

Cheng-Ting Yeh

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

7,125
citations

318942

23
h-index

488211

31
g-index

33
all docs

33
docs citations

33
times ranked

10266
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 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. <i>PLoS Genetics</i> , 2009, 5, e1000734. | 1.5 | 484 |
| 3 | Genome-wide discovery and characterization of maize long non-coding RNAs. <i>Genome Biology</i> , 2014, 15, R40. | 13.9 | 419 |
| 4 | Parallel domestication of the Shattering1 genes in cereals. <i>Nature Genetics</i> , 2012, 44, 720-724. | 9.4 | 401 |
| 5 | Gene Mapping via Bulk Segregant RNA-Seq (BSR-Seq). <i>PLoS ONE</i> , 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. <i>PLoS Genetics</i> , 2009, 5, e1000733. | 1.5 | 196 |
| 7 | 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 |
| 8 | Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. <i>PLoS Genetics</i> , 2012, 8, e1003127. | 1.5 | 166 |
| 9 | 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 |
| 10 | Heritable Epigenetic Variation among Maize Inbreds. <i>PLoS Genetics</i> , 2011, 7, e1002372. | 1.5 | 150 |
| 11 | Genic and nongenic contributions to natural variation of quantitative traits in maize. <i>Genome Research</i> , 2012, 22, 2436-2444. | 2.4 | 125 |
| 12 | A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. <i>Frontiers in Plant Science</i> , 2017, 8, 694. | 1.7 | 109 |
| 13 | 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 |
| 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. <i>Plant Journal</i> , 2015, 84, 587-596. | 2.8 | 93 |
| 15 | Repeat subtraction-mediated sequence capture from a complex genome. <i>Plant Journal</i> , 2010, 62, 898-909. | 2.8 | 89 |
| 16 | Nonsyntenic Genes Drive Highly Dynamic Complementation of Gene Expression in Maize Hybrids. <i>Plant Cell</i> , 2014, 26, 3939-3948. | 3.1 | 80 |
| 17 | B73-Mo17 Near-Isogenic Lines Demonstrate Dispersed Structural Variation in Maize. <i>Plant Physiology</i> , 2011, 156, 1679-1690. | 2.3 | 76 |
| 18 | The Aux/IAA 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 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | Detailed Analysis of a Contiguous 22-Mb Region of the Maize Genome. <i>PLoS Genetics</i> , 2009, 5, e1000728. | 1.5 | 39 |
| 22 | 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 |
| 23 | 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 |
| 24 | Linked read technology for assembling large complex and polyploid genomes. <i>BMC Genomics</i> , 2018, 19, 651. | 1.2 | 31 |
| 25 | 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 |
| 26 | Changes in genome content generated via segregation of non-allelic homologs. <i>Plant Journal</i> , 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. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3567-3575. | 0.8 | 19 |
| 28 | High-Resolution Genotyping via Whole Genome Hybridizations to Microarrays Containing Long Oligonucleotide Probes. <i>PLoS ONE</i> , 2010, 5, e14178. | 1.1 | 11 |
| 29 | KAT4IA: K-Means Assisted Training for Image Analysis of Field-Grown Plant Phenotypes. <i>Plant Phenomics</i> , 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 <i>Tragopogon castellanus</i> Populations of Independent Origins. <i>Frontiers in Plant Science</i> , 2021, 12, 679047. | 1.7 | 3 |