Nam-Soo Kim

List of Publications by Year
in descending order

65 papers	1,091 citations	471509 17 h-index	454955 30 g-index
67 all docs	67 docs citations	67 times ranked	1199 citing authors

#	Article	IF	Citations
1	Transposable Elements and Genome Size Variations in Plants. Genomics and Informatics, 2014, 12, 87.	0.8	163
2	Simple Sequence Repeat Polymorphisms (SSRPs) for Evaluation of Molecular Diversity and Germplasm Classification of Minor Crops. Molecules, 2009, 14, 4546-4569.	3.8	124
3	Genetic Diversity of Perilla and Related Weedy Types in Korea Determined by AFLP Analyses. Crop Science, 2002, 42, 2161-2166.	1.8	56
4	Rim 2/Hipa CACTA transposon display: a new genetic marker technique in Oryza species. BMC Genetics, 2005, 6, 15.	2.7	49
5	A bioinformatics approach for identifying transgene insertion sites using whole genome sequencing data. BMC Biotechnology, 2017, 17, 67.	3.3	42
6	Rapid and Efficient FISH using Pre-Labeled Oligomer Probes. Scientific Reports, 2018, 8, 8224.	3.3	42
7	Marker utility of transposable elements for plant genetics, breeding, and ecology: a review. Genes and Genomics, 2015, 37, 141-151.	1.4	36
8	Chromosomal Localization and Sequence Variation of 5S rRNA Gene in Five Capsicum Species. Molecules and Cells, 2000, 10, 18-24.	2.6	34
9	Intron loss mediated structural dynamics and functional differentiation of the polygalacturonase gene family in land plants. Genes and Genomics, 2010, 32, 570-577.	1.4	33
10	Genetic diversity and phylogenetic relationship in AA Oryza species as revealed by Rim2/Hipa CACTA transposon display. Genes and Genetic Systems, 2006, 81, 93-101.	0.7	28
11	Genetic diversity of maize kernel starch-synthesis genes with SNAPs. Genome, 2006, 49, 1287-1296.	2.0	28
12	Development of expressed sequence tag derived-simple sequence repeats in the genus Lilium. Genes and Genomics, 2011, 33, 727-733.	1.4	27
13	Isolation and characterization of microsatellite markers in Perilla frutescens Brit. Molecular Ecology Notes, 2005, 5, 455-457.	1.7	25
14	Genetic mapping of the Isaac-CACTA transposon in maize. Theoretical and Applied Genetics, 2006, 113, 16-22.	3.6	24
15	Genetic and cytogenetic analyses of the A genome of Triticum monococcum. VIII. Localization of rDNAs and characterization of 5S rRNA genes. Genome, 1993, 36, 77-86.	2.0	21
16	The C- and G-value paradox with polyploidy, repeatomes, introns, phenomes and cell economy. Genes and Genomics, 2020, 42, 699-714.	1.4	21
17	Chloroplast genomes of Lilium lancifolium, L. amabile, L. callosum, and L. philadelphicum: Molecular characterization and their use in phylogenetic analysis in the genus Lilium and other allied genera in the order Liliales. PLoS ONE, 2017, 12, e0186788.	2.5	19
18	Comprehensive genomic analyses with 115 plastomes from algae to seed plants: structure, gene contents, GC contents, and introns. Genes and Genomics, 2020, 42, 553-570.	1.4	19

#	Article	IF	Citations
19	Genetic variation in Oryza species detected by MITE-AFLP.. Genes and Genetic Systems, 2003, 78, 235-243.	0.7	18
20	LTR-retrotransposons and inter-retrotransposon amplified polymorphism (IRAP) analysis in Lilium species. Genetica, 2015, 143, 343-352.	1.1	18
21	Isolation and characterization of novelTy1-copia-like retrotransposons from lily. Genome, 2013, 56, 495-503.	2.0	17
22	CACTA and MITE transposon distributions on a genetic map of rice using F15 RILs derived from Milyang 23 and Gihobyeo hybrids. Molecules and Cells, 2006, 21, 360-6.	2.6	17
23	Species relationships among Allium species by ISSR analysis. Horticulture Environment and Biotechnology, 2012, 53, 256-262.	2.1	16
24	Isaac-CACTA transposons: new genetic markers in maize and sorghum. Genome, 2005, 48, 455-460.	2.0	14
25	The genomes and transposable elements in plants: are they friends or foes?. Genes and Genomics, 2017, 39, 359-370.	1.4	14
26	Sequence Variation and Comparison of the 5S rRNA Sequences in Allium Species and their Chromosomal Distribution in Four Allium Species. Journal of Plant Biology, 2012, 55, 15-25.	2.1	13
27	Genetic and epigenetic diversity among dent, waxy, and sweet corns. Genes and Genomics, 2015, 37, 865-874.	1.4	13
28	Isolation of cold-responsive genes from garlic, Allium sativum. Genes and Genomics, 2012, 34, 93-101.	1.4	10
29	Natural triploid <scp>L</scp>ilium leichtlinii var. maximowiczii populations in <scp>K</scp>orea. Plant Species Biology, 2016, 31, 98-106.	1.0	10
30	Ribosomal DNA locus variation and REMAP analysis of the diploid and triploid complexes ofLilium lancifolium. Genome, 2016, 59, 551-564.	2.0	10
31	Development of CACTA transposon derived SCAR markers and their use in population structure analysis in Zea mays. Genetica, 2018, 146, 1-12.	1.1	10
32	Plastid Genomes of the Early Vascular Plant Genus Selaginella Have Unusual Direct Repeat Structures and Drastically Reduced Gene Numbers. International Journal of Molecular Sciences, 2021, 22, 641.	4.1	10
33	Gene Expression and Isoform Identification of PacBio Full-Length cDNA Sequences for Berberine Biosynthesis in Berberis koreana. Plants, 2021, 10, 1314.	3.5	10
34	Genetic diversity and structure analyses on the natural populations of diploids and triploids of tiger lily, Lilium lancifolium Thunb., from Korea, China, and Japan. Genes and Genomics, 2016, 38, 467-477.	1.4	9
35	Sequence diversification of 45S rRNA ITS, trnH-psbA spacer, and matK genic regions in several Allium species. Genes and Genomics, 2010, 32, 165-172.	1.4	8
36	Comparison of molecular genetic utilities of TD, AFLP, and MSAP among the accessions of japonica, indica, and Tongil of Oryza sativa L.. Genes and Genomics, 2016, 38, 819-830.	1.4	8

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37	NGS sequencing reveals that many of the genetic variations in transgenic rice plants match the variations found in natural rice population. Genes and Genomics, 2019, 41, 213-222.	1.4	8
38	A new MITE family, Pangrangja, in Gramineae species. Molecules and Cells, 2003, 15, 373-80.	2.6	7
39	Construction of genetic linkage map and identification of QTLs related to agronomic traits in maize using DNA transposon-based markers. Breeding Science, 2018, 68, 465-473.	1.9	6
40	De novo transcriptome sequencing and gene expression profiling with/without B-chromosome plants of Lilium amabile. Genomics and Informatics, 2019, 17, e27.	0.8	6
41	CACTA transposon-derived Ti-SCARs for cultivar fingerprinting in rapeseed. Genes and Genomics, 2012, 34, 575-579.	1.4	5
42	A new active CACTA element and transposition activity in ecotype differentiation of Arabidopsis. Genes and Genomics, 2014, 36, 229-238.	1.4	4
43	Genetic diversity analysis of maize lines using AFLP and TE-based molecular marker systems. Genes and Genomics, 2016, 38, 1005-1012.	1.4	4
44	Ty3/Gypsy retrotransposons in the Pacific abalone Haliotis discus hannai: characterization and use for species identification in the genus Haliotis. Genes and Genomics, 2018, 40, 177-187.	1.4	4
45	Karyotype and B chromosome variation in Lilium amabile Palibin. Genes and Genomics, 2019, 41, 647-655.	1.4	4
46	Characterization of chloroplast genomes of Alnus rubra and Betula cordifolia, and their use in phylogenetic analyses in Betulaceae. Genes and Genomics, 2019, 41, 305-316.	1.4	4
47	Identification of resurrection genes from the transcriptome of dehydrated and rehydrated Selaginella tamariscina. Plant Signaling and Behavior, 2021, 16, 1973703.	2.4	4
48	Retrotransposons in Betula nana, and interspecific relationships in the Betuloideae, based on inter-retrotransposon amplified polymorphism (IRAP) markers. Genes and Genomics, 2018, 40, 511-519.	1.4	3
49	Sequence Diversity of a Domesticated Transposase Gene, MUG1, in Oryza Species. Molecules and Cells, 2009, 27, 459-466.	2.6	2
50	Differentiation of CACTA-like Elements in Arabidopsis. , 2012, , 325-341.		2
51	Transposable elements and genomics. Genes and Genomics, 2015, 37, 111-112.	1.4	2
52	Translational genomics for human diseases: toward a new era of precision medicine. Genes and Genomics, 2016, 38, 573-575.	1.4	2
53	Cytological variations and long terminal repeat (LTR) retrotransposon diversities among diploids and B-chromosome aneuploids in Lilium amabile Palibin. Genes and Genomics, 2019, 41, 941-950.	1.4	2
54	Detection of mPing mobilization in transgenic rice plants. Genes and Genomics, 2020, 42, 47-54.	1.4	2

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55	Sequence variation in ITS spacers and 5.8S rDNA and relationship of E, St, P, Ns, Xm, and H genomes in the genera of Agropyron, Elytrigia, Leymus, Pascopyrum, Psathyrostachys, and Hordeum. Genes and Genomics, 2010, 32, 477-485.	1.4	1
56	Sequence-Specific Amplified Polymorphism (SSAP) and Sequence Characterized Amplified Region (SCAR) Markers in Zea mays. Methods in Molecular Biology, 2021, 2250, 207-218.	0.9	1
57	Genomic perspectives on epigenetics. Genes and Genomics, 2022, 44, 247-249.	1.4	1
58	Meeting report : Innovation in biology for the next generation!. Genes and Genomics, 2011, 33, 457-459.	1.4	0
59	Pong-like elements in Arabidopsis and Brassica rapa: its regulation of F-box protein gene in different ecotypes of Arabidopsis thaliana. Genes and Genomics, 2013, 35, 787-794.	1.4	0
60	Meeting report: genetics and genome engineering. Genes and Genomics, 2013, 35, 411-413.	1.4	0
61	Meeting report: Frontiers in genetics: genomics and epigenomics. Genes and Genomics, 2013, 35, 559-562.	1.4	0
62	Meeting report: stem cell biology and epigenetics. Genes and Genomics, 2013, 35, 681-684.	1.4	0
63	Meeting report: plant genetics and molecular biology. Genes and Genomics, 2014, 36, 125-127.	1.4	0
64	Meeting report: The biology of genomes and proteomes. Genes and Genomics, 2015, 37, 567-570.	1.4	0
65	Advancement of chromosome science in the genomics era. Genes and Genomics, 2021, 43, 195-198.	1.4	0