

Tae-Jin Yang

List of Publications by Year in descending order

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167
papers

7,101
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94433

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171
docs citations

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7833
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#	ARTICLE	IF	CITATIONS
1	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. <i>BMC Genomics</i> , 2015, 16, 1.	2.8	1,445
2	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
3	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. <i>Genome Biology</i> , 2017, 18, 210.	8.8	255
4	Sequence-Level Analysis of the Diploidization Process in the Triplicated <i>FLOWERING LOCUS C</i> Region of <i>Brassica rapa</i> . <i>Plant Cell</i> , 2006, 18, 1339-1347.	6.6	223
5	The Complete Chloroplast Genome Sequences of Five <i>Epimedium</i> Species: Lights into Phylogenetic and Taxonomic Analyses. <i>Frontiers in Plant Science</i> , 2016, 7, 306.	3.6	185
6	Genome-wide comparative analysis of the <i>Brassica rapa</i> gene space reveals genome shrinkage and differential loss of duplicated genes after whole genome triplication. <i>Genome Biology</i> , 2009, 10, R111.	9.6	183
7	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of <i>Oryza</i> AA genome species. <i>Scientific Reports</i> , 2015, 5, 15655.	3.3	169
8	Comprehensive Survey of Genetic Diversity in Chloroplast Genomes and 45S nrDNAs within <i>Panax ginseng</i> Species. <i>PLoS ONE</i> , 2015, 10, e0117159.	2.5	151
9	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	8.3	136
10	Complete Chloroplast Genome Sequence of Tartary Buckwheat (<i>Fagopyrum tataricum</i>) and Comparative Analysis with Common Buckwheat (<i>F. esculentum</i>). <i>PLoS ONE</i> , 2015, 10, e0125332.	2.5	119
11	Characterization of the centromere and pericentromere retrotransposons in <i>Brassica rapa</i> and their distribution in related <i>Brassica</i> species. <i>Plant Journal</i> , 2007, 49, 173-183.	5.7	116
12	Characterization of dihydroflavonol 4-reductase (DFR) genes and their association with cold and freezing stress in <i>Brassica rapa</i> . <i>Gene</i> , 2014, 550, 46-55.	2.2	96
13	Genotyping-by-sequencing map permits identification of clubroot resistance QTLs and revision of the reference genome assembly in cabbage (<i>Brassica oleracea</i> L.). <i>DNA Research</i> , 2016, 23, dsv034.	3.4	94
14	Comprehensive comparative analysis of chloroplast genomes from seven <i>Panax</i> species and development of an authentication system based on species-unique single nucleotide polymorphism markers. <i>Journal of Ginseng Research</i> , 2020, 44, 135-144.	5.7	76
15	Genome-wide characterization of long intergenic non-coding RNAs (lincRNAs) provides new insight into viral diseases in honey bees <i>Apis cerana</i> and <i>Apis mellifera</i> . <i>BMC Genomics</i> , 2015, 16, 680.	2.8	73
16	Ginseng Genome Database: an open-access platform for genomics of <i>Panax ginseng</i> . <i>BMC Plant Biology</i> , 2018, 18, 62.	3.6	73
17	Characterization of rDNAs and tandem repeats in the heterochromatin of <i>Brassica rapa</i> . <i>Molecules and Cells</i> , 2005, 19, 436-44.	2.6	70
18	The Korea <i>Brassica</i> Genome Project: a Glimpse of the <i>Brassica</i> Genome Based on Comparative Genome Analysis With <i>Arabidopsis</i> . <i>Comparative and Functional Genomics</i> , 2005, 6, 138-146.	2.0	69

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19	Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , 2010, 11, R94.	9.6	66
20	Major repeat components covering one-third of the ginseng (<i>Panax ginseng</i> C.A.) Tj ETQq0 0 0 r g B T / Overlock 10	9.7	66
21	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015, 15, 32.	3.6	63
22	Identification and Expression Analysis of Glucosinolate Biosynthetic Genes and Estimation of Glucosinolate Contents in Edible Organs of <i>Brassica oleracea</i> Subspecies. <i>Molecules</i> , 2015, 20, 13089-13111.	3.8	61
23	Completion of the mitochondrial genome sequence of onion (<i>Allium cepa</i> L.) containing the CMS-S male-sterile cytoplasm and identification of an independent event of the ccmF N gene split. <i>Current Genetics</i> , 2016, 62, 873-885.	1.7	59
24	Complete mitochondrial genome sequence and identification of a candidate gene responsible for cytoplasmic male sterility in radish (<i>Raphanus sativus</i> L.) containing DCGMS cytoplasm. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1763-1774.	3.6	57
25	Comprehensive analysis of <i>Panax ginseng</i> root transcriptomes. <i>BMC Plant Biology</i> , 2015, 15, 138.	3.6	55
26	Authentication Markers for Five Major <i>Panax</i> Species Developed via Comparative Analysis of Complete Chloroplast Genome Sequences. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 6298-6306.	5.2	55
27	Transcriptome profiling and comparative analysis of <i>Panax ginseng</i> adventitious roots. <i>Journal of Ginseng Research</i> , 2014, 38, 278-288.	5.7	53
28	Evolution of the Araliaceae family inferred from complete chloroplast genomes and 45S nrDNAs of 10 <i>Panax</i> -related species. <i>Scientific Reports</i> , 2017, 7, 4917.	3.3	53
29	In-depth sequence analysis of the tomato chromosome 12 centromeric region: identification of a large CAA block and characterization of pericentromere retrotransposons. <i>Chromosoma</i> , 2005, 114, 103-117.	2.2	52
30	Evolution of the large genome in <i>Capsicum annum</i> occurred through accumulation of single-type long terminal repeat retrotransposons and their derivatives. <i>Plant Journal</i> , 2012, 69, 1018-1029.	5.7	51
31	Development of Reproducible EST-derived SSR Markers and Assessment of Genetic Diversity in <i>Panax ginseng</i> Cultivars and Related Species. <i>Journal of Ginseng Research</i> , 2011, 35, 399-412.	5.7	49
32	Transcriptome sequencing of two parental lines of cabbage (<i>Brassica oleracea</i> L. var. capitata L.) and construction of an EST-based genetic map. <i>BMC Genomics</i> , 2014, 15, 149.	2.8	46
33	Practical application of DNA markers for high-throughput authentication of <i>Panax ginseng</i> and <i>Panax quinquefolius</i> from commercial ginseng products. <i>Journal of Ginseng Research</i> , 2014, 38, 123-129.	5.7	46
34	Evolutionary relationship of <i>Panax ginseng</i> and <i>P. quinquefolius</i> inferred from sequencing and comparative analysis of expressed sequence tags. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1377-1387.	1.6	45
35	Microsatellite-based analysis of genetic diversity in 91 commercial <i>Brassica oleracea</i> L. cultivars belonging to six varietal groups. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 1967-1986.	1.6	45
36	Rapid and Efficient FISH using Pre-Labeled Oligomer Probes. <i>Scientific Reports</i> , 2018, 8, 8224.	3.3	42

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37	Identification of candidate UDP-glycosyltransferases involved in protopanaxadiol-type ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>Scientific Reports</i> , 2018, 8, 11744.	3.3	41
38	EST-SSR Marker Sets for Practical Authentication of All Nine Registered Ginseng Cultivars in Korea. <i>Journal of Ginseng Research</i> , 2012, 36, 298-307.	5.7	40
39	Enhancement of Anti-Inflammatory Activity of <i>Aloe vera</i> Adventitious Root Extracts through the Alteration of Primary and Secondary Metabolites via Salicylic Acid Elicitation. <i>PLoS ONE</i> , 2013, 8, e82479.	2.5	40
40	Genome-Wide Comparative Analysis of 20 Miniature Inverted-Repeat Transposable Element Families in <i>Brassica rapa</i> and <i>B. oleracea</i> . <i>PLoS ONE</i> , 2014, 9, e94499.	2.5	38
41	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. <i>DNA Research</i> , 2017, 24, dsw049.	3.4	38
42	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in <i>Platycodon grandiflorus</i> , a medicinal plant. <i>Horticulture Research</i> , 2020, 7, 112.	6.3	38
43	Transcriptome analysis of newly classified bZIP transcription factors of <i>Brassica rapa</i> in cold stress response. <i>Genomics</i> , 2014, 104, 194-202.	2.9	37
44	Integrated Transcriptomic and Metabolomic Analysis of Five <i>Panax ginseng</i> Cultivars Reveals the Dynamics of Ginsenoside Biosynthesis. <i>Frontiers in Plant Science</i> , 2017, 8, 1048.	3.6	37
45	Re-exploration of Uâ€™s Triangle Brassica Species Based on Chloroplast Genomes and 45S nrDNA Sequences. <i>Scientific Reports</i> , 2018, 8, 7353.	3.3	36
46	Progress in Understanding and Sequencing the Genome of <i>Brassica rapa</i> . <i>International Journal of Plant Genomics</i> , 2008, 2008, 1-9.	2.2	35
47	Comparative analysis of pepper and tomato reveals euchromatin expansion of pepper genome caused by differential accumulation of Ty3/Gypsy-like elements. <i>BMC Genomics</i> , 2011, 12, 85.	2.8	34
48	Karyotype analysis of <i>Panax ginseng</i> C.A.Meyer, 1843 (Araliaceae) based on rDNA loci and DAPI band distribution. <i>Comparative Cytogenetics</i> , 2012, 6, 425-441.	0.8	32
49	Characterization of a new high copy Stowaway family MITE, BRAMI-1 in <i>Brassica</i> genome. <i>BMC Plant Biology</i> , 2013, 13, 56.	3.6	32
50	Evidence of genome duplication revealed by sequence analysis of multi-loci expressed sequence tagâ€™simple sequence repeat bands in <i>Panax ginseng</i> Meyer. <i>Journal of Ginseng Research</i> , 2014, 38, 130-135.	5.7	32
51	Dynamic Chloroplast Genome Rearrangement and DNA Barcoding for Three Apiaceae Species Known as the Medicinal Herb â€™Bang-Poongâ€™. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2196.	4.1	32
52	Detection of QTLs associated with mungbean yellow mosaic virus (MYMV) resistance using the interspecific cross of <i>Vigna radiata</i> Å– <i>Vigna umbellata</i> . <i>Journal of Applied Genetics</i> , 2019, 60, 255-268.	1.9	31
53	Characterization of terminal-repeat retrotransposon in miniature (TRIM) in <i>Brassica</i> relatives. <i>Theoretical and Applied Genetics</i> , 2007, 114, 627-636.	3.6	30
54	Diversity and evolution of major <i>Panax</i> species revealed by scanning the entire chloroplast intergenic spacer sequences. <i>Genetic Resources and Crop Evolution</i> , 2013, 60, 413-425.	1.6	30

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55	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. <i>Scientific Reports</i> , 2020, 10, 6112.	3.3	30
56	Terminal repeat retrotransposon in miniature (TRIM) as DNA markers in Brassica relatives. <i>Molecular Genetics and Genomics</i> , 2007, 278, 361-370.	2.1	28
57	Uncovering the Differential Molecular Basis of Adaptive Diversity in Three Echinochloa Leaf Transcriptomes. <i>PLoS ONE</i> , 2015, 10, e0134419.	2.5	28
58	Development and characterization of new microsatellite markers in Panax ginseng (C.A. Meyer) from BAC end sequences. <i>Conservation Genetics</i> , 2010, 11, 1223-1225.	1.5	26
59	Characterization of three active transposable elements recently inserted in three independent DFR-A alleles and one high-copy DNA transposon isolated from the Pink allele of the ANS gene in onion (<i>Allium cepa</i> L.). <i>Molecular Genetics and Genomics</i> , 2015, 290, 1027-1037.	2.1	26
60	Identification of a gene responsible for cytoplasmic male-sterility in onions (<i>Allium cepa</i> L.) using comparative analysis of mitochondrial genome sequences of two recently diverged cytoplasms. <i>Theoretical and Applied Genetics</i> , 2019, 132, 313-322.	3.6	26
61	Association of molecular markers derived from the BrCRISTO1 gene with prolycopene-enriched orange-colored leaves in Brassica rapa. <i>Theoretical and Applied Genetics</i> , 2014, 127, 179-191.	3.6	25
62	Expeditious discrimination of four species of the Panax genus using direct infusion-MS/MS combined with multivariate statistical analysis. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 1002, 329-336.	2.3	24
63	Rapid amplification of four retrotransposon families promoted speciation and genome size expansion in the genus Panax. <i>Scientific Reports</i> , 2017, 7, 9045.	3.3	24
64	Elucidating the major hidden genomic components of the A, C, and AC genomes and their influence on Brassica evolution. <i>Scientific Reports</i> , 2017, 7, 17986.	3.3	24
65	Transcriptomes of Indian barnyard millet and barnyardgrass reveal putative genes involved in drought adaptation and micronutrient accumulation. <i>Acta Physiologiae Plantarum</i> , 2019, 41, 1.	2.1	22
66	Comparative analysis of the transcriptomes and primary metabolite profiles of adventitious roots of five Panax ginseng cultivars. <i>Journal of Ginseng Research</i> , 2017, 41, 60-68.	5.7	20
67	Authentication of <i>Zanthoxylum</i> Species Based on Integrated Analysis of Complete Chloroplast Genome Sequences and Metabolite Profiles. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 10350-10359.	5.2	20
68	Comparative transcriptome analysis of heat stress responsiveness between two contrasting ginseng cultivars. <i>Journal of Ginseng Research</i> , 2019, 43, 572-579.	5.7	20
69	Genetic diversity among cultivated and wild Panax ginseng populations revealed by high-resolution microsatellite markers. <i>Journal of Ginseng Research</i> , 2020, 44, 637-643.	5.7	20
70	Repeat Evolution in <i>Brassica rapa</i> (AA), <i>B. oleracea</i> (CC), and <i>B. napus</i> (AACC) Genomes. <i>Plant Breeding and Biotechnology</i> , 2016, 4, 107-122.	0.9	19
71	Authentication of Golden-Berry <i>P. ginseng</i> Cultivar "Gumpoong"™ from a Landrace "Hwangsook"™ Based on Pooling Method Using Chloroplast-Derived Markers. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 16-24.	0.9	19
72	Construction and utility of 10-kb libraries for efficient clone-gap closure for rice genome sequencing. <i>Theoretical and Applied Genetics</i> , 2003, 107, 652-660.	3.6	18

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73	BrassicaTED - a public database for utilization of miniature transposable elements in Brassica species. BMC Research Notes, 2014, 7, 379.	1.4	18
74	Inheritance of chloroplast and mitochondrial genomes in cucumber revealed by four reciprocal F1 hybrid combinations. Scientific Reports, 2021, 11, 2506.	3.3	17
75	A Glimpse of <i>Panax ginseng</i> Genome Structure Revealed from Ten BAC Clone Sequences Obtained by SMRT Sequencing Platform. Plant Breeding and Biotechnology, 2017, 5, 25-35.	0.9	17
76	A refined <i>Panax ginseng</i> karyotype based on an ultra-high copy 167-bp tandem repeat and ribosomal DNAs. Journal of Ginseng Research, 2017, 41, 469-476.	5.7	16
77	Evolutionary Comparison of the Chloroplast Genome in the Woody Sonchus Alliance (Asteraceae) on the Canary Islands. Genes, 2019, 10, 217.	2.4	16
78	Comparative analysis and phylogenetic investigation of Hong Kong <i>Ilex</i> chloroplast genomes. Scientific Reports, 2021, 11, 5153.	3.3	16
79	The complete chloroplast genome sequence of <i>Zanthoxylum piperitum</i> . Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3525-3526.	0.7	15
80	The complete mitochondrial genome of <i>Wolfiporia cocos</i> (Polypolales: Polyporaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1010-1011.	0.4	15
81	Determination of cytoplasmic male sterile factors in onion plants (<i>Allium cepa</i> L.) using PCR-RFLP and SNP markers. Molecules and Cells, 2006, 21, 411-7.	2.6	14
82	Diversity and Inheritance of Intergenic Spacer Sequences of 45S Ribosomal DNA among Accessions of <i>Brassica oleracea</i> L. var. <i>capitata</i> . International Journal of Molecular Sciences, 2015, 16, 28783-28799.	4.1	13
83	Characterization of Chromosome-Specific Microsatellite Repeats and Telomere Repeats Based on Low Coverage Whole Genome Sequence Reads in <i>Panax ginseng</i> . Plant Breeding and Biotechnology, 2018, 6, 74-81.	0.9	13
84	Retrotransposons - a major driving force in plant genome evolution and a useful tool for genome analysis. Journal of Crop Science and Biotechnology, 2009, 12, 1-8.	1.5	12
85	The complete chloroplast genome sequence of <i>Capsicum chinense</i> Jacq. (Solanaceae). Mitochondrial DNA Part B: Resources, 2016, 1, 164-165.	0.4	12
86	The complete chloroplast genome sequence of <i>Cynanchum auriculatum</i> Royle ex Wight (Apocynaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4549-4550.	0.7	12
87	The complete chloroplast genome sequence of Indian barnyard millet, <i>Echinochloa frumentacea</i> (Poaceae). Mitochondrial DNA Part B: Resources, 2016, 1, 79-80.	0.4	12
88	The complete chloroplast genome sequence of an important medicinal plant <i>Cynanchum wilfordii</i> (Maxim.) Hemsl. (Apocynaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3747-3748.	0.7	12
89	QTL mapping in <i>Vigna radiata</i> × <i>Vigna umbellata</i> population uncovers major genomic regions associated with bruchid resistance. Molecular Breeding, 2019, 39, 1.	2.1	12
90	Dynamic evolution of <i>Panax</i> species. Genes and Genomics, 2021, 43, 209-215.	1.4	12

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91	The complete chloroplast genome of <i>Lilium distichum</i> Nakai (Liliaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4633-4634.	0.7	11
92	The complete chloroplast genome sequence of Magic Lily (<i>Lycoris squamigera</i>). Mitochondrial DNA Part B: Resources, 2018, 3, 1210-1211.	0.4	11
93	Characterization of the Long Terminal Repeat of the Endogenous Retrovirus-derived microRNAs in the Olive Flounder. Scientific Reports, 2019, 9, 14007.	3.3	11
94	Pre-labelled oligo probe-FISH karyotype analyses of four Araliaceae species using rDNA and telomeric repeat. Genes and Genomics, 2019, 41, 839-847.	1.4	11
95	Nuclear and chloroplast genome diversity revealed by low-coverage whole-genome shotgun sequence in 44 Brassica oleracea breeding lines. Horticultural Plant Journal, 2021, 7, 539-551.	5.0	11
96	Miniature Inverted-repeat Transposable Elements (MITEs) as Valuable Genomic Resources for the Evolution and Breeding of Brassica Crops. Plant Breeding and Biotechnology, 2014, 2, 322-333.	0.9	11
97	The complete chloroplast genome sequences of <i>Artemisia gmelinii</i> and <i>Artemisia capillaris</i> (Asteraceae). Mitochondrial DNA Part B: Resources, 2016, 1, 410-411.	0.4	10
98	The complete chloroplast genome of a medicinal plant <i>Epimedium koreanum</i> Nakai (Berberidaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4342-4343.	0.7	10
99	The complete chloroplast genome sequence of <i>Lilium hansonii</i> Leichtlin ex D.D.T.Moore. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3678-3679.	0.7	10
100	The complete chloroplast genome sequence of <i>Panax vietnamensis</i> Ha et Grushv (Araliaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 85-86.	0.7	10
101	Two complete chloroplast genome sequences and intra-species diversity for <i>Rehmannia glutinosa</i> (Orobanchaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 176-177.	0.4	10
102	Plastid Genomes of the Early Vascular Plant Genus <i>Selaginella</i> Have Unusual Direct Repeat Structures and Drastically Reduced Gene Numbers. International Journal of Molecular Sciences, 2021, 22, 641.	4.1	10
103	The complete chloroplast genome sequence of <i>Rhus chinensis</i> Mill (Anacardiaceae). Mitochondrial DNA Part B: Resources, 2016, 1, 696-697.	0.4	9
104	Complete chloroplast genome sequence of <i>Artemisia fukudo</i> Makino (Asteraceae). Mitochondrial DNA Part B: Resources, 2016, 1, 376-377.	0.4	9
105	The complete chloroplast genome sequence of <i>Ligularia fischeri</i> (Ledeb.) Turcz. (Asteraceae). Mitochondrial DNA Part B: Resources, 2016, 1, 4-5.	0.4	9
106	The complete chloroplast genome sequence of <i>Panax quinquefolius</i> (L.). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3033-3034.	0.7	9
107	The complete chloroplast genome sequence of Korean <i>Lonicera japonica</i> and intra-species diversity. Mitochondrial DNA Part B: Resources, 2018, 3, 941-942.	0.4	9
108	Whole-genome sequencing of <i>Brassica oleracea</i> var. <i>capitata</i> reveals new diversity of the mitogenome. PLoS ONE, 2018, 13, e0194356.	2.5	8

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109	Comparative analysis of Cassandra TRIMs in three Brassicaceae genomes. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S146-S150.	0.8	7
110	The complete chloroplast genomes of two <i>Taraxacum</i> species, <i>T. platycarpum</i> Dahlst. and <i>T. mongolicum</i> Hand.-Mazz. (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 412-413.	0.4	7
111	The complete chloroplast genome of <i>Eclipta prostrata</i> L. (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 414-415.	0.4	7
112	The complete chloroplast genomes of three Korean <i>Echinochloa crus-galli</i> accessions. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4357-4358.	0.7	7
113	Characterization of Imcrop, a Mutator-like MITE family in the rice genome. <i>Genes and Genomics</i> , 2012, 34, 189-198.	1.4	6
114	Discrimination between genetically identical peony roots from different regions of origin based on 1H-nuclear magnetic resonance spectroscopy-based metabolomics: determination of the geographical origins and estimation of the mixing proportions of blended samples. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 7523-7534.	3.7	6
115	Arginosecologanin, a secoiridoid-derived guanidine alkaloid from the roots of <i>Lonicera insularis</i> . <i>Natural Product Research</i> , 2018, 32, 788-794.	1.8	6
116	Genome-Wide Identification and Expression Analyses of the Fibrillin Family Genes Suggest Their Involvement in Photoprotection in Cucumber. <i>Plants</i> , 2018, 7, 50.	3.5	6
117	Chemical and genomic diversity of six <i>Lonicera</i> species occurring in Korea. <i>Phytochemistry</i> , 2018, 155, 126-135.	2.9	6
118	Five-color fluorescence in situ hybridization system for karyotyping of <i>Panax ginseng</i> . <i>Horticulture Environment and Biotechnology</i> , 2020, 61, 869-877.	2.1	6
119	The complete chloroplast genome of <i>Epimedium pubescens</i> Maxim. (Berberidaceae), a traditional Chinese medicine herb. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2042-2044.	0.4	6
120	Assessing the genetic and chemical diversity of <i>Taraxacum</i> species in the Korean Peninsula. <i>Phytochemistry</i> , 2021, 181, 112576.	2.9	6
121	Genomic Survey of the Hidden Components of the <i>B. rapa</i> Genome. <i>Compendium of Plant Genomes</i> , 2015, , 83-96.	0.5	6
122	Genetic and chemical markers for authentication of three <i>Artemisia</i> species: <i>A. capillaris</i> , <i>A. gmelinii</i> , and <i>A. fukudo</i> . <i>PLoS ONE</i> , 2022, 17, e0264576.	2.5	6
123	The complete chloroplast genome sequence of the <i>Taraxacum officinale</i> F.H.Wigg (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 228-229.	0.4	5
124	The complete chloroplast genome sequence of <i>Ledebouriella seseloides</i> (Hoffm.) H. Wolff. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3498-3499.	0.7	5
125	The complete chloroplast genome sequence of <i>Dendropanax morbifera</i> (L'Éveill��). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2923-2924.	0.7	5
126	Phylogenetic relationship of 40 species of genus <i>Aloe</i> L. and the origin of an allodiploid species revealed by nucleotide sequence variation in chloroplast intergenic space and cytogenetic in situ hybridization. <i>Genetic Resources and Crop Evolution</i> , 2016, 63, 235-242.	1.6	5

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127	Quantity, Distribution, and Evolution of Major Repeats in <i>Brassica napus</i> . <i>Compendium of Plant Genomes</i> , 2018, , 111-129.	0.5	5
128	Diversity and authentication of <i>Rubus</i> accessions revealed by complete plastid genome and rDNA sequences. <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 1454-1459.	0.4	5
129	Mitochondrial genome recombination in somatic hybrids of <i>Solanum commersonii</i> and <i>S. tuberosum</i> . <i>Scientific Reports</i> , 2022, 12, .	3.3	5
130	Comparative transcriptome and metabolome analyses of four <i>Panax</i> species explore the dynamics of metabolite biosynthesis. <i>Journal of Ginseng Research</i> , 2023, 47, 44-53.	5.7	5
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