Shaun J Curtin

List of Publications by Year in descending order

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SHALIN I CLIDTIN

#	Article	IF	CITATIONS
1	Selection-free zinc-finger-nuclease engineering by context-dependent assembly (CoDA). Nature Methods, 2011, 8, 67-69.	19.0	480
2	A Multipurpose Toolkit to Enable Advanced Genome Engineering in Plants. Plant Cell, 2017, 29, 1196-1217.	6.6	469
3	RNA interferenceâ€inducing hairpin RNAs in plants act through the viral defence pathway. EMBO Reports, 2006, 7, 1168-1175.	4.5	284
4	The evolution and diversification of Dicers in plants. FEBS Letters, 2006, 580, 2442-2450.	2.8	283
5	Targeted Mutagenesis of Duplicated Genes in Soybean with Zinc-Finger Nucleases Â. Plant Physiology, 2011, 156, 466-473.	4.8	260
6	The <i>Arabidopsis thaliana</i> double-stranded RNA binding protein DRB1 directs guide strand selection from microRNA duplexes. Rna, 2009, 15, 2219-2235.	3.5	198
7	CRISPR/Cas mutagenesis of soybean and Medicago truncatula using a new web-tool and a modified Cas9 enzyme. GM Crops and Food, 2015, 6, 243-252.	3.8	162
8	<scp>CRISPR</scp> /Cas9 and <scp>TALEN</scp> s generate heritable mutations for genes involved in small <scp>RNA</scp> processing of <i>Glycine max</i> and <i>Medicago truncatula</i> . Plant Biotechnology Journal, 2018, 16, 1125-1137.	8.3	147
9	Genome Engineering of Crops with Designer Nucleases. Plant Genome, 2012, 5, 42-50.	2.8	102
10	The roles of plant dsRNAâ€binding proteins in RNAiâ€like pathways. FEBS Letters, 2008, 582, 2753-2760.	2.8	90
11	Phylogenetic relationships and pathogenicity of Colletotrichum acutatum isolates from grape in subtropical Australia. Plant Pathology, 2007, 56, 448-463.	2.4	85
12	Validating Genome-Wide Association Candidates Controlling Quantitative Variation in Nodulation. Plant Physiology, 2017, 173, 921-931.	4.8	71
13	DRB2 Is Required for MicroRNA Biogenesis in Arabidopsis thaliana. PLoS ONE, 2012, 7, e35933.	2.5	68
14	Identical Substitutions in Magnesium Chelatase Paralogs Result in Chlorophyll-Deficient Soybean Mutants. G3: Genes, Genomes, Genetics, 2015, 5, 123-131.	1.8	57
15	Genomic variation and DNA repair associated with soybean transgenesis: a comparison to cultivars and mutagenized plants. BMC Biotechnology, 2016, 16, 41.	3.3	54
16	Pathways to de novo domestication of crop wild relatives. Plant Physiology, 2022, 188, 1746-1756.	4.8	27
17	MicroRNA Maturation and MicroRNA Target Gene Expression Regulation Are Severely Disrupted in Soybean dicer-like1 Double Mutants. G3: Genes, Genomes, Genetics, 2016, 6, 423-433.	1.8	23
18	Targeted Mutagenesis for Functional Analysis of Gene Duplication in Legumes. Methods in Molecular Biology, 2013, 1069, 25-42.	0.9	20

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19	Co-expression of soybean Dicer-like genes in response to stress and development. Functional and Integrative Genomics, 2012, 12, 671-682.	3.5	19
20	Potato improvement through genetic engineering. GM Crops and Food, 2021, 12, 479-496.	3.8	11
21	Alfalfa (<i>Medicago sativa</i> L.) <i>pho2</i> mutant plants hyperaccumulate phosphate. G3: Genes, Genomes, Genetics, 2022, , .	1.8	10
22	Design and Assembly of CRISPR/Cas9 Reagents for Gene Knockout, Targeted Insertion, and Replacement in Wheat. Methods in Molecular Biology, 2017, 1679, 187-212.	0.9	7
23	Editing the Medicago truncatula Genome: Targeted Mutagenesis Using the CRISPR-Cas9 Reagent. Methods in Molecular Biology, 2018, 1822, 161-174.	0.9	7
24	The Arabidopsis thaliana Double-Stranded RNA Binding (DRB) Domain Protein Family. , 2011, , 385-406.		5
25	<i>SELF PRUNING 3C</i> is a flowering repressor that modulates seed germination, root architecture, and drought responses. Journal of Experimental Botany, 2022, 73, 6226-6240.	4.8	5
26	Further Disruption of the TAS3 Pathway via the Addition of the AGO7 Mutation to the DRB1, DRB2 or DRB4 Mutations Severely Impairs the Reproductive Competence of Arabidopsis thaliana. Agronomy, 2019, 9, 680.	3.0	3
27	Targeted Mutagenesis of Alfalfa. Compendium of Plant Genomes, 2021, , 271-283.	0.5	3
28	Isolation and Analysis of Small RNAs from Virus-Infected Plants. Methods in Molecular Biology, 2012, 894, 173-189.	0.9	2
29	RNA Silencing and Its Application in Functional Genomics. , 2007, , 291-332.		1