Tzung-Fu Hsieh

List of Publications by Year
in descending order

41	4,696	257101 24	329751 37
papers	citations	h-index	g-index

47	47	47	5155
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	DEMETER DNA Glycosylase Establishes MEDEA Polycomb Gene Self-Imprinting by Allele-Specific Demethylation. Cell, 2006, 124, 495-506.	13.5	665
2	Genome-Wide Demethylation of Arabidopsis Endosperm. Science, 2009, 324, 1451-1454.	6.0	628
3	A CRISPR/Cas9 Toolbox for Multiplexed Plant Genome Editing and Transcriptional Regulation. Plant Physiology, 2015, 169, 971-985.	2.3	532
4	Active DNA Demethylation in Plant Companion Cells Reinforces Transposon Methylation in Gametes. Science, 2012, 337, 1360-1364.	6.0	445
5	Regulation of imprinted gene expression in Arabidopsis endosperm. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1755-1762.	3.3	317
6	Molecular characterization of AtNAM: a member of the Arabidopsis NAC domain superfamily. Plant Molecular Biology, 2002, 50, 237-248.	2.0	288
7	Arabidopsis LEAFY COTYLEDON2 induces maturation traits and auxin activity: Implications for somatic embryogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3151-3156.	3.3	282
8	Dynamic DNA Methylation in Plant Growth and Development. International Journal of Molecular Sciences, 2018, 19, 2144.	1.8	187
9	Robust Transcriptional Activation in Plants Using Multiplexed CRISPR-Act2.0 and mTALE-Act Systems. Molecular Plant, 2018, 11, 245-256.	3.9	179
10	Cellular Programming of Plant Gene Imprinting. Cell, 2008, 132, 735-744.	13.5	146
11	Similarity between soybean and Arabidopsis seed methylomes and loss of non-CG methylation does not affect seed development. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9730-E9739.	3.3	111
12	Characterization and Subcellular Compartmentation of Recombinant 4-Hydroxyphenylpyruvate Dioxygenase from Arabidopsis in Transgenic Tobacco1. Plant Physiology, 1999, 119, 1507-1516.	2.3	94
13	A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. Plant Genome, 2016, 9, plantgenome2015.10.0102.	1.6	85
14	MethylCoder: software pipeline for bisulfite-treated sequences. Bioinformatics, 2011, 27, 2435-2436.	1.8	76
15	The AAA-ATPase molecular chaperone Cdc48/p97 disassembles sumoylated centromeres, decondenses heterochromatin, and activates ribosomal RNA genes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16166-16171.	3.3	74
16	Gene expression in the developing mouse retina by EST sequencing and microarray analysis. Nucleic Acids Research, 2001, 29, 4983-4993.	6.5	68
17	From flour to flower: how Polycomb group proteins influence multiple aspects of plant development. Trends in Plant Science, 2003, 8, 439-445.	4.3	68
18	BIOLOGY OF CHROMATIN DYNAMICS. Annual Review of Plant Biology, 2005, 56, 327-351.	8.6	63

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19	Endosperm gene imprinting and seed development. Current Opinion in Genetics and Development, 2007, 17, 480-485.	1.5	58
20	Comparative Methylome Analyses Identify Epigenetic Regulatory Loci of Human Brain Evolution. Molecular Biology and Evolution, 2016, 33, 2947-2959.	3.5	49
21	Identification of estrogen-induced genes downregulated by AhR agonists in MCF-7 breast cancer cells using suppression subtractive hybridization. Gene, 2001, 262, 207-214.	1.0	46
22	A naturally occurring conditional albino mutant in rice caused by defects in the plastid-localized OsABCI8 transporter. Plant Molecular Biology, 2017, 94, 137-148.	2.0	31
23	Mutation in a putative glycosyltransferase-like gene causes programmed cell death and early leaf senescence in rice. Rice, 2019, 12, 7.	1.7	29
24	Heritable Epigenetic Variation and its Potential Applications for Crop Improvement. Plant Breeding and Biotechnology, 2013, 1, 307-319.	0.3	28
25	Rice OsPEX1, an extensin-like protein, affects lignin biosynthesis and plant growth. Plant Molecular Biology, 2019, 100, 151-161.	2.0	25
26	The catalytic core of DEMETER guides active DNA demethylation in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17563-17571.	3.3	23
27	Epigenetic modification of ESP, encoding a putative long noncoding RNA, affects panicle architecture in rice. Rice, 2019, 12, 20.	1.7	18
28	Epigenetics Regulates Reproductive Development in Plants. Plants, 2019, 8, 564.	1.6	18
29	FIE, a nuclear PRC2 protein, forms cytoplasmic complexes inArabidopsis thaliana. Journal of Experimental Botany, 2016, 67, 6111-6123.	2.4	16
30	Identification of mixed linkage Î²â€glucan quantitative trait loci and evaluation of AsCslF6 homoeologs in hexaploid oat. Crop Science, 2020, 60, 914-933.	0.8	16
31	Control of Paternally Expressed Imprinted UPWARD CURLY LEAF1, a Gene Encoding an F-Box Protein That Regulates CURLY LEAF Polycomb Protein, in the Arabidopsis Endosperm. PLoS ONE, 2015, 10, e0117431.	1.1	6
32	Comparative Phylogenomic Analysis Reveals Evolutionary Genomic Changes and Novel Toxin Families in Endophytic Liberibacter Pathogens. Microbiology Spectrum, 2021, 9, e0050921.	1.2	6
33	Sexual and Non-sexual Reproduction. Advances in Botanical Research, 2018, 88, 117-163.	0.5	4
34	Whole-Genome DNA Methylation Profiling with Nucleotide Resolution. Methods in Molecular Biology, 2015, 1284, 27-40.	0.4	4
35	Epigenetics: A tug of war for DNA methylation. Nature Plants, 2016, 2, 16171.	4.7	3
36	Admixture of divergent genomes facilitates hybridization across species in the family Brassicaceae. New Phytologist, 2022, 235, 743-758.	3.5	3

#	Article	IF	Citations
37	Genomic Analysis of Arabidopsis Gene Expression in Response to a Systemic Fungicide. , 2003, , .		2
38	Genomic Imprinting in Arabidopsis thaliana and Zea mays. , 2007, , 219-239.		1
39	Epigenetic Reprogramming During Plant Reproduction. RNA Technologies, 2017, , 405-425.	0.2	1
40	Patenting Applied to Genetic Sequence Information. Biotechnology and Genetic Engineering Reviews, 2006, 23, 317-330.	2.4	0
41	Epigenetic remodeling by DNA glycosylases during rice reproduction. Molecular Plant, 2021, 14, 1433-1435.	3.9	0