

Tae-Ho Lee

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

12,054
citations

471509

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610901

24
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all docs

24
docs citations

24
times ranked

10845
citing authors

#	ARTICLE	IF	CITATIONS
1	MCSanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. <i>Nucleic Acids Research</i> , 2012, 40, e49-e49.	14.5	4,252
2	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
3	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
4	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
5	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
6	PGDD: a database of gene and genome duplication in plants. <i>Nucleic Acids Research</i> , 2012, 41, D1152-D1158.	14.5	544
7	SNPhylo: a pipeline to construct a phylogenetic tree from huge SNP data. <i>BMC Genomics</i> , 2014, 15, 162.	2.8	410
8	Genome and evolution of the shade-requiring medicinal herb <i>Panax ginseng</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1904-1917.	8.3	136
9	Genome Alignment Spanning Major Poaceae Lineages Reveals Heterogeneous Evolutionary Rates and Alters Inferred Dates for Key Evolutionary Events. <i>Molecular Plant</i> , 2015, 8, 885-898.	8.3	131
10	RiceArrayNet: A Database for Correlating Gene Expression from Transcriptome Profiling, and Its Application to the Analysis of Coexpressed Genes in Rice. <i>Plant Physiology</i> , 2009, 151, 16-33.	4.8	91
11	Comparative Analysis of <i>Miscanthus</i> and <i>Saccharum</i> Reveals a Shared Whole-Genome Duplication but Different Evolutionary Fates. <i>Plant Cell</i> , 2014, 26, 2420-2429.	6.6	88
12	Comparative genomic deconvolution of the cotton genome revealed a decaploid ancestor and widespread chromosomal fractionation. <i>New Phytologist</i> , 2016, 209, 1252-1263.	7.3	65
13	Function Relaxation Followed by Diversifying Selection after Whole-Genome Duplication in Flowering Plants. <i>Plant Physiology</i> , 2013, 162, 769-778.	4.8	44
14	Genetic analysis of vegetative branching in sorghum. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2387-2403.	3.6	35
15	The Evolution of an Invasive Plant, <i>Sorghum halepense</i> L. (Johnsongrass™). <i>Frontiers in Genetics</i> , 2020, 11, 317.	2.3	30
16	Plant Genome Duplication Database. <i>Methods in Molecular Biology</i> , 2017, 1533, 267-277.	0.9	30
17	Genome-wide identification of grain filling genes regulated by the OsSMF1 transcription factor in rice. <i>Rice</i> , 2017, 10, 16.	4.0	23
18	Comparative transcriptome analysis reveals whole-genome duplications and gene selection patterns in cultivated and wild <i>Chrysanthemum</i> species. <i>Plant Molecular Biology</i> , 2017, 95, 451-461.	3.9	21

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19	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
20	NABIC: A New Access Portal to Search, Visualize, and Share Agricultural Genomics Data. Evolutionary Bioinformatics, 2016, 12, EBO.S34493.	1.2	10
21	RapaNet: A Web Tool for the Co-Expression Analysis of Brassica rapa Genes. Evolutionary Bioinformatics, 2017, 13, 117693431771542.	1.2	9
22	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
23	Characterization of twenty Camelina spp. accessions using single nucleotide polymorphism genotyping. Horticulture Environment and Biotechnology, 2017, 58, 187-194.	2.1	4
24	Current status on expression profiling using rice microarray. Journal of Plant Biotechnology, 2010, 37, 144-152.	0.4	2