

Yang-Jae Kang

List of Publications by Year in descending order

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Version: 2024-02-01

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 of the world's smallest flowering plant, <i>Wolffia australiana</i> , helps explain its specialized physiology and unique morphology. <i>Communications Biology</i> , 2021, 4, 900.	4.4	16
2	The Semi-Supervised Strategy of Machine Learning on the Gene Family Diversity to Unravel Resveratrol Synthesis. <i>Plants</i> , 2021, 10, 2058.	3.5	2
3	Optimizing the Experimental Method for Stomata-Profiling Automation of Soybean Leaves Based on Deep Learning. <i>Plants</i> , 2021, 10, 2714.	3.5	4
4	Machine learning-based identification of hip arthroplasty designs. <i>Journal of Orthopaedic Translation</i> , 2020, 21, 13-17.	3.9	37
5	Database: web application for visualization of the cumulated RNAseq data against the salicylic acid (SA) and methyl jasmonate (MeJA) treatment of <i>Arabidopsis thaliana</i> . <i>BMC Plant Biology</i> , 2020, 20, 453.	3.6	2
6	Highly efficient homology-directed repair using CRISPR/Cpf1-geminiviral replicon in tomato. <i>Plant Biotechnology Journal</i> , 2020, 18, 2133-2143.	8.3	134
7	Mapping and Validation of QTLs for the Amino Acid and Total Protein Content in Brown Rice. <i>Frontiers in Genetics</i> , 2020, 11, 240.	2.3	21
8	Characterization of the complete chloroplast genome sequence of <i>Wolffia globosa</i> (Lemnoideae) and its phylogenetic relationships to other Araceae family. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1905-1907.	0.4	4
9	Comparative and phylogenetic analysis of the complete chloroplast genome of <i>Wolffia brasiliensis</i> (duckweed) in Araceae. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 1767-1768.	0.4	1
10	Identification of plastid genomic regions inferring species identity from de novo plastid genome assembly of 14 Korean-native Iris species (Iridaceae). <i>PLoS ONE</i> , 2020, 15, e0241178.	2.5	9
11	Soybean-VCF2Genomes: a database to identify the closest accession in soybean germplasm collection. <i>BMC Bioinformatics</i> , 2019, 20, 384.	2.6	3
12	Sugarcane ORF finder: the web-application for mining genes from sugarcane genome. <i>Plant Biotechnology Reports</i> , 2019, 13, 553-558.	1.5	1
13	Identification of Key Genes for the Precise Classification between <i>Solenopsis invicta</i> and <i>S. geminata</i> Facilitating the Quarantine Process. <i>Genes</i> , 2019, 10, 812.	2.4	2
14	p38 Stabilizes Snail by Suppressing DYRK2-Mediated Phosphorylation That Is Required for GSK3 β -Induced Snail Degradation. <i>Cancer Research</i> , 2019, 79, 4135-4148.	0.9	32
15	Drought resistance is mediated by divergent strategies in closely related Brassicaceae. <i>New Phytologist</i> , 2019, 223, 783-797.	7.3	34
16	Genetic diversity of <i>Jatropha curcas</i> collections from different islands in Indonesia. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2018, 16, 334-342.	0.8	6
17	<i>Bacillus velezensis</i> YC7010 Enhances Plant Defenses Against Brown Planthopper Through Transcriptomic and Metabolic Changes in Rice. <i>Frontiers in Plant Science</i> , 2018, 9, 1904.	3.6	41
18	Genome-wide DNA methylation profile in mungbean. <i>Scientific Reports</i> , 2017, 7, 40503.	3.3	10

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19	Translational genomics for plant breeding with the genome sequence explosion. <i>Plant Biotechnology Journal</i> , 2016, 14, 1057-1069.	8.3	46
20	Genome-wide SSR marker development in oil palm by Illumina HiSeq for parental selection. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2016, 14, 157-160.	0.8	2
21	Optimization of a Virus-Induced Gene Silencing System with Soybean yellow common mosaic virus for Gene Function Studies in Soybeans. <i>Plant Pathology Journal</i> , 2016, 32, 112-122.	1.7	15
22	Draft genome sequence of adzuki bean, <i>Vigna angularis</i> . <i>Scientific Reports</i> , 2015, 5, 8069.	3.3	144
23	Underlying genetic variation in the response of cultivated and wild soybean to enhanced ultraviolet-B radiation. <i>Euphytica</i> , 2015, 202, 207-217.	1.2	10
24	Genome-wide analysis of mutations in a dwarf soybean mutant induced by fast neutron bombardment. <i>Euphytica</i> , 2015, 203, 399-408.	1.2	28
25	Small-Scale duplication as a genomic signature for crop improvement. <i>Journal of Crop Science and Biotechnology</i> , 2015, 18, 45-51.	1.5	2
26	Genetic diversity of mungbean (<i>Vigna radiata</i> L.) germplasm in Indonesia. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S91-S94.	0.8	13
27	Genome-wide comparative analysis of flowering genes between <i>Arabidopsis</i> and mungbean. <i>Genes and Genomics</i> , 2014, 36, 799-808.	1.4	14
28	Genome sequence of mungbean and insights into evolution within <i>Vigna</i> species. <i>Nature Communications</i> , 2014, 5, 5443.	12.8	453
29	Circadian clock and photoperiodic flowering genes in adzuki bean (<i>Vigna angularis</i> [Willd.] Tj ETQq1 1 0.784314 rgBT /Overlock	0.8	1
30	Identification of tissue-specific gene clusters and orthologues of nodulation-related genes in <i>Vigna angularis</i> . <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S21-S26.	0.8	2
31	Genome-wide single nucleotide polymorphism discovery and validation in adzuki bean. <i>Molecular Breeding</i> , 2014, 33, 497-501.	2.1	22
32	Genome-wide SNP discovery in mungbean by Illumina HiSeq. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2017-2027.	3.6	37
33	Gene divergence of homeologous regions associated with a major seed protein content QTL in soybean. <i>Frontiers in Plant Science</i> , 2013, 4, 176.	3.6	23
34	Divergence of Flowering-Related Genes in Three Legume Species. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0008.	2.8	37
35	Genome-wide scan of the soybean genome using degenerate oligonucleotide primed PCR: an example for studying large complex genome structure. <i>Genes and Genomics</i> , 2012, 34, 467-474.	1.4	3
36	Genome-wide mapping of NBS-LRR genes and their association with disease resistance in soybean. <i>BMC Plant Biology</i> , 2012, 12, 139.	3.6	143

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37	Divergence of flowering genes in soybean. <i>Journal of Biosciences</i> , 2012, 37, 857-870.	1.1	46
38	QTL identification of flowering time at three different latitudes reveals homeologous genomic regions that control flowering in soybean. <i>Theoretical and Applied Genetics</i> , 2011, 123, 545-553.	3.6	30
39	RNA-Seq Analysis of a Soybean Near-Isogenic Line Carrying Bacterial Leaf Pustule-Resistant and -Susceptible Alleles. <i>DNA Research</i> , 2011, 18, 483-497.	3.4	96
40	Whole-genome sequencing and intensive analysis of the undomesticated soybean (<i>Glycine soja</i>) Tj ETQq0 0 0 rgBT /Overlock 10 America, 2010, 107, 22032-22037.	7.1	299