

Cheng-Ting Yeh

List of Publications by Year in descending order

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31
papers

7,125
citations

318942

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h-index

488211

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docs citations

33
times ranked

10266
citing authors

#	ARTICLE	IF	CITATIONS
1	Trajectories of Homoeolog-Specific Expression in Allotetraploid <i>Tragopogon castellanus</i> Populations of Independent Origins. <i>Frontiers in Plant Science</i> , 2021, 12, 679047.	1.7	3
2	KAT4IA: K-Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , 2021, 2021, 9805489.	2.5	5
3	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. <i>BMC Research Notes</i> , 2020, 13, 71.	0.6	38
4	Co-expression analysis aids in the identification of genes in the cuticular wax pathway in maize. <i>Plant Journal</i> , 2019, 97, 530-542.	2.8	34
5	Empirical Comparisons of Different Statistical Models To Identify and Validate Kernel Row Number-Associated Variants from Structured Multi-parent Mapping Populations of Maize. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3567-3575.	0.8	19
6	Linked read technology for assembling large complex and polyploid genomes. <i>BMC Genomics</i> , 2018, 19, 651.	1.2	31
7	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2513-2522.	0.8	41
8	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. <i>BMC Research Notes</i> , 2018, 11, 452.	0.6	25
9	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 694.	1.7	109
10	Extreme phenotype genome-wide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. <i>Plant Journal</i> , 2015, 84, 587-596.	2.8	93
11	The maize <i>brown midrib4</i> (<i>bm4</i>) gene encodes a functional folylpolyglutamate synthase. <i>Plant Journal</i> , 2015, 81, 493-504.	2.8	42
12	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948.	3.1	80
13	The <i>Aux/IAA</i> gene <i>rum1</i> involved in seminal and lateral root formation controls vascular patterning in maize (<i>Zea mays</i> L.) primary roots. <i>Journal of Experimental Botany</i> , 2014, 65, 4919-4930.	2.4	69
14	Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40.	13.9	419
15	The maize <i>brown midrib2</i> (<i>bm2</i>) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. <i>Plant Journal</i> , 2014, 77, 380-392.	2.8	94
16	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. <i>PLoS Genetics</i> , 2012, 8, e1003127.	1.5	166
17	Complementation contributes to transcriptome complexity in maize (<i>Zea mays</i> L.) hybrids relative to their inbred parents. <i>Genome Research</i> , 2012, 22, 2445-2454.	2.4	154
18	Genic and nongenetic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012, 22, 2436-2444.	2.4	125

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19	Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 2012, 72, 390-399.	2.8	24
20	Parallel domestication of the <i>Shattering1</i> genes in cereals. <i>Nature Genetics</i> , 2012, 44, 720-724.	9.4	401
21	Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 2012, 7, e36406.	1.1	297
22	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies. , 2011, , .		4
23	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize \hat{A} \hat{A} . <i>Plant Physiology</i> , 2011, 156, 1679-1690.	2.3	76
24	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. <i>Plant Cell</i> , 2011, 23, 4221-4233.	3.1	189
25	Heritable Epigenetic Variation among Maize Inbreds. <i>PLoS Genetics</i> , 2011, 7, e1002372.	1.5	150
26	Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , 2010, 62, 898-909.	2.8	89
27	High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. <i>PLoS ONE</i> , 2010, 5, e14178.	1.1	11
28	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728.	1.5	39
29	Maize Inbreds Exhibit High Levels of Copy Number Variation (CNV) and Presence/Absence Variation (PAV) in Genome Content. <i>PLoS Genetics</i> , 2009, 5, e1000734.	1.5	484
30	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	6.0	3,612
31	Mu Transposon Insertion Sites and Meiotic Recombination Events Co-Localize with Epigenetic Marks for Open Chromatin across the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000733.	1.5	196