Yang-Jae Kang

List of Publications by Year
in descending order

40 papers	1,825 citations	394421 19 h-index	302126 39 g-index
40 all docs	40 docs citations	40 times ranked	2469 citing authors

#	Article	IF	Citations
1	Genome sequence of mungbean and insights into evolution within Vigna species. Nature Communications, 2014, 5, 5443.	12.8	453
2	Whole-genome sequencing and intensive analysis of the undomesticated soybean (*Glycine soja*) Tj ETQq0 0 0 rgBT /Overlock 10 America, 2010, 107, 22032-22037.	7.1	299
3	Draft genome sequence of adzuki bean, Vigna angularis. Scientific Reports, 2015, 5, 8069.	3.3	144
4	Genome-wide mapping of NBS-LRR genes and their association with disease resistance in soybean. BMC Plant Biology, 2012, 12, 139.	3.6	143
5	Highly efficient homologyâ€directed repair using CRISPR/Cpf1â€geminiviral replicon in tomato. Plant Biotechnology Journal, 2020, 18, 2133-2143.	8.3	134
6	RNA-Seq Analysis of a Soybean Near-Isogenic Line Carrying Bacterial Leaf Pustule-Resistant and -Susceptible Alleles. DNA Research, 2011, 18, 483-497.	3.4	96
7	Divergence of flowering genes in soybean. Journal of Biosciences, 2012, 37, 857-870.	1.1	46
8	Translational genomics for plant breeding with the genome sequence explosion. Plant Biotechnology Journal, 2016, 14, 1057-1069.	8.3	46
9	Bacillus velezensis YC7010 Enhances Plant Defenses Against Brown Planthopper Through Transcriptomic and Metabolic Changes in Rice. Frontiers in Plant Science, 2018, 9, 1904.	3.6	41
10	Genome-wide SNP discovery in mungbean by Illumina HiSeq. Theoretical and Applied Genetics, 2013, 126, 2017-2027.	3.6	37
11	Divergence of Floweringâ€Related Genes in Three Legume Species. Plant Genome, 2013, 6, plantgenome2013.03.0008.	2.8	37
12	Machine learningâ€"based identification of hip arthroplasty designs. Journal of Orthopaedic Translation, 2020, 21, 13-17.	3.9	37
13	Drought resistance is mediated by divergent strategies in closely related Brassicaceae. New Phytologist, 2019, 223, 783-797.	7.3	34
14	p38 Stabilizes Snail by Suppressing DYRK2-Mediated Phosphorylation That Is Required for GSK3Î²-Î²TrCPâ€"Induced Snail Degradation. Cancer Research, 2019, 79, 4135-4148.	0.9	32
15	QTL identification of flowering time at three different latitudes reveals homeologous genomic regions that control flowering in soybean. Theoretical and Applied Genetics, 2011, 123, 545-553.	3.6	30
16	Genome-wide analysis of mutations in a dwarf soybean mutant induced by fast neutron bombardment. Euphytica, 2015, 203, 399-408.	1.2	28
17	Gene divergence of homeologous regions associated with a major seed protein content QTL in soybean. Frontiers in Plant Science, 2013, 4, 176.	3.6	23
18	Genome-wide single nucleotide polymorphism discovery and validation in adzuki bean. Molecular Breeding, 2014, 33, 497-501.	2.1	22

#	Article	IF	Citations
19	Mapping and Validation of QTLs for the Amino Acid and Total Protein Content in Brown Rice. Frontiers in Genetics, 2020, 11, 240.	2.3	21
20	Genome of the world's smallest flowering plant, Wolffia australiana, helps explain its specialized physiology and unique morphology. Communications Biology, 2021, 4, 900.	4.4	16
21	Optimization of a Virus-Induced Gene Silencing System with Soybean yellow common mosaic virus for Gene Function Studies in Soybeans. Plant Pathology Journal, 2016, 32, 112-122.	1.7	15
22	Genome-wide comparative analysis of flowering genes between Arabidopsis and mungbean. Genes and Genomics, 2014, 36, 799-808.	1.4	14
23	Genetic diversity of mungbean (*Vigna radiata* L.) germplasm in Indonesia. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, S91-S94.	0.8	13
24	Underlying genetic variation in the response of cultivated and wild soybean to enhanced ultraviolet-B radiation. Euphytica, 2015, 202, 207-217.	1.2	10
25	Genome-wide DNA methylation profile in mungbean. Scientific Reports, 2017, 7, 40503.	3.3	10
26	Identification of plastid genomic regions inferring species identity from de novo plastid genome assembly of 14 Korean-native Iris species (Iridaceae). PLoS ONE, 2020, 15, e0241178.	2.5	9
27	Genetic diversity of Jatropha curcas collections from different islands in Indonesia. Plant Genetic Resources: Characterisation and Utilisation, 2018, 16, 334-342.	0.8	6
28	Characterization of the complete chloroplast genome sequence of *Wolffia globosa* (Lemnoideae) and its phylogenetic relationships to other Araceae family. Mitochondrial DNA Part B: Resources, 2020, 5, 1905-1907.	0.4	4
29	Optimizing the Experimental Method for Stomata-Profiling Automation of Soybean Leaves Based on Deep Learning. Plants, 2021, 10, 2714.	3.5	4
30	Genome-wide scan of the soybean genome using degenerate oligonucleotide primed PCR: an example for studying large complex genome structure. Genes and Genomics, 2012, 34, 467-474.	1.4	3
31	Soybean-VCF2Genomes: a database to identify the closest accession in soybean germplasm collection. BMC Bioinformatics, 2019, 20, 384.	2.6	3
32	Identification of tissue-specific gene clusters and orthologues of nodulation-related genes in Vigna angularis. Plant Genetic Resources: Characterisation and Utilisation, 2014, 12, S21-S26.	0.8	2
33	Small-Scale duplication as a genomic signature for crop improvement. Journal of Crop Science and Biotechnology, 2015, 18, 45-51.	1.5	2
34	Genome-wide SSR marker development in oil palm by Illumina HiSeq for parental selection. Plant Genetic Resources: Characterisation and Utilisation, 2016, 14, 157-160.	0.8	2
35	Identification of Key Genes for the Precise Classification between Solenopsis invicta and S. geminata Facilitating the Quarantine Process. Genes, 2019, 10, 812.	2.4	2
36	Database: web application for visualization of the cumulated RNAseq data against the salicylic acid (SA) and methyl jasmonate (MeJA) treatment of Arabidopsis thaliana. BMC Plant Biology, 2020, 20, 453.	3.6	2

#	Article	IF	Citations
37	The Semi-Supervised Strategy of Machine Learning on the Gene Family Diversity to Unravel Resveratrol Synthesis. Plants, 2021, 10, 2058.	3.5	2
38	Circadian clock and photoperiodic flowering genes in adzuki bean (*Vigna angularis* [Willd.]) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	1
39	Sugarcane ORF finder: the web-application for mining genes from sugarcane genome. Plant Biotechnology Reports, 2019, 13, 553-558.	1.5	1
40	Comparative and phylogenetic analysis of the complete chloroplast genome of *Wolffia brasiliensis* (duckweed) in Araceae. Mitochondrial DNA Part B: Resources, 2020, 5, 1767-1768.	0.4	1