Cheng-Ting Yeh

List of Publications by Year
in descending order

31 papers	7,125 citations	279487 23 h-index	433756 31 g-index
33 all docs	33 docs citations	33 times ranked	9164 citing authors

#	Article	IF	Citations
1	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	6.0	3,612
2	Maize Inbreds Exhibit High Levels of Copy Number Variation (CNV) and Presence/Absence Variation (PAV) in Genome Content. PLoS Genetics, 2009, 5, e1000734.	1.5	484
3	Genome-wide discovery and characterization of maize long non-coding RNAs. Genome Biology, 2014, 15, R40.	13.9	419
4	Parallel domestication of the Shattering1 genes in cereals. Nature Genetics, 2012, 44, 720-724.	9.4	401
5	Gene Mapping via Bulked Segregant RNA-Seq (BSR-Seq). PLoS ONE, 2012, 7, e36406.	1.1	297
6	Mu Transposon Insertion Sites and Meiotic Recombination Events Co-Localize with Epigenetic Marks for Open Chromatin across the Maize Genome. PLoS Genetics, 2009, 5, e1000733.	1.5	196
7	Parent-of-Origin Effects on Gene Expression and DNA Methylation in the Maize Endosperm. Plant Cell, 2011, 23, 4221-4233.	3.1	189
8	Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. PLoS Genetics, 2012, 8, e1003127.	1.5	166
9	Complementation contributes to transcriptome complexity in maize (*Zea mays* L.) hybrids relative to their inbred parents. Genome Research, 2012, 22, 2445-2454.	2.4	154
10	Heritable Epigenetic Variation among Maize Inbreds. PLoS Genetics, 2011, 7, e1002372.	1.5	150
11	Genic and nongenic contributions to natural variation of quantitative traits in maize. Genome Research, 2012, 22, 2436-2444.	2.4	125
12	A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. Frontiers in Plant Science, 2017, 8, 694.	1.7	109
13	The maize *brown midrib2* (*bm2*) gene encodes a methylenetetrahydrofolate reductase that contributes to lignin accumulation. Plant Journal, 2014, 77, 380-392.	2.8	94
14	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. Plant Journal, 2015, 84, 587-596.	2.8	93
15	Repeat subtraction-mediated sequence capture from a complex genome. Plant Journal, 2010, 62, 898-909.	2.8	89
16	Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. Plant Cell, 2014, 26, 3939-3948.	3.1	80
17	B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize Â Â. Plant Physiology, 2011, 156, 1679-1690.	2.3	76
18	The Aux/IAA gene rum1 involved in seminal and lateral root formation controls vascular patterning in maize (Zea mays L.) primary roots. Journal of Experimental Botany, 2014, 65, 4919-4930.	2.4	69

#	Article	IF	Citations
19	The maize <i>brown midrib4</i> (<i>bm4)</i> gene encodes a functional folylpolyglutamate synthase. Plant Journal, 2015, 81, 493-504.	2.8	42
20	Phenotypic Data from Inbred Parents Can Improve Genomic Prediction in Pearl Millet Hybrids. G3: Genes, Genomes, Genetics, 2018, 8, 2513-2522.	0.8	41
21	Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. PLoS Genetics, 2009, 5, e1000728.	1.5	39
22	Maize genomes to fields (G2F): 2014â€"2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. BMC Research Notes, 2020, 13, 71.	0.6	38
23	Coâ€expression analysis aids in the identification of genes in the cuticular wax pathway in maize. Plant Journal, 2019, 97, 530-542.	2.8	34
24	Linked read technology for assembling large complex and polyploid genomes. BMC Genomics, 2018, 19, 651.	1.2	31
25	Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. BMC Research Notes, 2018, 11, 452.	0.6	25
26	Changes in genome content generated via segregation of nonâ€allelic homologs. Plant Journal, 2012, 72, 390-399.	2.8	24
27	Empirical Comparisons of Different Statistical Models To Identify and Validate Kernel Row Number-Associated Variants from Structured Multi-parent Mapping Populations of Maize. G3: Genes, Genomes, Genetics, 2018, 8, 3567-3575.	0.8	19
28	High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. PLoS ONE, 2010, 5, e14178.	1.1	11
29	KAT4IA: K-Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. Plant Phenomics, 2021, 2021, 9805489.	2.5	5
30	An Efficient and Scalable Implementation of SNP-Pair Interaction Testing for Genetic Association Studies. , 2011, , .		4
31	Trajectories of Homoeolog-Specific Expression in Allotetraploid Tragopogon castellanus Populations of Independent Origins. Frontiers in Plant Science, 2021, 12, 679047.	1.7	3