

Ray Ming

List of Publications by Year in descending order

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Version: 2024-02-01

193
papers

16,280
citations

38660

50
h-index

19136

118
g-index

218
all docs

218
docs citations

218
times ranked

16180
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sorghum bicolor genome and the diversification of grasses. Nature, 2009, 457, 551-556.	13.7	2,642
2	TRY plant trait database – enhanced coverage and open access. Global Change Biology, 2020, 26, 119-188.	4.2	1,038
3	The draft genome of the transgenic tropical fruit tree papaya (<i>Carica papaya</i> Linnaeus). Nature, 2008, 452, 991-996.	13.7	964
4	The genome of the pear (<i>Pyrus bretschneideri</i> Rehd.). Genome Research, 2013, 23, 396-408.	2.4	832
5	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	6.0	520
6	Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps. Genome Research, 2008, 18, 1944-1954.	2.4	515
7	The pineapple genome and the evolution of CAM photosynthesis. Nature Genetics, 2015, 47, 1435-1442.	9.4	472
8	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. Nature Genetics, 2018, 50, 1565-1573.	9.4	463
9	Sex Chromosomes in Land Plants. Annual Review of Plant Biology, 2011, 62, 485-514.	8.6	405
10	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. Nature Genetics, 2019, 51, 865-876.	9.4	398
11	A primitive Y chromosome in papaya marks incipient sex chromosome evolution. Nature, 2004, 427, 348-352.	13.7	351
12	ALLMAPS: robust scaffold ordering based on multiple maps. Genome Biology, 2015, 16, 3.	3.8	340
13	Genome of the long-living sacred lotus (<i>Nelumbo nucifera</i> Gaertn.). Genome Biology, 2013, 14, R41.	13.9	329
14	Assembly of allele-aware, chromosomal-scale autopolyploid genomes based on Hi-C data. Nature Plants, 2019, 5, 833-845.	4.7	292
15	Sequencing papaya X and Y chromosomes reveals molecular basis of incipient sex chromosome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13710-13715.	3.3	264
16	A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. New Phytologist, 2015, 207, 491-504.	3.5	211
17	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. BMC Genomics, 2010, 11, 261.	1.2	175
18	The <i>Kalanchoe</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. Nature Communications, 2017, 8, 1899.	5.8	159

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19	Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant <i>Camellia sinensis</i> . <i>Nature Genetics</i> , 2021, 53, 1250-1259.	9.4	157
20	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
21	Comparison of Cytochrome P450 Genes from Six Plant Genomes. <i>Tropical Plant Biology</i> , 2008, 1, 216-235.	1.0	138
22	High-Density Linkage Mapping Revealed Suppression of Recombination at the Sex Determination Locus in Papaya. <i>Genetics</i> , 2004, 166, 419-436.	1.2	132
23	Sex determination in papaya. <i>Seminars in Cell and Developmental Biology</i> , 2007, 18, 401-408.	2.3	124
24	Sex chromosomes in flowering plants. <i>American Journal of Botany</i> , 2007, 94, 141-150.	0.8	111
25	The pomegranate (<i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. <i>Plant Journal</i> , 2017, 91, 1108-1128.	2.8	109
26	DNA methylation and heterochromatinization in the male-specific region of the primitive Y chromosome of papaya. <i>Genome Research</i> , 2008, 18, 1938-1943.	2.4	107
27	Assembly of the 373k gene space of the polyploid sugarcane genome reveals reservoirs of functional diversity in the world's leading biomass crop. <i>GigaScience</i> , 2019, 8, .	3.3	106
28	PacBio Sequencing Reveals Transposable Elements as a Key Contributor to Genomic Plasticity and Virulence Variation in <i>Magnaporthe oryzae</i> . <i>Molecular Plant</i> , 2017, 10, 1465-1468.	3.9	100
29	Genome size variation in three <i>Saccharum</i> species. <i>Euphytica</i> , 2012, 185, 511-519.	0.6	93
30	Improving sugarcane for biofuel: engineering for an even better feedstock. <i>GCB Bioenergy</i> , 2009, 1, 251-255.	2.5	92
31	The Sugarcane Genome Challenge: Strategies for Sequencing a Highly Complex Genome. <i>Tropical Plant Biology</i> , 2011, 4, 145-156.	1.0	91
32	Cloning of the Papaya Chromoplast-Specific Lycopene β -Cyclase, <i>CpCYC-b</i> , Controlling Fruit Flesh Color Reveals Conserved Microsynteny and a Recombination Hot Spot. <i>Plant Physiology</i> , 2010, 152, 2013-2022.	2.3	90
33	Genome-Wide Identification, Evolution and Functional Divergence of MYB Transcription Factors in Chinese White Pear (<i>Pyrus bretschneideri</i>). <i>Plant and Cell Physiology</i> , 2016, 57, 824-847.	1.5	89
34	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. <i>Nature Genetics</i> , 2022, 54, 73-83.	9.4	88
35	A framework genetic map for <i>Miscanthus sinensis</i> from RNAseq-based markers shows recent tetraploidy. <i>BMC Genomics</i> , 2012, 13, 142.	1.2	87
36	Origin and domestication of papaya Y chromosome. <i>Genome Research</i> , 2015, 25, 524-533.	2.4	87

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37	Comparison of the Mitochondrial Genome Sequences of Six <i>Annulohyphomyces stygium</i> Isolates Suggests Short Fragment Insertions as a Potential Factor Leading to Larger Genomic Size. <i>Frontiers in Microbiology</i> , 2018, 9, 2079.	1.5	84
38	A physical map of the papaya genome with integrated genetic map and genome sequence. <i>BMC Genomics</i> , 2009, 10, 371.	1.2	81
39	Low X/Y divergence in four pairs of papaya sex-linked genes. <i>Plant Journal</i> , 2008, 53, 124-132.	2.8	78
40	Sex determination in flowering plants: Papaya as a model system. <i>Plant Science</i> , 2014, 217-218, 56-62.	1.7	78
41	Temporal and spatial transcriptomic and microRNA dynamics of CAM photosynthesis in pineapple. <i>Plant Journal</i> , 2017, 92, 19-30.	2.8	78
42	Construction of a Sequence-Tagged High-Density Genetic Map of Papaya for Comparative Structural and Evolutionary Genomics in Brassicales. <i>Genetics</i> , 2007, 177, 2481-2491.	1.2	73
43	Genomes of the Banyan Tree and Pollinator Wasp Provide Insights into Fig-Wasp Coevolution. <i>Cell</i> , 2020, 183, 875-889.e17.	13.5	71
44	Macroevolutionary synthesis of flowering plant sexual systems. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 898-912.	1.1	68
45	Transcriptome dynamics of <i>Camellia sinensis</i> in response to continuous salinity and drought stress. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	67
46	Genomics of sex chromosomes. <i>Current Opinion in Plant Biology</i> , 2007, 10, 123-130.	3.5	64
47	Genome-Wide Identification and Expression Profile Analysis of WRKY Family Genes in the Autopolyploid <i>Saccharum spontaneum</i> . <i>Plant and Cell Physiology</i> , 2020, 61, 616-630.	1.5	63
48	Recent Origin of Dioecious and Gynodioecious Y Chromosomes in Papaya. <i>Tropical Plant Biology</i> , 2008, 1, 49-57.	1.0	62
49	Analysis of papaya BAC end sequences reveals first insights into the organization of a fruit tree genome. <i>Molecular Genetics and Genomics</i> , 2006, 276, 1-12.	1.0	61
50	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
51	Genomic impact of stress-induced transposable element mobility in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2021, 49, 10431-10447.	6.5	60
52	Papaya CpbHLH1/2 regulate carotenoid biosynthesis-related genes during papaya fruit ripening. <i>Horticulture Research</i> , 2019, 6, 80.	2.9	59
53	The genome of kenaf (<i>Hibiscus cannabinus</i> L.) provides insights into bast fibre and leaf shape biogenesis. <i>Plant Biotechnology Journal</i> , 2020, 18, 1796-1809.	4.1	55
54	Comparative Analysis of GC Content Variations in Plant Genomes. <i>Tropical Plant Biology</i> , 2016, 9, 136-149.	1.0	54

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55	The genome of Shanputao (<i>Vitis amurensis</i>) provides a new insight into cold tolerance of grapevine. <i>Plant Journal</i> , 2021, 105, 1495-1506.	2.8	52
56	Structure, phylogeny, allelic haplotypes and expression of sucrose transporter gene families in <i>Saccharum</i> . <i>BMC Genomics</i> , 2016, 17, 88.	1.2	48
57	Somatic variations led to the selection of acidic and acidless orange cultivars. <i>Nature Plants</i> , 2021, 7, 954-965.	4.7	48
58	Haplotype analysis of sucrose synthase gene family in three <i>Saccharum</i> species. <i>BMC Genomics</i> , 2013, 14, 314.	1.2	47
59	Unraveling a genetic roadmap for improved taste in the domesticated apple. <i>Molecular Plant</i> , 2021, 14, 1454-1471.	3.9	47
60	The evolutionary origin and domestication history of goldfish (<i>Carassius auratus</i>). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29775-29785.	3.3	47
61	Genomic analyses of the CAM plant pineapple. <i>Journal of Experimental Botany</i> , 2014, 65, 3395-3404.	2.4	46
62	Development and application of microsatellite markers for genomic analysis of papaya. <i>Tree Genetics and Genomes</i> , 2008, 4, 333-341.	0.6	45
63	Analysis of the Mitochondrial Genome in <i>Hypomyces aurantius</i> Reveals a Novel Twintron Complex in Fungi. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1049.	1.8	45
64	Diurnal Cycling Transcription Factors of Pineapple Revealed by Genome-Wide Annotation and Global Transcriptomic Analysis. <i>Genome Biology and Evolution</i> , 2017, 9, 2170-2190.	1.1	43
65	New insights into the evolution and functional divergence of the SWEET family in <i>Saccharum</i> based on comparative genomics. <i>BMC Plant Biology</i> , 2018, 18, 270.	1.6	42
66	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
67	Genomics of sex determination. <i>Current Opinion in Plant Biology</i> , 2014, 18, 110-116.	3.5	41
68	Genetic mapping of quantitative trait loci controlling fruit size and shape in papaya. <i>Molecular Breeding</i> , 2012, 29, 457-466.	1.0	40
69	Recent polyploidization events in three <i>Saccharum</i> founding species. <i>Plant Biotechnology Journal</i> , 2019, 17, 264-274.	4.1	40
70	Construction of physical maps for the sex-specific regions of papaya sex chromosomes. <i>BMC Genomics</i> , 2012, 13, 176.	1.2	39
71	Evolution and expression of the fructokinase gene family in <i>Saccharum</i> . <i>BMC Genomics</i> , 2017, 18, 197.	1.2	39
72	The sex-specific region of sex chromosomes in animals and plants. <i>Chromosome Research</i> , 2012, 20, 57-69.	1.0	38

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73	Diversity of metabolite accumulation patterns in inner and outer seed coats of pomegranate: exploring their relationship with genetic mechanisms of seed coat development. <i>Horticulture Research</i> , 2020, 7, 10.	2.9	38
74	Dioecy does not consistently accelerate or slow lineage diversification across multiple genera of angiosperms. <i>New Phytologist</i> , 2016, 209, 1290-1300.	3.5	37
75	Genome-Wide Comparative Analyses of Microsatellites in Papaya. <i>Tropical Plant Biology</i> , 2008, 1, 278-292.	1.0	34
76	Integration of Genetic and Cytological Maps and Development of a Pachytene Chromosome-based Karyotype in Papaya. <i>Tropical Plant Biology</i> , 2010, 3, 166-170.	1.0	34
77	Isolation of ripening-related genes from ethylene/1-MCP treated papaya through RNA-seq. <i>BMC Genomics</i> , 2017, 18, 671.	1.2	33
78	Target enrichment sequencing of 307 germplasm accessions identified ancestry of ancient and modern hybrids and signatures of adaptation and selection in sugarcane (<i>Saccharum</i> spp.), a "sweet" crop with "bitter" genomes. <i>Plant Biotechnology Journal</i> , 2019, 17, 488-498.	4.1	33
79	Genomic insights into the recent chromosome reduction of autopolyploid sugarcane <i>Saccharum spontaneum</i> . <i>Nature Genetics</i> , 2022, 54, 885-896.	9.4	33
80	Identification of microRNAs, phasiRNAs and Their Targets in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 176-186.	1.0	32
81	Exploring the differential mechanisms of carotenoid biosynthesis in the yellow peel and red flesh of papaya. <i>BMC Genomics</i> , 2019, 20, 49.	1.2	32
82	Intra-specific DNA polymorphism in pineapple (<i>Ananas comosus</i> (L.) Merr.) assessed by AFLP markers. <i>Genetic Resources and Crop Evolution</i> , 2005, 51, 815-825.	0.8	31
83	Fruit Development, Ripening and Quality Related Genes in the Papaya Genome. <i>Tropical Plant Biology</i> , 2008, 1, 246-277.	1.0	31
84	Genomic evidence of prevalent hybridization throughout the evolutionary history of the fig-wasp pollination mutualism. <i>Nature Communications</i> , 2021, 12, 718.	5.8	31
85	Development of male-specific markers and identification of sex reversal mutants in papaya. <i>Euphytica</i> , 2017, 213, 1.	0.6	30
86	Molecular mechanisms of mutualistic and antagonistic interactions in a plant-pollinator association. <i>Nature Ecology and Evolution</i> , 2021, 5, 974-986.	3.4	30
87	Sex specific expression and distribution of small RNAs in papaya. <i>BMC Genomics</i> , 2014, 15, 20.	1.2	28
88	Accumulation of interspersed and sex-specific repeats in the non-recombining region of papaya sex chromosomes. <i>BMC Genomics</i> , 2014, 15, 335.	1.2	28
89	Transcriptome Profiling Revealed Stress-Induced and Disease Resistance Genes Up-Regulated in PRSV Resistant Transgenic Papaya. <i>Frontiers in Plant Science</i> , 2016, 7, 855.	1.7	28
90	Papain-like cysteine proteases in <i>Carica papaya</i> : lineage-specific gene duplication and expansion. <i>BMC Genomics</i> , 2018, 19, 26.	1.2	28

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91	Comparative analysis of sucrose phosphate synthase (SPS) gene family between <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> . <i>BMC Plant Biology</i> , 2020, 20, 422.	1.6	27
92	The genomic architecture of the sex-determining region and sex-related metabolic variation in <i>Ginkgo biloba</i> . <i>Plant Journal</i> , 2020, 104, 1399-1409.	2.8	26
93	SunUp and Sunset genomes revealed impact of particle bombardment mediated transformation and domestication history in papaya. <i>Nature Genetics</i> , 2022, 54, 715-724.	9.4	26
94	Characterization of Insertion Sites in Rainbow Papaya, the First Commercialized Transgenic Fruit Crop. <i>Tropical Plant Biology</i> , 2008, 1, 293-309.	1.0	25
95	Genome-Wide Analysis of MicroRNAs in Sacred Lotus, <i>Nelumbo nucifera</i> (Gaertn). <i>Tropical Plant Biology</i> , 2013, 6, 117-130.	1.0	25
96	Toward systems-level analysis of agricultural production from crassulacean acid metabolism (CAM): scaling from cell to commercial production. <i>New Phytologist</i> , 2015, 208, 66-72.	3.5	25
97	PGD: Pineapple Genomics Database. <i>Horticulture Research</i> , 2018, 5, 66.	2.9	25
98	Reference genomes of the two cultivated jute species. <i>Plant Biotechnology Journal</i> , 2021, 19, 2235-2248.	4.1	25
99	Genome-Wide Analysis of Repetitive Elements in Papaya. <i>Tropical Plant Biology</i> , 2008, 1, 191-201.	1.0	24
100	Development of Chromosome-specific Cytogenetic Markers and Merging of Linkage Fragments in Papaya. <i>Tropical Plant Biology</i> , 2010, 3, 171-181.	1.0	24
101	Evidence for Emergence of Sex-Determining Gene(s) in a Centromeric Region in <i>Vasconcellea parviflora</i> . <i>Genetics</i> , 2015, 199, 413-421.	1.2	23
102	Development and Applications of Chromosome-Specific Cytogenetic BAC-FISH Probes in <i>S. spontaneum</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 218.	1.7	23
103	Comparative genomics revealed the gene evolution and functional divergence of magnesium transporter families in <i>Saccharum</i> . <i>BMC Genomics</i> , 2019, 20, 83.	1.2	23
104	The reference genome of <i>Miscanthus floridulus</i> illuminates the evolution of Saccharinae. <i>Nature Plants</i> , 2021, 7, 608-618.	4.7	23
105	B-class MADS-box genes in trioecious papaya: two paleoAP3 paralogs, CpTM6-1 and CpTM6-2, and a PI ortholog CpPI. <i>Planta</i> , 2008, 227, 741-753.	1.6	22
106	Mitochondrial genome in <i>Hypsizygus marmoreus</i> and its evolution in Dikarya. <i>BMC Genomics</i> , 2019, 20, 765.	1.2	22
107	Genome of papaya, a fast growing tropical fruit tree. <i>Tree Genetics and Genomes</i> , 2012, 8, 445-462.	0.6	21
108	Assembling allopolyploid genomes: no longer formidable. <i>Genome Biology</i> , 2015, 16, 27.	3.8	21

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109	Extremely low nucleotide diversity in the X-linked region of papaya caused by a strong selective sweep. <i>Genome Biology</i> , 2016, 17, 230.	3.8	21
110	Cell wall metabolism and hexose allocation contribute to biomass accumulation in high yielding extreme segregants of a <i>Saccharum</i> interspecific F2 population. <i>BMC Genomics</i> , 2017, 18, 773.	1.2	21
111	Inpactor, Integrated and Parallel Analyzer and Classifier of LTR Retrotransposons and Its Application for Pineapple LTR Retrotransposons Diversity and Dynamics. <i>Biology</i> , 2018, 7, 32.	1.3	21
112	Genome-Wide Analysis of Nitrate Transporter (NRT/NPF) Family in Sugarcane <i>Saccharum spontaneum</i> L.. <i>Tropical Plant Biology</i> , 2019, 12, 133-149.	1.0	21
113	Analysis of MADS-box genes revealed modified flowering gene network and diurnal expression in pineapple. <i>BMC Genomics</i> , 2020, 21, 8.	1.2	21
114	Comparative analyses of American and Asian lotus genomes reveal insights into petal color, carpel thermogenesis and domestication. <i>Plant Journal</i> , 2022, 110, 1498-1515.	2.8	21
115	DNA methylome and transcriptome landscapes revealed differential characteristics of dioecious flowers in papaya. <i>Horticulture Research</i> , 2020, 7, 81.	2.9	20
116	Evolutionary expansion and functional divergence of sugar transporters in <i>Saccharum</i> (<i>S.</i>) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	2.8	20
117	Chloroplast Genome of Rambutan and Comparative Analyses in Sapindaceae. <i>Plants</i> , 2021, 10, 283.	1.6	20
118	Allele-defined genome reveals biallelic differentiation during cassava evolution. <i>Molecular Plant</i> , 2021, 14, 851-854.	3.9	20
119	Pineapple Genome: A Reference for Monocots and CAM Photosynthesis. <i>Trends in Genetics</i> , 2016, 32, 690-696.	2.9	19
120	The role of cis-elements in the evolution of crassulacean acid metabolism photosynthesis. <i>Horticulture Research</i> , 2020, 7, 5.	2.9	19
121	Development of microsatellite markers in autopolyploid sugarcane and comparative analysis of conserved microsatellites in sorghum and sugarcane. <i>Molecular Breeding</i> , 2012, 30, 661-669.	1.0	18
122	Organelle DNA accumulation in the recently evolved papaya sex chromosomes. <i>Molecular Genetics and Genomics</i> , 2013, 288, 277-284.	1.0	18
123	Analysis of Alternative Splicing Landscape in Pineapple (<i>Ananas comosus</i>). <i>Tropical Plant Biology</i> , 2016, 9, 150-160.	1.0	18
124	Coffee Germplasm Resources, <i>Genomics and Breeding</i> . , 0, , 415-447.		18
125	Transcriptomic analysis of transgressive segregants revealed the central role of photosynthetic capacity and efficiency in biomass accumulation in sugarcane. <i>Scientific Reports</i> , 2018, 8, 4415.	1.6	17
126	Genomics of Macadamia, a Recently Domesticated Tree Nut Crop. , 2008, , 313-332.		17

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127	The effects of artificial selection on sugar metabolism and transporter genes in grape. <i>Tree Genetics and Genomes</i> , 2013, 9, 1343-1349.	0.6	16
128	Development of an X-specific marker and identification of YY individuals in spinach. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1987-1994.	1.8	16
129	Genomic footprints of repeated evolution of <i><scp>CAM</scp></i> photosynthesis in a Neotropical species radiation. <i>Plant, Cell and Environment</i> , 2020, 43, 2987-3001.	2.8	15
130	Resequencing of 388 cassava accessions identifies valuable loci and selection for variation in heterozygosity. <i>Genome Biology</i> , 2021, 22, 316.	3.8	15
131	The spinach YY genome reveals sex chromosome evolution, domestication, and introgression history of the species. <i>Genome Biology</i> , 2022, 23, 75.	3.8	15
132	Floral MADS-box Genes in Trioecious Papaya: Characterization of AG and AP1 Subfamily Genes Revealed a Sex-type-specific Gene. <i>Tropical Plant Biology</i> , 2008, 1, 97-107.	1.0	14
133	Genome size variation among sex types in dioecious and trioecious Caricaceae species. <i>Euphytica</i> , 2013, 189, 461-469.	0.6	14
134	Allele specific expression of Dof genes responding to hormones and abiotic stresses in sugarcane. <i>PLoS ONE</i> , 2020, 15, e0227716.	1.1	14
135	Identifying a melanogenesis-related candidate gene by a high-quality genome assembly and population diversity analysis in <i>Hypsizygus marmoreus</i> . <i>Journal of Genetics and Genomics</i> , 2021, 48, 75-87.	1.7	14
136	Signatures of selection in recently domesticated macadamia. <i>Nature Communications</i> , 2022, 13, 242.	5.8	14
137	Genome-Wide Comparative Analysis of Microsatellites in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 117-135.	1.0	13
138	Auxin regulation involved in gynoecium morphogenesis of papaya flowers. <i>Horticulture Research</i> , 2019, 6, 119.	2.9	12
139	Evolution and Expression Analysis of Starch Synthase Gene Families in <i>Saccharum spontaneum</i> . <i>Tropical Plant Biology</i> , 2019, 12, 158-173.	1.0	12
140	Differential gene expression among three sex types reveals a MALE STERILITY 1 (CpMS1) for sex differentiation in papaya. <i>BMC Plant Biology</i> , 2019, 19, 545.	1.6	12
141	Construction of high-density genetic maps defined sex determination region of the Y chromosome in spinach. <i>Molecular Genetics and Genomics</i> , 2021, 296, 41-53.	1.0	12
142	Ultra-long DNA molecule isolation from plant nuclei for ultra-long read genome sequencing. <i>STAR Protocols</i> , 2021, 2, 100343.	0.5	12
143	Auxin regulated metabolic changes underlying sepal retention and development after pollination in spinach. <i>BMC Plant Biology</i> , 2021, 21, 166.	1.6	12
144	Sex biased expression of hormone related genes at early stage of sex differentiation in papaya flowers. <i>Horticulture Research</i> , 2021, 8, 147.	2.9	12

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145	Comparative Analysis of the MADS-Box Genes Revealed Their Potential Functions for Flower and Fruit Development in Longan (<i>Dimocarpus longan</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 813798.	1.7	12
146	Genome-Wide Identification and Characterization of Nucleotide-Binding Site (NBS) Resistance Genes in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 187-199.	1.0	11
147	Structural variations in papaya genomes. <i>BMC Genomics</i> , 2021, 22, 335.	1.2	11
148	The Fruits of Tropical Plant Genomics. <i>Tropical Plant Biology</i> , 2008, 1, 3-19.	1.0	10
149	Genome-Wide Identification and Analysis of Genes Encoding Proteolytic Enzymes in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 161-175.	1.0	10
150	Draft genome sequence of <i>Cercospora sojina</i> isolate S9, a fungus causing frog-eye leaf spot (FLS) disease of soybean. <i>Genomics Data</i> , 2017, 12, 79-80.	1.3	10
151	Identification and Expression Analysis of TCP Genes in <i>Saccharum spontaneum</i> L. <i>Tropical Plant Biology</i> , 2019, 12, 206-218.	1.0	10
152	Genomic and Allelic Analyses of Laccase Genes in Sugarcane (<i>Saccharum spontaneum</i> L.). <i>Tropical Plant Biology</i> , 2019, 12, 219-229.	1.0	10
153	Expression profiling of MADS-box gene family revealed its role in vegetative development and stem ripening in <i>S. spontaneum</i> . <i>Scientific Reports</i> , 2020, 10, 20536.	1.6	10
154	Identification and genes expression analysis of ATP-dependent phosphofructokinase family members among three <i>Saccharum</i> species. <i>Functional Plant Biology</i> , 2013, 40, 369.	1.1	9
155	Comparative Analysis of SUS Gene Family between <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> . <i>Tropical Plant Biology</i> , 2019, 12, 174-185.	1.0	9
156	Expression profiling of the Dof gene family under abiotic stresses in spinach. <i>Scientific Reports</i> , 2021, 11, 14429.	1.6	9
157	Methylation related genes affect sex differentiation in dioecious and gynodioecious papaya. <i>Horticulture Research</i> , 2022, 9, .	2.9	9
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