	A RAPID METHOD FOR THE DETERMINATION OF DIASTATIC POWER. Journal of the Institute of Brewing, 1984, 90, 37-39.	2.3	33
504	RAPID SMALL-SCALE DETERMINATION OF MALT EXTRACT IN BARLEY BREEDING. Journal of the Institute of Brewing, 1984, 90, 371-374.	2.3	15

#	Article	IF	Citations
505	A SIMPLIFIED ENZYMIC METHOD FOR THE DETERMINATION OF (1â†'3) (1â†'4)-Î²-GLUCANS IN BARLEY. Journal of the Institute of Brewing, 1984, 90, 178-180.	2.3	31
506	Proton Motive Potential Difference Across the Plasma Membrane of Plant Cells: a Comparison of Cultured Cells and Protoplasts From Italian Ryegrass (Lolium multiflorum Lam.) Endosperm. Functional Plant Biology, 1984, 11, 119.	2.1	4
507	A simple and rapid preparation of alditol acetates for monosaccharide analysis. Carbohydrate Research, 1983, 113, 291-299.	2.3	1,846
508	Separation of alditol acetates from plasticizers and other contaminants by capillary gas chromatography. Journal of Chromatography A, 1983, 262, 249-256.	3.7	15
509	Detection of neutral and aminosugars from glycoproteins and polysaccharides as their alditol acetates. Journal of Chromatography A, 1983, 256, 419-427.	3.7	64
510	Localization of Î²-glucan synthases on the membranes of cultured Lolium multiflorum (ryegrass) endosperm cells. Biochemical Journal, 1983, 209, 627-633.	3.7	18
511	Factors Influencing Î²-Glucan Synthesis by Particulate Enzymes from Suspension-Cultured Lolium multiflorum Endosperm Cells. Plant Physiology, 1982, 69, 632-636.	4.8	53
512	Solubilization of Î²-glucan synthases from the membranes of cultured ryegrass endosperm cells. Biochemical Journal, 1982, 203, 629-636.	3.7	35
513	Gas chromatography of alditol acetates on a high-polarity bonded-phase vitreous-silica column. Journal of Chromatography A, 1982, 249, 180-182.	3.7	21
514	DIFFERENCES IN FRUCTAN CONTENT AND SYNTHESIS IN SOME ALLIUM SPECIES. New Phytologist, 1981, 87, 249-256.	7.3	130
515	Sucrose:sucrose fructosyltransferase and fructan:fructan fructosyltransferase from allium cepa. Phytochemistry, 1980, 19, 1017-1020.	2.9	61
516	Water-soluble polysaccharide in nine commercial sweet corn cultivars and its suitability for estimating kernel maturity. Australian Journal of Experimental Agriculture, 1979, 19, 373.	1.0	1
517	Diurnal Variations in Non-Structural Carbohydrates, Leaf Extension, and Leaf Cavity Carbon Dioxide Concentrations inAllium cepaL.. Journal of Experimental Botany, 1979, 30, 109-118.	4.8	15
518	The association of fructans with high percentage dry weight in onion cultivars suitable for dehydrating. Journal of the Science of Food and Agriculture, 1979, 30, 1035-1038.	3.5	68
519	The distribution of fructan metabolising enzymes in the onion plant. Plant Science Letters, 1979, 14, 155-158.	1.8	17
520	THE DISTRIBUTION OF FRUCTANS IN ONIONS. New Phytologist, 1978, 81, 29-34.	7.3	147
521	An assay for glycosyltransferases using phenel partition and gas-liquid chromatography. Analytical Biochemistry, 1978, 90, 234-238.	2.4	10
522	Water-soluble polysaccharide determination as a technique for evaluation of sweet corn maturity. Australian Journal of Agricultural Research, 1978, 29, 517.	1.5	3

#	Article	IF	Citations
523	Salinity Tolerance in Canola: Insights from Proteomic Studies. , 0, , .		3
524	Improvements in the sequencing and assembly of plant genomes. GigaByte, 0, 2021, 1-10.	0.0	15
525	Flavor Development in Rice. , 0, , 130-146.		3
526	Genomics and Gene-Editing Technologies Accelerating Grain Product Innovation. Cereal Foods World, 0, , .	0.2	1