

Tae-Jin Yang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

162 papers	4,779 citations	33 h-index	65 g-index
171 ext. papers	5,995 ext. citations	3.4 avg, IF	5.19 L-index

#	Paper	IF	Citations
162	Cell cycle synchronization in Panax ginseng roots for cytogenomics research. <i>Horticulture Environment and Biotechnology</i> , 2022 , 63, 137-145	2	
161	Genome structure and diversity among Cynanchum wilfordii accessions.. <i>BMC Plant Biology</i> , 2022 , 22, 4	5.3	1
160	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	3	
159	Genetic and chemical markers for authentication of three Artemisia species: A. capillaris, A. gmelinii, and A. fukudo.. <i>PLoS ONE</i> , 2022 , 17, e0264576	3.7	1
158	Complete plastid and 45S rDNA sequences allow authentication of Liriope platyphylla and Ophiopogon japonicus. <i>Current Plant Biology</i> , 2022 , 30, 100244	3.3	0
157	The complete plastid genome sequence of Nakai (Apiaceae), an endemic and rare species in Korea.. <i>Mitochondrial DNA Part B: Resources</i> , 2022 , 7, 766-768	0.5	
156	Comparative analysis and phylogenetic investigation of Hong Kong Ilex chloroplast genomes. <i>Scientific Reports</i> , 2021 , 11, 5153	4.9	4
155	Genomic Signature for Stem Swollen of Kohlrabi Morphotype in Brassica oleracea. <i>Plant Breeding and Biotechnology</i> , 2021 , 9, 45-54	1.2	
154	Diversity and authentication of accessions revealed by complete plastid genome and rDNA sequences. <i>Mitochondrial DNA Part B: Resources</i> , 2021 , 6, 1454-1459	0.5	2
153	Assessing the genetic and chemical diversity of Taraxacum species in the Korean Peninsula. <i>Phytochemistry</i> , 2021 , 181, 112576	4	4
152	Molecular Cytogenetics of Panax Ginseng. <i>Compendium of Plant Genomes</i> , 2021 , 55-69	0.8	0
151	Genomic Resources for Ginseng Genome Studies. <i>Compendium of Plant Genomes</i> , 2021 , 143-148	0.8	
150	Chloroplast Genome Diversity in Panax Genus. <i>Compendium of Plant Genomes</i> , 2021 , 95-105	0.8	
149	Ginseng Genome Structure and Evolution. <i>Compendium of Plant Genomes</i> , 2021 , 85-93	0.8	
148	Plastid Genomes of the Early Vascular Plant Genus Have Unusual Direct Repeat Structures and Drastically Reduced Gene Numbers. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	5
147	Inheritance of chloroplast and mitochondrial genomes in cucumber revealed by four reciprocal F hybrid combinations. <i>Scientific Reports</i> , 2021 , 11, 2506	4.9	3
146	Composition and Organization of Major Repeat Components in the Brassica oleracea Genome. <i>Compendium of Plant Genomes</i> , 2021 , 51-66	0.8	

145	Mining of Miniature Transposable Elements in Brassica Species at BrassicaTED. <i>Methods in Molecular Biology</i> , 2021 , 2250, 69-74	1.4	
144	Breeding of Superior Ginseng Cultivars. <i>Compendium of Plant Genomes</i> , 2021 , 45-54	0.8	1
143	Dynamic evolution of Panax species. <i>Genes and Genomics</i> , 2021 , 43, 209-215	2.1	2
142	Nuclear and Chloroplast Genome Diversity Revealed by Low-Coverage Whole-Genome Shotgun Sequence in 44 Brassica oleracea Breeding Lines. <i>Horticultural Plant Journal</i> , 2021 , 7, 539-539	4.3	2
141	The complete chloroplast genome of Maxim. (Berberidaceae), a traditional Chinese medicine herb. <i>Mitochondrial DNA Part B: Resources</i> , 2020 , 5, 2042-2044	0.5	6
140	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in , a medicinal plant. <i>Horticulture Research</i> , 2020 , 7, 112	7.7	15
139	RNA editing may stabilize membrane-embedded proteins by increasing phydrophobicity: A study of Zanthoxylum piperitum and Z. schinifolium chloroplast NdhG. <i>Gene</i> , 2020 , 746, 144638	3.8	1
138	Characterization of B-Genome Specific High Copy hAT MITE Families in Genome. <i>Frontiers in Plant Science</i> , 2020 , 11, 1104	6.2	0
137	Five-color fluorescence in situ hybridization system for karyotyping of Panax ginseng. <i>Horticulture Environment and Biotechnology</i> , 2020 , 61, 869-877	2	3
136	Genetic diversity among cultivated and wild populations revealed by high-resolution microsatellite markers. <i>Journal of Ginseng Research</i> , 2020 , 44, 637-643	5.8	12
135	Comprehensive comparative analysis of chloroplast genomes from seven 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	5.8	38
134	Mitochondrial plastid DNA can cause DNA barcoding paradox in plants. <i>Scientific Reports</i> , 2020 , 10, 61124.9	4.9	13
133	Characterization of the Long Terminal Repeat of the Endogenous Retrovirus-derived microRNAs in the Olive Flounder. <i>Scientific Reports</i> , 2019 , 9, 14007	4.9	7
132	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,	6.3	22
131	Evolutionary Comparison of the Chloroplast Genome in the Woody Alliance (Asteraceae) on the Canary Islands. <i>Genes</i> , 2019 , 10,	4.2	10
130	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	2.1	7
129	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	2.6	10
128	The complete chloroplast genome sequence of a medicinal herb (Asparagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019 , 5, 85-86	0.5	1

127	Comparative transcriptome analysis of heat stress responsiveness between two contrasting ginseng cultivars. <i>Journal of Ginseng Research</i> , 2019 , 43, 572-579	5.8	9
126	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	3.4	7
125	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	2.5	16
124	The complete chloroplast genome of subsp. (H.L.) T. S. Ying & Boufford (Berberidaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2019 , 4, 3933-3935	0.5	2
123	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	6	16
122	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018 , 16, 1904-1917	11.6	77
121	Ginseng Genome Database: an open-access platform for genomics of <i>Panax ginseng</i> . <i>BMC Plant Biology</i> , 2018 , 18, 62	5.3	47
120	Genome-Wide Identification and Expression Analyses of the Fibrillin Family Genes Suggest Their Involvement in Photoprotection in Cucumber. <i>Plants</i> , 2018 , 7,	4.5	3
119	Re-exploration of U's Triangle Brassica Species Based on Chloroplast Genomes and 45S nrDNA Sequences. <i>Scientific Reports</i> , 2018 , 8, 7353	4.9	17
118	Chemical and genomic diversity of six <i>Lonicera</i> species occurring in Korea. <i>Phytochemistry</i> , 2018 , 155, 126-135	4	4
117	Identification of candidate UDP-glycosyltransferases involved in protopanaxadiol-type ginsenoside biosynthesis in <i>Panax ginseng</i> . <i>Scientific Reports</i> , 2018 , 8, 11744	4.9	19
116	Whole-genome sequencing of <i>Brassica oleracea</i> var. capitata reveals new diversity of the mitogenome. <i>PLoS ONE</i> , 2018 , 13, e0194356	3.7	7
115	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	1.2	11
114	Argininoscologanin, a secoiridoid-derived guanidine alkaloid from the roots of <i>Lonicera insularis</i> . <i>Natural Product Research</i> , 2018 , 32, 788-794	2.3	4
113	The complete chloroplast genome sequence of (Koidz.) Nakai (Asparagaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2018 , 3, 1052-1053	0.5	1
112	The complete chloroplast genome sequence of Magic Lily (). <i>Mitochondrial DNA Part B: Resources</i> , 2018 , 3, 1210-1211	0.5	8
111	The complete chloroplast genome of Maxim., a traditional Chinese medicinal herb. <i>Mitochondrial DNA Part B: Resources</i> , 2018 , 3, 112-114	0.5	
110	Diversity and Evolution of <i>B. napus</i> Chloroplast Genome. <i>Compendium of Plant Genomes</i> , 2018 , 177-188	0.8	

109	The complete chloroplast genome sequence of Korean and intra-species diversity. <i>Mitochondrial DNA Part B: Resources</i> , 2018 , 3, 941-942	0.5	9
108	Quantity, Distribution, and Evolution of Major Repeats in <i>Brassica napus</i> . <i>Compendium of Plant Genomes</i> , 2018 , 111-129	0.8	4
107	Rapid and Efficient FISH using Pre-Labeled Oligomer Probes. <i>Scientific Reports</i> , 2018 , 8, 8224	4.9	30
106	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	1.3	6
105	Comparative analysis of the transcriptomes and primary metabolite profiles of adventitious roots of five cultivars. <i>Journal of Ginseng Research</i> , 2017 , 41, 60-68	5.8	17
104	-Prenyltransferase interacts with a Nogo-B receptor homolog for dolichol biosynthesis in Meyer. <i>Journal of Ginseng Research</i> , 2017 , 41, 403-410	5.8	4
103	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	5.7	40
102	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 ¹¹	5.7	11
101	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	18.3	142
100	The complete chloroplast genome sequence with a novel 24-bp deletion of a Korean solid green-type cucumber variety (var.). <i>Mitochondrial DNA Part B: Resources</i> , 2017 , 2, 755-756	0.5	3
99	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	4.9	15
98	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	4.9	35
97	A refined karyotype based on an ultra-high copy 167-bp tandem repeat and ribosomal DNAs. <i>Journal of Ginseng Research</i> , 2017 , 41, 469-476	5.8	13
96	Elucidating the major hidden genomic components of the A, C, and AC genomes and their influence on <i>Brassica</i> evolution. <i>Scientific Reports</i> , 2017 , 7, 17986	4.9	19
95	Integrated Transcriptomic and Metabolomic Analysis of Five Cultivars Reveals the Dynamics of Ginsenoside Biosynthesis. <i>Frontiers in Plant Science</i> , 2017 , 8, 1048	6.2	27
94	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	1.2	3
93	Authentication of Golden-Berry <i>P. ginseng</i> Cultivar "Jumpoong" From a Landrace "Wangsook" Based on Pooling Method Using Chloroplast-Derived Markers. <i>Plant Breeding and Biotechnology</i> , 2017 , 5, 16-24	1.2	13
92	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	1.2	13

91	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	1.2	2
90	Genome analysis of <i>Hibiscus syriacus</i> provides insights of polyploidization and indeterminate flowering in woody plants. <i>DNA Research</i> , 2017 , 24, 71-80	4.5	32
89	The complete chloroplast genome sequence of the medicinal plant <i>Glehnia littoralis</i> F.Schmidt ex Miq. (Apiaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3674-5	1.3	4
88	The complete chloroplast genome sequence of an important medicinal plant <i>Cynanchum wilfordii</i> (Maxim.) Hemsl. (Apocynaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3747-8	1.3	8
87	The complete chloroplast genome of a medicinal plant <i>Epimedium koreanum</i> Nakai (Berberidaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 4342-4343	1.3	8
86	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	1.3	6
85	The complete chloroplast genome sequence of <i>Lilium hansonii</i> Leichtlin ex D.D.T.Moore. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3678-9	1.3	10
84	The complete chloroplast genome of <i>Eleutherococcus gracilistylus</i> (W.W.Sm.) S.Y.Hu (Araliaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3741-2	1.3	2
83	The complete chloroplast genome sequence of <i>Zanthoxylum piperitum</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3525-6	1.3	12
82	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, 3498-9	1.3	4
81	The complete chloroplast genome sequence of <i>Panax quinquefolius</i> (L.). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 3033-4	1.3	8
80	The complete chloroplast genome sequence of <i>Dendropanax moribifera</i> (Léveill.) <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 2923-4	1.3	3
79	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	2	5
78	The complete chloroplast genome of Korean popular hybrid Hallabong mandarin [(♂)] (Rutaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 29-30	0.5	0
77	The complete chloroplast genome sequence of the <i>F.H.Wigg</i> (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 228-229	0.5	4
76	The complete chloroplast genome sequences of and (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 410-411	0.5	5
75	The complete chloroplast genome sequence of <i>Mill</i> (Anacardiaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 696-697	0.5	6
74	Complete chloroplast genome sequence of <i>Makino</i> (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 376-377	0.5	7

73	The complete chloroplast genomes of Gilg (Liliaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 336-337	0.5	3
72	The complete chloroplast genome sequence of (Ledeb.) Turcz. (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 4-5	0.5	2
71	The complete chloroplast genomes of two species, Dahlst. and Hand.-Mazz. (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 412-413	0.5	3
70	The complete chloroplast genome of L. (Asteraceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 414-415	0.5	3
69	The complete chloroplast genome sequence of <i>Cynanchum auriculatum</i> Royle ex Wight (Apocynaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 4549-4550	1.3	9
68	The complete chloroplast genome sequence of a Korean indigenous ornamental plant for. Nakai (Hydrangeaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 27-28	0.5	1
67	The complete chloroplast genome of <i>Lilium distichum</i> Nakai (Liliaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 4633-4634	1.3	10
66	The complete chloroplast genome sequence of Indian barnyard millet, (Poaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 79-80	0.5	8
65	The complete chloroplast genomes of two Wisteria species, W. floribunda and W. sinensis (Fabaceae). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 4353-4354	1.3	2
64	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, 29-41	4.5	65
63	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	1.2	16
62	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	1.2	2
61	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	6.2	116
60	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 gene split. <i>Current Genetics</i> , 2016 , 62, 873-885	2.9	44
59	The complete chloroplast genome sequence of Jacq. (Solanaceae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 164-165	0.5	9
58	Uncovering the novel characteristics of Asian honey bee, <i>Apis cerana</i> , by whole genome sequencing. <i>BMC Genomics</i> , 2015 , 16, 1	4.5	738
57	Genome-wide SNP identification and QTL mapping for black rot resistance in cabbage. <i>BMC Plant Biology</i> , 2015 , 15, 32	5.3	45
56	Miniature Transposable Elements (mTEs): Impacts and Uses in the <i>Brassica</i> Genome. <i>Compendium of Plant Genomes</i> , 2015 , 65-81	0.8	3

55	Comprehensive analysis of Panax ginseng root transcriptomes. <i>BMC Plant Biology</i> , 2015 , 15, 138	5.3	44
54	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, 329-36	3.2	19
53	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, 1027-37	3.1	22
52	Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of Oryza AA genome species. <i>Scientific Reports</i> , 2015 , 5, 15655	4.9	124
51	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	4.5	54
50	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, 28783-99	6.3	9
49	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, 13089-111	4.8	46
48	Comprehensive Survey of Genetic Diversity in Chloroplast Genomes and 45S nrDNAs within Panax ginseng Species. <i>PLoS ONE</i> , 2015 , 10, e0117159	3.7	115
47	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	3.7	82
46	Uncovering the differential molecular basis of adaptive diversity in three <i>Echinochloa</i> leaf transcriptomes. <i>PLoS ONE</i> , 2015 , 10, e0134419	3.7	17
45	Genomic Survey of the Hidden Components of the <i>B. rapa</i> Genome. <i>Compendium of Plant Genomes</i> , 2015 , 83-96	0.8	6
44	Transcriptome sequencing of two parental lines of cabbage (<i>Brassica oleracea</i> L. var. <i>capitata</i> L.) and construction of an EST-based genetic map. <i>BMC Genomics</i> , 2014 , 15, 149	4.5	39
43	Major repeat components covering one-third of the ginseng (<i>Panax ginseng</i> C.A. Meyer) genome and evidence for allotetraploidy. <i>Plant Journal</i> , 2014 , 77, 906-16	6.9	45
42	Analysis of expressed sequence tags from a normalized cDNA library of perilla (<i>Perilla frutescens</i>) 2014 , 57, 312-320		4
41	Transcriptome analysis of newly classified bZIP transcription factors of <i>Brassica rapa</i> in cold stress response. <i>Genomics</i> , 2014 , 104, 194-202	4.3	25
40	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	3.8	59
39	BrassicaTED - a public database for utilization of miniature transposable elements in <i>Brassica</i> species. <i>BMC Research Notes</i> , 2014 , 7, 379	2.3	17
38	Practical application of DNA markers for high-throughput authentication of Panax ginseng and Panax quinquefolius from commercial ginseng products. <i>Journal of Ginseng Research</i> , 2014 , 38, 123-9	5.8	35

37	Evidence of genome duplication revealed by sequence analysis of multi-loci expressed sequence tag-simple sequence repeat bands in <i>Panax ginseng</i> Meyer. <i>Journal of Ginseng Research</i> , 2014 , 38, 130-5	5.8	21
36	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014 , 5, 3930	17.4	676
35	Transcriptome profiling and comparative analysis of <i>Panax ginseng</i> adventitious roots. <i>Journal of Ginseng Research</i> , 2014 , 38, 278-88	5.8	48
34	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	3.7	30
33	Comparative analysis of <i>Cassandra</i> TRIMs in three Brassicaceae genomes. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014 , 12, S146-S150	1	7
32	Association of molecular markers derived from the BrCRTISO1 gene with prolycopene-enriched orange-colored leaves in <i>Brassica rapa</i> [corrected]. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 179-91	6	19
31	Miniature Inverted-repeat Transposable Elements (MITEs) as Valuable Genomic Resources for the Evolution and Breeding of Brassica Crops. <i>Plant Breeding and Biotechnology</i> , 2014 , 2, 322-333	1.2	7
30	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, 7523-34	4.4	4
29	Characterization of a new high copy Stowaway family MITE, BRAMI-1 in Brassica genome. <i>BMC Plant Biology</i> , 2013 , 13, 56	5.3	26
28	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, 1763-74	6	48
27	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	2	26
26	Optimal protocol for mass propagation of <i>Aloe vera</i> . <i>Journal of Crop Science and Biotechnology</i> , 2013 , 16, 285-290	1.2	1
25	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	2	26
24	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	2	28
23	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	3.7	29
22	Evolution of the large genome in <i>Capsicum annuum</i> occurred through accumulation of single-type long terminal repeat retrotransposons and their derivatives. <i>Plant Journal</i> , 2012 , 69, 1018-29	6.9	46
21	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	5.8	33
20	Characterization of Imcrop, a Mutator-like MITE family in the rice genome. <i>Genes and Genomics</i> , 2012 , 34, 189-198	2.1	4

19	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, 425-41	1	28
18	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	4.5	30
17	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	5.8	39
16	Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , 2010 , 11, R94	18.3	53
15	Development and characterization of new microsatellite markers in <i>Panax ginseng</i> (C.A. Meyer) from BAC end sequences. <i>Conservation Genetics</i> , 2010 , 11, 1223-1225	2.6	23
14	Retrotransposons - a major driving force in plant genome evolution and a useful tool for genome analysis. <i>Journal of Crop Science and Biotechnology</i> , 2009 , 12, 1-8	1.2	10
13	In silico-selection of <i>Brassica rapa</i> organelle genome-derived BACs using their end sequences and sequence level comparative analysis of the 124 kb mitochondrial genome sequences in the family Brassicaceae. <i>Journal of Crop Science and Biotechnology</i> , 2009 , 12, 207-215	1.2	
12	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	18.3	155
11	Progress in understanding and sequencing the genome of <i>Brassica rapa</i> . <i>International Journal of Plant Genomics</i> , 2008 , 2008, 582837		27
10	Characterization of the centromere and peri-centromere retrotransposons in <i>Brassica rapa</i> and their distribution in related <i>Brassica</i> species. <i>Plant Journal</i> , 2007 , 49, 173-83	6.9	95
9	Characterization of terminal-repeat retrotransposon in miniature (TRIM) in <i>Brassica</i> relatives. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 627-36	6	28
8	Terminal repeat retrotransposon in miniature (TRIM) as DNA markers in <i>Brassica</i> relatives. <i>Molecular Genetics and Genomics</i> , 2007 , 278, 361-70	3.1	24
7	Sequence-level analysis of the diploidization process in the triplicated FLOWERING LOCUS C region of <i>Brassica rapa</i> . <i>Plant Cell</i> , 2006 , 18, 1339-47	11.6	192
6	Determination of cytoplasmic male sterile factors in onion plants (<i>Allium cepa</i> L.) using PCR-RFLP and SNP markers. <i>Molecules and Cells</i> , 2006 , 21, 411-7	3.5	13
5	The Korea brassica genome project: a glimpse of the brassica genome based on comparative genome analysis with <i>Arabidopsis</i> . <i>Comparative and Functional Genomics</i> , 2005 , 6, 138-46		61
4	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, 103-17 ²⁸		48
3	Characterization of rDNAs and tandem repeats in the heterochromatin of <i>Brassica rapa</i> . <i>Molecules and Cells</i> , 2005 , 19, 436-44	3.5	57
2	Construction and utility of 10-kb libraries for efficient clone-gap closure for rice genome sequencing. <i>Theoretical and Applied Genetics</i> , 2003 , 107, 652-60	6	16

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