Josh T Cuperus

List of Publications by Year
in descending order

25 papers	3,573 citations	361413 20 h-index	580821 25 g-index
34 all docs	34 docs citations	34 times ranked	4425 citing authors

#	Article	IF	Citations
1	Single-cell genomics in plants: current state, future directions, and hurdles to overcome. Plant Physiology, 2022, 188, 749-755.	4.8	24
2	A single-cell view of the transcriptome during lateral root initiation in <i>Arabidopsis thaliana</i>. Plant Cell, 2021, 33, 2197-2220.	6.6	75
3	Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. Nature Plants, 2021, 7, 842-855.	9.3	78
4	The regulatory landscape of Arabidopsis thaliana roots at single-cell resolution. Nature Communications, 2021, 12, 3334.	12.8	84
5	Vision, challenges and opportunities for a Plant Cell Atlas. ELife, 2021, 10, .	6.0	31
6	Effects of sequence motifs in the yeast 3â€² untranslated region determined from massively parallel assays of random sequences. Genome Biology, 2021, 22, 293.	8.8	6
7	The promise of single-cell genomics in plants. Current Opinion in Plant Biology, 2020, 54, 114-121.	7.1	26
8	Identification of Plant Enhancers and Their Constituent Elements by STARR-seq in Tobacco Leaves. Plant Cell, 2020, 32, 2120-2131.	6.6	53
9	Editorial overview: Technology development as a driver of biological discovery. Current Opinion in Plant Biology, 2020, 54, A1-A4.	7.1	1
10	Dynamics of Gene Expression in Single Root Cells of <i>Arabidopsis thaliana</i>. Plant Cell, 2019, 31, 993-1011.	6.6	279
11	Complex Relationships between Chromatin Accessibility, Sequence Divergence, and Gene Expression in Arabidopsis thaliana. Molecular Biology and Evolution, 2018, 35, 837-854.	8.9	33
12	Preferences in a trait decision determined by transcription factor variants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7997-E8006.	7.1	15
13	Deep learning of the regulatory grammar of yeast 5â€² untranslated regions from 500,000 random sequences. Genome Research, 2017, 27, 2015-2024.	5.5	166
14	A tetO Toolkit To Alter Expression of Genes in <i>Saccharomyces cerevisiae</i>. ACS Synthetic Biology, 2015, 4, 842-852.	3.8	18
15	New Generation of Artificial MicroRNA and Synthetic Trans-Acting Small Interfering RNA Vectors for Efficient Gene Silencing in Arabidopsis. Plant Physiology, 2014, 165, 15-29.	4.8	119
16	Phytophthora Have Distinct Endogenous Small RNA Populations That Include Short Interfering and microRNAs. PLoS ONE, 2013, 8, e77181.	2.5	88
17	Functional Analysis of Three <i>Arabidopsis</i> ARGONAUTES Using Slicer-Defective Mutants Â. Plant Cell, 2012, 24, 3613-3629.	6.6	249
18	Evolution and Functional Diversification of <i>MIRNA</i> Genes. Plant Cell, 2011, 23, 431-442.	6.6	645

#	Article	IF	Citations
19	Identification of genes required for de novo DNA methylation in Arabidopsis. Epigenetics, 2011, 6, 344-354.	2.7	64
20	Unique functionality of 22-nt miRNAs in triggering RDR6-dependent siRNA biogenesis from target transcripts in Arabidopsis. Nature Structural and Molecular Biology, 2010, 17, 997-1003.	8.2	448
21	Identification of <i>MIR390a</i> precursor processing-defective mutants in Arabidopsis by direct genome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 466-471.	7.1	137
22	Regulation and functional specialization of small RNA–target nodes during plant development. Current Opinion in Plant Biology, 2009, 12, 622-627.	7.1	111
23	Specificity of ARGONAUTE7-miR390 Interaction and Dual Functionality in TAS3 Trans-Acting siRNA Formation. Cell, 2008, 133, 128-141.	28.9	712
24	Agrobacterium rhizogenes GALLS Protein Substitutes for Agrobacterium tumefaciens Single-Stranded DNA-Binding Protein VirE2. Journal of Bacteriology, 2004, 186, 3065-3077.	2.2	52
25	Translation Start Sequences Affect the Efficiency of Silencing of Agrobacterium tumefaciens T-DNA Oncogenes. Plant Physiology, 2003, 133, 966-977.	4.8	29