

# 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	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
2	Methylation related genes affect sex differentiation in dioecious and gynodioecious papaya. <i>Horticulture Research</i> , 2022, 9, .	2.9	9
3	Signatures of selection in recently domesticated macadamia. <i>Nature Communications</i> , 2022, 13, 242.	5.8	14
4	Gene regulation network analyses of pistil development in papaya. <i>BMC Genomics</i> , 2022, 23, 8.	1.2	8
5	Transcriptome analyses shed light on floral organ morphogenesis and bract color formation in <i>Bougainvillea</i> . <i>BMC Plant Biology</i> , 2022, 22, 97.	1.6	3
6	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
7	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
8	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
9	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
10	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
11	Evolutionary expansion and functional divergence of sugar transporters in <i>Saccharum</i> ( <i>S.</i> ) Tj ETQq1 1 0.784314 rgBT /Overloc	2.8	20
12	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
13	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
14	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
15	Chloroplast Genome of Rambutan and Comparative Analyses in Sapindaceae. <i>Plants</i> , 2021, 10, 283.	1.6	20
16	The complete chloroplast genome sequence of <i>Camellia sinensis</i> var. <i>sinensis</i> cultivar Tieguanyin (Theaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 395-396.	0.2	5
17	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
18	Transcriptional regulation of dosage compensation in <i>Carica papaya</i> . <i>Scientific Reports</i> , 2021, 11, 5854.	1.6	5

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19	Ultra-long DNA molecule isolation from plant nuclei for ultra-long read genome sequencing. STAR Protocols, 2021, 2, 100343.	0.5	12
20	Cloning and physical localization of male-biased repetitive DNA sequences in <i>Spinacia oleracea</i> (Amaranthaceae). Comparative Cytogenetics, 2021, 15, 101-118.	0.3	2
21	Auxin regulated metabolic changes underlying sepal retention and development after pollination in spinach. BMC Plant Biology, 2021, 21, 166.	1.6	12
22	Structural variations in papaya genomes. BMC Genomics, 2021, 22, 335.	1.2	11
23	Editorial: Genomics-Enabled Crop Genetics. Frontiers in Genetics, 2021, 12, 687160.	1.1	2
24	Molecular mechanisms of mutualistic and antagonistic interactions in a plant-pollinator association. Nature Ecology and Evolution, 2021, 5, 974-986.	3.4	30
25	The reference genome of <i>Miscanthus floridulus</i> illuminates the evolution of Saccharinae. Nature Plants, 2021, 7, 608-618.	4.7	23
26	Allele-defined genome reveals biallelic differentiation during cassava evolution. Molecular Plant, 2021, 14, 851-854.	3.9	20
27	Somatic variations led to the selection of acidic and acidless orange cultivars. Nature Plants, 2021, 7, 954-965.	4.7	48
28	Reference genomes of the two cultivated jute species. Plant Biotechnology Journal, 2021, 19, 2235-2248.	4.1	25
29	Sex biased expression of hormone related genes at early stage of sex differentiation in papaya flowers. Horticulture Research, 2021, 8, 147.	2.9	12
30	Expression profiling of the Dof gene family under abiotic stresses in spinach. Scientific Reports, 2021, 11, 14429.	1.6	9
31	Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant <i>Camellia sinensis</i> . Nature Genetics, 2021, 53, 1250-1259.	9.4	157
32	Identification of structural variation and polymorphisms of a sex co-segregating scaffold in spinach. Plant Reproduction, 2021, , 1.	1.3	1
33	Unraveling a genetic roadmap for improved taste in the domesticated apple. Molecular Plant, 2021, 14, 1454-1471.	3.9	47
34	Rambutan genome revealed gene networks for spine formation and aril development. Plant Journal, 2021, 108, 1037-1052.	2.8	7
35	Genomic impact of stress-induced transposable element mobility in <i>Arabidopsis</i> . Nucleic Acids Research, 2021, 49, 10431-10447.	6.5	60
36	Karyotype and genome size determination of <i>Jarilla chocola</i> , an additional sister clade of <i>Carica papaya</i> . Plant OMICS, 2021, , 50-56.	0.4	1

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37	Expression profiling of WRKY transcription factors in Spinach. <i>Euphytica</i> , 2021, 217, 1.	0.6	1
38	The SAGA of pineapple: genome-wide identification and tissue-specific expression of Spt-Ada-Gcn5-acetyltransferase (SAGA) complex. <i>Euphytica</i> , 2021, 217, 1.	0.6	0
39	Resequencing of 388 cassava accessions identifies valuable loci and selection for variation in heterozygosity. <i>Genome Biology</i> , 2021, 22, 316.	3.8	15
40	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
41	The role of cis-elements in the evolution of crassulacean acid metabolism photosynthesis. <i>Horticulture Research</i> , 2020, 7, 5.	2.9	19
42	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
43	TRY plant trait database – enhanced coverage and open access. <i>Global Change Biology</i> , 2020, 26, 119-188.	4.2	1,038
44	Positional cloning and characterization of the papaya diminutive mutant reveal a truncating mutation in the CpMMS19 gene. <i>New Phytologist</i> , 2020, 225, 2006-2021.	3.5	0
45	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
46	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
47	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
48	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
49	Genomic footprints of repeated evolution of CAM photosynthesis in a Neotropical species radiation. <i>Plant, Cell and Environment</i> , 2020, 43, 2987-3001.	2.8	15
50	Comparative analysis of chloroplast genomes in <i>Vasconcellea pubescens</i> A.DC. and <i>Carica papaya</i> L.. <i>Scientific Reports</i> , 2020, 10, 15799.	1.6	7
51	Identification of Candidate Auxin Response Factors Involved in Pomegranate Seed Coat Development. <i>Frontiers in Plant Science</i> , 2020, 11, 536530.	1.7	3
52	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
53	Development and Evaluation of SSR Markers Based on Large Scale Full-Length Transcriptome Sequencing in Sugarcane. <i>Tropical Plant Biology</i> , 2020, 13, 343-352.	1.0	5
54	DNA methylome and transcriptome landscapes revealed differential characteristics of dioecious flowers in papaya. <i>Horticulture Research</i> , 2020, 7, 81.	2.9	20

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55	Genomic variation between PRSV resistant transgenic SunUp and its progenitor cultivar Sunset. <i>BMC Genomics</i> , 2020, 21, 398.	1.2	3
56	Intra-specific comparison of mitochondrial genomes reveals host gene fragment exchange via intron mobility in <i>Tremella fuciformis</i> . <i>BMC Genomics</i> , 2020, 21, 426.	1.2	7
57	Allele specific expression of Dof genes responding to hormones and abiotic stresses in sugarcane. <i>PLoS ONE</i> , 2020, 15, e0227716.	1.1	14
58	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
59	Genome-Wide Analysis of Transposable Elements and Satellite DNAs in <i>Spinacia</i> Species to Shed Light on Their Roles in Sex Chromosome Evolution. <i>Frontiers in Plant Science</i> , 2020, 11, 575462.	1.7	6
60	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
61	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
62	Recent polyploidization events in three <i>Saccharum</i> founding species. <i>Plant Biotechnology Journal</i> , 2019, 17, 264-274.	4.1	40
63	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
64	Assembly of allele-aware, chromosomal-scale autopolyploid genomes based on Hi-C data. <i>Nature Plants</i> , 2019, 5, 833-845.	4.7	292
65	Global identification and expression analysis of pineapple aquaporins revealed their roles in CAM photosynthesis, boron uptake and fruit domestication. <i>Euphytica</i> , 2019, 215, 1.	0.6	6
66	Papaya CpbHLH1/2 regulate carotenoid biosynthesis-related genes during papaya fruit ripening. <i>Horticulture Research</i> , 2019, 6, 80.	2.9	59
67	Auxin regulation involved in gynoceium morphogenesis of papaya flowers. <i>Horticulture Research</i> , 2019, 6, 119.	2.9	12
68	Mitochondrial genome in <i>Hypsizygus marmoreus</i> and its evolution in Dikarya. <i>BMC Genomics</i> , 2019, 20, 765.	1.2	22
69	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
70	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
71	The bracteatus pineapple genome and domestication of clonally propagated crops. <i>Nature Genetics</i> , 2019, 51, 1549-1558.	9.4	60
72	Analysis of genetic diversity of lychee ( <i>Litchi chinensis</i> Sonn.) and wild forest relatives in the Sapindaceae from Vietnam using microsatellites. <i>Genetic Resources and Crop Evolution</i> , 2019, 66, 1653-1669.	0.8	3

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73	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
74	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
75	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
76	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	9.4	398
77	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
78	The complete chloroplast genome of a gynodioecious deciduous orchid <i>Satyrium ciliatum</i> (Orchidaceae) female. <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3876-3877.	0.2	1
79	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
80	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
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	Differential expression of hormone related genes between extreme segregants of a <i>Saccharum</i> interspecific F2 population. <i>Euphytica</i> , 2018, 214, 1.	0.6	2
83	Differential methylation and expression of HUA1 ortholog in three sex types of papaya. <i>Plant Science</i> , 2018, 272, 99-106.	1.7	7
84	Pedigree, marker recruitment, and genetic diversity of modern sugarcane cultivars in China and the United States. <i>Euphytica</i> , 2018, 214, 1.	0.6	5
85	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
86	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
87	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
88	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
89	Comparison of the Mitochondrial Genome Sequences of Six <i>Annulohyphoxylon 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
90	PGD: Pineapple Genomics Database. <i>Horticulture Research</i> , 2018, 5, 66.	2.9	25

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91	Comparative Analysis of Homologous Sequences of <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> Reveals Independent Polyploidization Events. <i>Frontiers in Plant Science</i> , 2018, 9, 1414.	1.7	3
92	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
93	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
94	Diversification and independent domestication of Asian and European pears. <i>Genome Biology</i> , 2018, 19, 77.	3.8	149
95	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
96	Macroevolutionary synthesis of flowering plant sexual systems. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 898-912.	1.1	68
97	Development of male-specific markers and identification of sex reversal mutants in papaya. <i>Euphytica</i> , 2017, 213, 1.	0.6	30
98	Evolution and expression of the fructokinase gene family in <i>Saccharum</i> . <i>BMC Genomics</i> , 2017, 18, 197.	1.2	39
99	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
100	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
101	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
102	Identification and Characterization of microRNAs from <i>Saccharum officinarum</i> L by Deep Sequencing. <i>Tropical Plant Biology</i> , 2017, 10, 134-150.	1.0	4
103	Temporal and spatial transcriptomic and microRNA dynamics of CAM photosynthesis in pineapple. <i>Plant Journal</i> , 2017, 92, 19-30.	2.8	78
104	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	5.8	159
105	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
106	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
107	Isolation of ripening-related genes from ethylene/1-MCP treated papaya through RNA-seq. <i>BMC Genomics</i> , 2017, 18, 671.	1.2	33
108	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

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109	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
110	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
111	Comparative structural analysis of Bru1 region homeologs in <i>Saccharum spontaneum</i> and <i>S. officinarum</i> . <i>BMC Genomics</i> , 2016, 17, 446.	1.2	8
112	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
113	Comparative Analysis of GC Content Variations in Plant Genomes. <i>Tropical Plant Biology</i> , 2016, 9, 136-149.	1.0	54
114	Genome-Wide Comparative Analysis of Microsatellites in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 117-135.	1.0	13
115	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
116	Analysis of Alternative Splicing Landscape in Pineapple ( <i>Ananas comosus</i> ). <i>Tropical Plant Biology</i> , 2016, 9, 150-160.	1.0	18
117	Pineapple Genome: A Reference for Monocots and CAM Photosynthesis. <i>Trends in Genetics</i> , 2016, 32, 690-696.	2.9	19
118	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
119	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
120	Identification of microRNAs, phasiRNAs and Their Targets in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 176-186.	1.0	32
121	Genome-Wide Identification and Analysis of Genes Encoding Proteolytic Enzymes in Pineapple. <i>Tropical Plant Biology</i> , 2016, 9, 161-175.	1.0	10
122	Molecular basis of off-type microsatellite markers in papaya. <i>Euphytica</i> , 2016, 209, 323-339.	0.6	5
123	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
124	Balancing selection contributed to domestication of autopolyploid sugarcane ( <i>Saccharum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td	0.6	7
125	A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. <i>New Phytologist</i> , 2015, 207, 491-504.	3.5	211
126	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



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127	Assembling allopolyploid genomes: no longer formidable. <i>Genome Biology</i> , 2015, 16, 27.	3.8	21
128	ALLMAPS: robust scaffold ordering based on multiple maps. <i>Genome Biology</i> , 2015, 16, 3.	3.8	340
129	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
130	Origin and domestication of papaya Y chromosome. <i>Genome Research</i> , 2015, 25, 524-533.	2.4	87
131	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
132	Sex specific expression and distribution of small RNAs in papaya. <i>BMC Genomics</i> , 2014, 15, 20.	1.2	28
133	Genomics of sex determination. <i>Current Opinion in Plant Biology</i> , 2014, 18, 110-116.	3.5	41
134	Sex determination in flowering plants: Papaya as a model system. <i>Plant Science</i> , 2014, 217-218, 56-62.	1.7	78
135	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184.	6.0	520
136	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
137	Genomic analyses of the CAM plant pineapple. <i>Journal of Experimental Botany</i> , 2014, 65, 3395-3404.	2.4	46
138	The Effects of Gibberellic Acid on Sex Expression and Secondary Sexual Characteristics in Papaya. <i>Hortscience: A Publication of the American Society for Horticultural Science</i> , 2014, 49, 378-383.	0.5	5
139	Haplotype analysis of sucrose synthase gene family in three <i>Saccharum</i> species. <i>BMC Genomics</i> , 2013, 14, 314.	1.2	47
140	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
141	Nucleotide Composition of the <i>Nelumbo nucifera</i> Genome. <i>Tropical Plant Biology</i> , 2013, 6, 85-97.	1.0	2
142	Secretome Prediction and Analysis in Sacred Lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Tropical Plant Biology</i> , 2013, 6, 131-137.	1.0	6
143	Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	13.9	329
144	The genome of the pear ( <i>Pyrus bretschneideri</i> Rehd.). <i>Genome Research</i> , 2013, 23, 396-408.	2.4	832

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145	Genome size variation among sex types in dioecious and trioecious Caricaceae species. <i>Euphytica</i> , 2013, 189, 461-469.	0.6	14
146	Organelle DNA accumulation in the recently evolved papaya sex chromosomes. <i>Molecular Genetics and Genomics</i> , 2013, 288, 277-284.	1.0	18
147	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
148	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
149	Sequencing papaya X and Y chromosomes reveals molecular basis of incipient sex chromosome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13710-13715.	3.3	264
150	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
151	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
152	Construction of physical maps for the sex-specific regions of papaya sex chromosomes. <i>BMC Genomics</i> , 2012, 13, 176.	1.2	39
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