Tae-Ho Lee

List of Publications by Year
in descending order

24 papers	12,054 citations	471509 17 h-index	610901 24 g-index
24 all docs	24 docs citations	24 times ranked	10845 citing authors

#	Article	IF	Citations
1	The Evolution of an Invasive Plant, Sorghum halepense L. (â€˜Johnsongrassâ€™). Frontiers in Genetics, 2020, 11, 317.	2.3	30
2	Genome and evolution of the shadeâ€requiring medicinal herb *Panax ginseng*. Plant Biotechnology Journal, 2018, 16, 1904-1917.	8.3	136
3	Genome-wide identification of grain filling genes regulated by the OsSMF1 transcription factor in rice. Rice, 2017, 10, 16.	4.0	23
4	Comparative transcriptome analysis reveals whole-genome duplications and gene selection patterns in cultivated and wild Chrysanthemum species. Plant Molecular Biology, 2017, 95, 451-461.	3.9	21
5	RapaNet: A Web Tool for the Co-Expression Analysis of Brassica rapa Genes. Evolutionary Bioinformatics, 2017, 13, 117693431771542.	1.2	9
6	Characterization of twenty Camelina spp. accessions using single nucleotide polymorphism genotyping. Horticulture Environment and Biotechnology, 2017, 58, 187-194.	2.1	4
7	Plant Genome Duplication Database. Methods in Molecular Biology, 2017, 1533, 267-277.	0.9	30
8	MultiSyn: A Webtool for Multiple Synteny Detection and Visualization of User's Sequence of Interest Compared to Public Plant Species. Evolutionary Bioinformatics, 2016, 12, EBO.S40009.	1.2	8
9	Comparative genomic deâ€convolution of the cotton genome revealed a decaploid ancestor and widespread chromosomal fractionation. New Phytologist, 2016, 209, 1252-1263.	7.3	65
10	NABIC: A New Access Portal to Search, Visualize, and Share Agricultural Genomics Data. Evolutionary Bioinformatics, 2016, 12, EBO.S34493.	1.2	10
11	Genome Alignment Spanning Major Poaceae Lineages Reveals Heterogeneous Evolutionary Rates and Alters Inferred Dates for Key Evolutionary Events. Molecular Plant, 2015, 8, 885-898.	8.3	131
12	Genetic analysis of vegetative branching in sorghum. Theoretical and Applied Genetics, 2014, 127, 2387-2403.	3.6	35
13	SNPhylo: a pipeline to construct a phylogenetic tree from huge SNP data. BMC Genomics, 2014, 15, 162.	2.8	410
14	Sequencing of transcriptomes from two Miscanthus species reveals functional specificity in rhizomes, and clarifies evolutionary relationships. BMC Plant Biology, 2014, 14, 134.	3.6	17
15	Comparative Analysis of *Miscanthus* and *Saccharum* Reveals a Shared Whole-Genome Duplication but Different Evolutionary Fates. Plant Cell, 2014, 26, 2420-2429.	6.6	88
16	Early allopolyploid evolution in the post-Neolithic *Brassica napus* oilseed genome. Science, 2014, 345, 950-953.	12.6	2,089
17	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	12.8	918
18	Function Relaxation Followed by Diversifying Selection after Whole-Genome Duplication in Flowering Plants Â Â. Plant Physiology, 2013, 162, 769-778.	4.8	44

#	Article	IF	Citations
19	MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Research, 2012, 40, e49-e49.	14.5	4,252
20	PGDD: a database of gene and genome duplication in plants. Nucleic Acids Research, 2012, 41, D1152-D1158.	14.5	544
21	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
22	The genome of the mesopolyploid crop species Brassica rapa. Nature Genetics, 2011, 43, 1035-1039.	21.4	1,893
23	Current status on expression profiling using rice microarray. Journal of Plant Biotechnology, 2010, 37, 144-152.	0.4	2
24	RiceArrayNet: A Database for Correlating Gene Expression from Transcriptome Profiling, and Its Application to the Analysis of Coexpressed Genes in Rice Â Â Â. Plant Physiology, 2009, 151, 16-33.	4.8	91