

Tae-Jin Yang

List of Publications by Year in descending order

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167
papers

7,101
citations

94433

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71685

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171
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171
times ranked

7833
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#	ARTICLE	IF	CITATIONS
1	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
2	Genome structure and diversity among <i>Cynanchum wilfordii</i> accessions. <i>BMC Plant Biology</i> , 2022, 22, 4.	3.6	2
3	Cell cycle synchronization in <i>Panax ginseng</i> roots for cytogenomics research. <i>Horticulture Environment and Biotechnology</i> , 2022, 63, 137-145.	2.1	2
4	High-throughput SNP markers for authentication of Korean wheat cultivars based on seven complete plastomes and the nuclear genome. <i>Food Science and Biotechnology</i> , 2022, 31, 423-431.	2.6	0
5	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
6	Admixture of divergent genomes facilitates hybridization across species in the family Brassicaceae. <i>New Phytologist</i> , 2022, 235, 743-758.	7.3	3
7	Complete plastid and 45S rDNA sequences allow authentication of <i>Liriope platyphylla</i> and <i>Ophiopogon japonicus</i> . <i>Current Plant Biology</i> , 2022, 30, 100244.	4.7	2
8	The complete plastid genome sequence of <i>Peucedanum hakuunense</i> Nakai (Apiaceae), an endemic and rare species in Korea. <i>Mitochondrial DNA Part B: Resources</i> , 2022, 7, 766-768.	0.4	0
9	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
10	Assessing the genetic and chemical diversity of <i>Taraxacum</i> species in the Korean Peninsula. <i>Phytochemistry</i> , 2021, 181, 112576.	2.9	6
11	Molecular Cytogenetics of <i>Panax Ginseng</i> . <i>Compendium of Plant Genomes</i> , 2021, , 55-69.	0.5	1
12	Chloroplast Genome Diversity in <i>Panax</i> Genus. <i>Compendium of Plant Genomes</i> , 2021, , 95-105.	0.5	0
13	Ginseng Genome Structure and Evolution. <i>Compendium of Plant Genomes</i> , 2021, , 85-93.	0.5	0
14	Plastid Genomes of the Early Vascular Plant Genus <i>Selaginella</i> Have Unusual Direct Repeat Structures and Drastically Reduced Gene Numbers. <i>International Journal of Molecular Sciences</i> , 2021, 22, 641.	4.1	10
15	Inheritance of chloroplast and mitochondrial genomes in cucumber revealed by four reciprocal F1 hybrid combinations. <i>Scientific Reports</i> , 2021, 11, 2506.	3.3	17
16	Composition and Organization of Major Repeat Components in the <i>Brassica oleracea</i> Genome. <i>Compendium of Plant Genomes</i> , 2021, , 51-66.	0.5	0
17	Mining of Miniature Transposable Elements in <i>Brassica</i> Species at BrassicaTED. <i>Methods in Molecular Biology</i> , 2021, 2250, 69-74.	0.9	0
18	Breeding of Superior Ginseng Cultivars. <i>Compendium of Plant Genomes</i> , 2021, , 45-54.	0.5	2

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19	Dynamic evolution of <i>Panax</i> species. <i>Genes and Genomics</i> , 2021, 43, 209-215.	1.4	12
20	Nuclear and chloroplast genome diversity revealed by low-coverage whole-genome shotgun sequence in 44 <i>Brassica oleracea</i> breeding lines. <i>Horticultural Plant Journal</i> , 2021, 7, 539-551.	5.0	11
21	Comparative analysis and phylogenetic investigation of Hong Kong <i>Ilex</i> chloroplast genomes. <i>Scientific Reports</i> , 2021, 11, 5153.	3.3	16
22	Genomic Signature for Stem Swollen of Kohlrabi Morphotype in <i>Brassica oleracea</i> . <i>Plant Breeding and Biotechnology</i> , 2021, 9, 45-54.	0.9	0
23	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
24	Genetic diversity among cultivated and wild <i>Panax ginseng</i> populations revealed by high-resolution microsatellite markers. <i>Journal of Ginseng Research</i> , 2020, 44, 637-643.	5.7	20
25	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
26	Characterization of B-Genome Specific High Copy hAT MITE Families in <i>Brassica nigra</i> Genome. <i>Frontiers in Plant Science</i> , 2020, 11, 1104.	3.6	1
27	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
28	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
29	The complete chloroplast genome sequence of a medicinal herb <i>Liriope platyphylla</i> (Asparagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 85-86.	0.4	1
30	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
31	RNA editing may stabilize membrane-embedded proteins by increasing hydrophobicity: A study of <i>Zanthoxylum piperitum</i> and <i>Z. schinifolium</i> chloroplast NdhG. <i>Gene</i> , 2020, 746, 144638.	2.2	3
32	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. <i>Scientific Reports</i> , 2020, 10, 6112.	3.3	30
33	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
34	QTL mapping in <i>Vigna radiata</i> × <i>Vigna umbellata</i> population uncovers major genomic regions associated with bruchid resistance. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	12
35	Detection of QTLs associated with mungbean yellow mosaic virus (MYMV) resistance using the interspecific cross of <i>Vigna radiata</i> × <i>Vigna umbellata</i> . <i>Journal of Applied Genetics</i> , 2019, 60, 255-268.	1.9	31
36	The complete mitochondrial genome of <i>Wolfiporia cocos</i> (Polypolales: Polyporaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1010-1011.	0.4	15

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37	Characterization of the Long Terminal Repeat of the Endogenous Retrovirus-derived microRNAs in the Olive Flounder. <i>Scientific Reports</i> , 2019, 9, 14007.	3.3	11
38	Dynamic Chloroplast Genome Rearrangement and DNA Barcoding for Three Apiaceae Species Known as the Medicinal Herb "Bang-Poong": <i>International Journal of Molecular Sciences</i> , 2019, 20, 2196.	4.1	32
39	The complete chloroplast genome sequence of an invasive plant <i>Lonicera Maackii</i> (Caprifoliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 1008-1009.	0.4	1
40	Two complete chloroplast genome sequences and intra-species diversity for <i>Rehmannia glutinosa</i> (Orobanchaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 176-177.	0.4	10
41	Evolutionary Comparison of the Chloroplast Genome in the Woody Sonchus Alliance (Asteraceae) on the Canary Islands. <i>Genes</i> , 2019, 10, 217.	2.4	16
42	Pre-labelled oligo probe-FISH karyotype analyses of four Araliaceae species using rDNA and telomeric repeat. <i>Genes and Genomics</i> , 2019, 41, 839-847.	1.4	11
43	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
44	The complete chloroplast genome of <i>Mahonia eurybracteata</i> subsp. <i>Ganpinensis</i> (H.L. & v.) T. S. Ying & Boufford (Berberidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019, 4, 3933-3935.	0.4	2
45	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
46	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
47	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
48	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
49	The complete chloroplast genome sequence of <i>Hosta capitata</i> (Koidz.) Nakai (Asparagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1052-1053.	0.4	3
50	The complete chloroplast genome sequence of Magic Lily (<i>Lycoris squamigera</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 1210-1211.	0.4	11
51	The complete chloroplast genome of <i>Plagiorhegma dubia</i> Maxim., a traditional Chinese medicinal herb. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 112-114.	0.4	1
52	Diversity and Evolution of <i>B. napus</i> Chloroplast Genome. <i>Compendium of Plant Genomes</i> , 2018, , 177-188.	0.5	0
53	The complete chloroplast genome sequence of Korean <i>Lonicera japonica</i> and intra-species diversity. <i>Mitochondrial DNA Part B: Resources</i> , 2018, 3, 941-942.	0.4	9
54	Quantity, Distribution, and Evolution of Major Repeats in <i>Brassica napus</i> . <i>Compendium of Plant Genomes</i> , 2018, , 111-129.	0.5	5

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55	Rapid and Efficient FISH using Pre-Labeled Oligomer Probes. <i>Scientific Reports</i> , 2018, 8, 8224.	3.3	42
56	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
57	Re-exploration of Ua€™s Triangle Brassica Species Based on Chloroplast Genomes and 45S nrDNA Sequences. <i>Scientific Reports</i> , 2018, 8, 7353.	3.3	36
58	Chemical and genomic diversity of six <i>Lonicera</i> species occurring in Korea. <i>Phytochemistry</i> , 2018, 155, 126-135.	2.9	6
59	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
60	Whole-genome sequencing of <i>Brassica oleracea</i> var. capitata reveals new diversity of the mitogenome. <i>PLoS ONE</i> , 2018, 13, e0194356.	2.5	8
61	Characterization of Chromosome-Specific Microsatellite Repeats and Telomere Repeats Based on Low Coverage Whole Genome Sequence Reads in <i>Panax ginseng</i> . <i>Plant Breeding and Biotechnology</i> , 2018, 6, 74-81.	0.9	13
62	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
63	The complete chloroplast genome sequence of <i>Panax vietnamensis</i> Ha et Grushv (Araliaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 85-86.	0.7	10
64	Comparative analysis of the transcriptomes and primary metabolite profiles of adventitious roots of five <i>Panax ginseng</i> cultivars. <i>Journal of Ginseng Research</i> , 2017, 41, 60-68.	5.7	20
65	cis -Prenyltransferase interacts with a Nogo-B receptor homolog for dolichol biosynthesis in <i>Panax ginseng</i> Meyer. <i>Journal of Ginseng Research</i> , 2017, 41, 403-410.	5.7	4
66	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
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	Rapid amplification of four retrotransposon families promoted speciation and genome size expansion in the genus <i>Panax</i> . <i>Scientific Reports</i> , 2017, 7, 9045.	3.3	24
69	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
70	A refined <i>Panax ginseng</i> karyotype based on an ultra-high copy 167-bp tandem repeat and ribosomal DNAs. <i>Journal of Ginseng Research</i> , 2017, 41, 469-476.	5.7	16
71	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
72	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

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73	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
74	The complete chloroplast genome sequence with a novel 24-bp deletion of a Korean solid green-type cucumber variety (<i>Cucumis sativus</i> var. <i>sativus</i>). <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 755-756.	0.4	4
75	A Glimpse of <i>Panax ginseng</i> Genome Structure Revealed from Ten BAC Clone Sequences Obtained by SMRT Sequencing Platform. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 25-35.	0.9	3
76	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
77	A Glimpse of <i>Panax ginseng</i> Genome Structure Revealed from Ten BAC Clone Sequences Obtained by SMRT Sequencing Platform. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 25-35.	0.9	17
78	Discrimination and Authentication of <i>Eclipta prostrata</i> and <i>E. alba</i> Based on the Complete Chloroplast Genomes. <i>Plant Breeding and Biotechnology</i> , 2017, 5, 334-343.	0.9	4
79	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
80	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
81	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
82	The complete chloroplast genome sequence of <i>Capsicum chinense</i> Jacq. (Solanaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 164-165.	0.4	12
83	The complete chloroplast genome of Korean popular <i>Citrus</i> hybrid Hallabong mandarin [(<i>Citrus unshiu</i> — <i>C. sinensis</i>)— <i>C. reticulata</i>] (Rutaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 29-30.	0.4	2
84	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
85	The complete chloroplast genome sequences of <i>Artemisia gmelinii</i> and <i>Artemisia capillaris</i> (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 410-411.	0.4	10
86	The complete chloroplast genome sequence of <i>Rhus chinensis</i> Mill (Anacardiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 696-697.	0.4	9
87	Complete chloroplast genome sequence of <i>Artemisia fukudo</i> Makino (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 376-377.	0.4	9
88	The complete chloroplast genomes of <i>Lilium tsingtauense</i> Gilg (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 336-337.	0.4	3
89	The complete chloroplast genome sequence of <i>Ligularia fischeri</i> (Ledeb.) Turcz. (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 4-5.	0.4	9
90	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

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91	The complete chloroplast genome of <i>Eclipta prostrata</i> L. (Asteraceae). Mitochondrial DNA Part B: Resources, 2016, 1, 414-415.	0.4	7
92	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
93	The complete chloroplast genome sequence of a Korean indigenous ornamental plant <i>Hydrangea serrata</i> for. <i>fertilis</i> Nakai (Hydrangeaceae). Mitochondrial DNA Part B: Resources, 2016, 1, 27-28.	0.4	4
94	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
95	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
96	The complete chloroplast genomes of two <i>Wisteria</i> species, <i>W. floribunda</i> and <i>W. sinensis</i> (Fabaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4353-4354.	0.7	4
97	The complete chloroplast genome sequence of the medicinal plant <i>Glehnia littoralis</i> F.Schmidt ex Miq. (Apiaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3674-3675.	0.7	4
98	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
99	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
100	The complete chloroplast genomes of three Korean <i>Echinochloa crus-galli</i> accessions. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4357-4358.	0.7	7
101	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
102	The complete chloroplast genome of <i>Eleutherococcus gracilistylus</i> (W.W.Sm.) S.Y.Hu (Araliaceae). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3741-3742.	0.7	2
103	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
104	The complete chloroplast genome sequence of <i>Ledebouriella seseloides</i> (Hoffm.) H. Wolff. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3498-3499.	0.7	5
105	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
106	The complete chloroplast genome sequence of <i>Dendropanax morbifera</i> (L'Ã©veillÃ©). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 2923-2924.	0.7	5
107	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. Genetic Resources and Crop Evolution, 2016, 63, 235-242.	1.6	5
108	Repeat Evolution in <i>Brassica rapa</i> (AA), <i>B. oleracea</i> (CC), and <i>B. napus</i> (AACC) Genomes. Plant Breeding and Biotechnology, 2016, 4, 107-122.	0.9	19

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109	Next-Generation Sequencing Based Transposon Display to Detect High-Throughput Insertion Polymorphism Markers in <i>Brassica</i> . <i>Plant Breeding and Biotechnology</i> , 2016, 4, 285-296.	0.9	2
110	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
111	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
112	Diversity and Inheritance of Intergenic Spacer Sequences of 45S Ribosomal DNA among Accessions of <i>Brassica oleracea</i> L. var. <i>capitata</i> . <i>International Journal of Molecular Sciences</i> , 2015, 16, 28783-28799.	4.1	13
113	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
114	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
115	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
116	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015, 15, 32.	3.6	63
117	Miniature Transposable Elements (mTEs): Impacts and Uses in the <i>Brassica</i> Genome. <i>Compendium of Plant Genomes</i> , 2015, , 65-81.	0.5	3
118	Comprehensive analysis of <i>Panax ginseng</i> root transcriptomes. <i>BMC Plant Biology</i> , 2015, 15, 138.	3.6	55
119	Expedition discrimination of four species of the <i>Panax</i> 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
120	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
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	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
123	Uncovering the Differential Molecular Basis of Adaptive Diversity in Three <i>Echinochloa</i> Leaf Transcriptomes. <i>PLoS ONE</i> , 2015, 10, e0134419.	2.5	28
124	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
125	Comparative analysis of Cassandra TRIMs in three Brassicaceae genomes. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S146-S150.	0.8	7
126	Association of molecular markers derived from the BrCRISTO1 gene with prolycopene-enriched orange-colored leaves in <i>Brassica rapa</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 179-191.	3.6	25

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128	Major repeat components covering one-third of the ginseng (<i>Panax ginseng</i> C.A.) genome. <i>PLoS ONE</i> , 2014, 9, e1000000.	3.7	66
129	Analysis of expressed sequence tags from a normalized cDNA library of perilla (<i>Perilla frutescens</i>). <i>Journal of Plant Biology</i> , 2014, 57, 312-320.	2.1	4
130	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
131	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
132	BrassicaTED - a public database for utilization of miniature transposable elements in <i>Brassica</i> species. <i>BMC Research Notes</i> , 2014, 7, 379.	1.4	18
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134	Evidence of genome duplication revealed by sequence analysis of multi-loci expressed sequence tags: simple sequence repeat bands in <i>Panax ginseng</i> Meyer. <i>Journal of Ginseng Research</i> , 2014, 38, 130-135.	5.7	32
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136	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
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141	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
142	Optimal protocol for mass propagation of <i>Aloe vera</i> . <i>Journal of Crop Science and Biotechnology</i> , 2013, 16, 285-290.	1.5	1
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144	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

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146	Karyotype analysis of <i>Panax ginseng</i> C.A.Meyer, 1843 (Araliaceae) based on rDNA loci and DAPI band distribution. Comparative Cytogenetics, 2012, 6, 425-441.	0.8	32
147	EST-SSR Marker Sets for Practical Authentication of All Nine Registered Ginseng Cultivars in Korea. Journal of Ginseng Research, 2012, 36, 298-307.	5.7	40
148	Characterization of Imcrop, a Mutator-like MITE family in the rice genome. Genes and Genomics, 2012, 34, 189-198.	1.4	6
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