Josh T Cuperus

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Specificity of ARGONAUTE7-miR390 Interaction and Dual Functionality in TAS3 Trans-Acting siRNA Formation. Cell, 2008, 133, 128-141.	28.9	712
2	Evolution and Functional Diversification of <i>MIRNA</i> Genes. Plant Cell, 2011, 23, 431-442.	6.6	645
3	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
4	Dynamics of Gene Expression in Single Root Cells of <i>Arabidopsis thaliana</i> . Plant Cell, 2019, 31, 993-1011.	6.6	279
5	Functional Analysis of Three <i>Arabidopsis</i> ARGONAUTES Using Slicer-Defective Mutants Â. Plant Cell, 2012, 24, 3613-3629.	6.6	249
6	Deep learning of the regulatory grammar of yeast 5′ untranslated regions from 500,000 random sequences. Genome Research, 2017, 27, 2015-2024.	5.5	166
7	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
8	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
9	Regulation and functional specialization of small RNA–target nodes during plant development. Current Opinion in Plant Biology, 2009, 12, 622-627.	7.1	111
10	Phytophthora Have Distinct Endogenous Small RNA Populations That Include Short Interfering and microRNAs. PLoS ONE, 2013, 8, e77181.	2.5	88
11	The regulatory landscape of Arabidopsis thaliana roots at single-cell resolution. Nature Communications, 2021, 12, 3334.	12.8	84
12	Synthetic promoter designs enabled by a comprehensive analysis of plant core promoters. Nature Plants, 2021, 7, 842-855.	9.3	78
13	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
14	Identification of genes required for de novo DNA methylation in Arabidopsis. Epigenetics, 2011, 6, 344-354.	2.7	64
15	Identification of Plant Enhancers and Their Constituent Elements by STARR-seq in Tobacco Leaves. Plant Cell, 2020, 32, 2120-2131.	6.6	53
16	Agrobacterium rhizogenes GALLS Protein Substitutes for Agrobacterium tumefaciens Single-Stranded DNA-Binding Protein VirE2. Journal of Bacteriology, 2004, 186, 3065-3077.	2.2	52
17	Complex Relationships between Chromatin Accessibility, Sequence Divergence, and Gene Expression in Arabidopsis thaliana. Molecular Biology and Evolution, 2018, 35, 837-854.	8.9	33
18	Vision, challenges and opportunities for a Plant Cell Atlas. ELife, 2021, 10, .	6.0	31

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19	Translation Start Sequences Affect the Efficiency of Silencing of Agrobacterium tumefaciens T-DNA Oncogenes. Plant Physiology, 2003, 133, 966-977.	4.8	29
20	The promise of single-cell genomics in plants. Current Opinion in Plant Biology, 2020, 54, 114-121.	7.1	26
21	Single-cell genomics in plants: current state, future directions, and hurdles to overcome. Plant Physiology, 2022, 188, 749-755.	4.8	24
22	A tetO Toolkit To Alter Expression of Genes in <i>Saccharomyces cerevisiae</i> . ACS Synthetic Biology, 2015, 4, 842-852.	3.8	18
23	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
24	Effects of sequence motifs in the yeast 3′ untranslated region determined from massively parallel assays of random sequences. Genome Biology, 2021, 22, 293.	8.8	6
25	Editorial overview: Technology development as a driver of biological discovery. Current Opinion in Plant Biology, 2020, 54, A1-A4.	7.1	1