Sang-Ho Kang

List of Publications by Year
in descending order

35	459	758635 12	794141 19
papers	citations	h-index	g-index

38	38	38	551
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Long-read transcriptome sequencing provides insight into lignan biosynthesis during fruit development in Schisandra chinensis. BMC Genomics, 2022, 23, 17.	1.2	10
2	Chromosomal Mapping of Tandem Repeats Revealed Massive Chromosomal Rearrangements and Insights Into Senna tora Dysploidy. Frontiers in Plant Science, 2021, 12, 629898.	1.7	26
3	Transcriptome Changes Reveal the Molecular Mechanisms of Humic Acid-Induced Salt Stress Tolerance in Arabidopsis. Molecules, 2021, 26, 782.	1.7	9
4	Machine learning, transcriptome, and genotyping chip analyses provide insights into SNP markers identifying flower color in Platycodon grandiflorus. Scientific Reports, 2021, 11, 8019.	1.6	5
5	Systemic Expression of Genes Involved in the Plant Defense Response Induced by Wounding in Senna tora. International Journal of Molecular Sciences, 2021, 22, 10073.	1.8	12
6	De novo Transcriptome Assembly of Senna occidentalis Sheds Light on the Anthraquinone Biosynthesis Pathway. Frontiers in Plant Science, 2021, 12, 773553.	1.7	4
7	Genome-enabled discovery of anthraquinone biosynthesis in Senna tora. Nature Communications, 2020, 11, 5875.	5.8	57
8	Humic acid enhances heat stress tolerance via transcriptional activation of Heat-Shock Proteins in Arabidopsis. Scientific Reports, 2020, 10, 15042.	1.6	31
9	De novo transcriptome sequence of Senna tora provides insights into anthraquinone biosynthesis. PLoS ONE, 2020, 15, e0225564.	1.1	14
10	Whole-genome, transcriptome, and methylome analyses provide insights into the evolution of platycoside biosynthesis in Platycodon grandiflorus, a medicinal plant. Horticulture Research, 2020, 7, 112.	2.9	38
11	The complete chloroplast genomes of the medicinal plants, Senna tora and Senna occidentalis species. Mitochondrial DNA Part B: Resources, 2020, 5, 1673-1674.	0.2	1
12	Genome Assembly and Annotation of Soft-Shelled Adlay (Coix lacryma-jobi Variety ma-yuen), a Cereal and Medicinal Crop in the Poaceae Family. Frontiers in Plant Science, 2020, 11, 630.	1.7	20
13	The complete mitochondrial genome sequence of Schisandra chinensis (Austrobaileyales:) Tj ETQq1 1 0.784314 rgBT /Overloc	0.2	1
14	The complete mitochondrial genome sequence of Senna occidentalis (Fabales: Fabaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 85-86.	0.2	1
15	The complete mitochondrial genome sequences of Senna tora (Fabales: Fabaceae). Mitochondrial DNA Part B: Resources, 2019, 4, 1283-1284.	0.2	2
16	HOS15 Interacts with the Histone Deacetylase HDA9 and the Evening Complex to Epigenetically Regulate the Floral Activator GIGANTEA. Plant Cell, 2019, 31, 37-51.	3.1	65
17	Complete chloroplast genome and 45S nrDNA sequences of the medicinal plant species <i>Glycyrrhiza</i> <i>glabra</i> and <i>Glycyrrhiza uralensis</i>. Genes and Genetic Systems, 2018, 93, 83-89.	0.2	16
18	Identification of repetitive DNA sequences in the Chrysanthemum boreale genome. Scientia Horticulturae, 2018, 236, 238-243.	1.7	6

#	Article	IF	Citations
19	The complete chloroplast genome sequence of Coix lacryma-jobi L. (Poaceae), a cereal and medicinal crop. Mitochondrial DNA Part B: Resources, 2018, 3, 980-981.	0.2	9
20	De novo transcriptome assembly of the Chinese pearl barley, adlay, by full-length isoform and short-read RNA sequencing. PLoS ONE, 2018, 13, e0208344.	1.1	12
21	Identification of Root-specific Promoters Derived from Arabidopsis thaliana. Han'guk Yukchong Hakhoe Chi, 2018, 50, 21-32.	0.2	1
22	High-Throughput Profiling of Wheat Gliadin Proteins Using LabChip System in Chinese Spring and Its Aneuploid Lines. Han'guk Yukchong Hakhoe Chi, 2018, 50, 81-89.	0.2	0
23	The complete chloroplast genome of two Brassica species, Brassica nigra and B. Oleracea. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 167-168.	0.7	19
24	Comparative transcriptome analysis reveals whole-genome duplications and gene selection patterns in cultivated and wild Chrysanthemum species. Plant Molecular Biology, 2017, 95, 451-461.	2.0	21
25	The multipartite mitochondrial genome of Cynanchum wilfordii (Gentianales: Apocynaceae). Mitochondrial DNA Part B: Resources, 2017, 2, 720-721.	0.2	2
26	The complete mitochondrial genome of Wonwhang (Pyrus pyrifolia). Mitochondrial DNA Part B: Resources, 2017, 2, 902-903.	0.2	6
27	Analysis of flavonoids in double haploid population derived from microspore culture of F1 hybrid of Brassica rapa. Journal of Plant Biotechnology, 2017, 44, 35-41.	0.1	3
28	The Complete Chloroplast Genome of the Hareâ€™s Ear Root, Bupleurum falcatum: Its Molecular Features. Genes, 2016, 7, 20.	1.0	14
29	The complete chloroplast genome sequence of medicinal plant, Artemisia argyi. Mitochondrial DNA Part B: Resources, 2016, 1, 257-258.	0.2	8
30	Current status and prospects of chrysanthemum genomics. Journal of Plant Biotechnology, 2016, 43, 272-280.	0.1	5
31	Rediscovery of haploid breeding in the genomics era. Journal of Plant Biotechnology, 2016, 43, 12-20.	0.1	1
32	Development of Tissue Culture Technology for haploid production in Brassica species. Journal of the Korean Society of International Agriculture, 2015, 27, 522-528.	0.1	2
33	NABIC Microarray: an integrated database of high-throughput data for gene expression profiles. Bioinformation, 2015, 11, 509-511.	0.2	0
34	The suppression of the glutelin storage protein gene in transgenic rice seeds results in a higher yield of recombinant protein. Plant Biotechnology Reports, 2012, 6, 347-353.	0.9	15
35	The Arabidopsis beta-carotene hydroxylase gene promoter for a strong constitutive expression of transgene. Plant Biotechnology Reports, 2009, 3, 325-331.	0.9	20