

# Jennifer S Hawkins

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

2,028  
citations

687363

13  
h-index

752698

20  
g-index

22  
all docs

22  
docs citations

22  
times ranked

2883  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	17.5	864
2	Differential lineage-specific amplification of transposable elements is responsible for genome size variation in <i>Gossypium</i> . <i>Genome Research</i> , 2006, 16, 1252-1261.	5.5	378
3	Rapid DNA loss as a counterbalance to genome expansion through retrotransposon proliferation in plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17811-17816.	7.1	164
4	Interactions among plants, bacteria, and fungi reduce extracellular enzyme activities under long-term N fertilization. <i>Global Change Biology</i> , 2018, 24, 2721-2734.	9.5	126
5	The regulatory landscape of a core maize domestication module controlling bud dormancy and growth repression. <i>Nature Communications</i> , 2019, 10, 3810.	12.8	116
6	Repeated big bangs and the expanding universe: Directionality in plant genome size evolution. <i>Plant Science</i> , 2008, 174, 557-562.	3.6	71
7	Phylogenetic determination of the pace of transposable element proliferation in plants: <i>copia</i> and LINE-like elements in <i>Gossypium</i> . <i>Genome</i> , 2008, 51, 11-18.	2.0	52
8	Global alteration of microRNAs and transposon-derived small RNAs in cotton ( <i>Gossypium hirsutum</i> ) during Cotton leafroll dwarf polerovirus (CLRVD) infection. <i>Plant Molecular Biology</i> , 2012, 80, 443-460.	3.9	46
9	The history and disposition of transposable elements in polyploid <i>Gossypium</i> . <i>Genome</i> , 2010, 53, 599-607.	2.0	43
10	Phylogenetic, morphological, and chemotaxonomic incongruence in the North American endemic genus <i>Echinacea</i> . <i>American Journal of Botany</i> , 2008, 95, 756-765.	1.7	34
11	Genetic Diversity in <i>Hypericum</i> and AFLP Markers for Species-Specific Identification of <i>H. perforatum</i> L. <i>Planta Medica</i> , 2007, 73, 1614-1621.	1.3	30
12	Differences in microbial community response to nitrogen fertilization result in unique enzyme shifts between arbuscular and ectomycorrhizal-dominated soils. <i>Global Change Biology</i> , 2021, 27, 2049-2060.	9.5	24
13	Phylogenetic reconstruction using four low-copy nuclear loci strongly supports a polyphyletic origin of the genus <i>Sorghum</i> . <i>Annals of Botany</i> , 2015, 116, 291-299.	2.9	23
14	Variation in allelic expression associated with a recombination hotspot in <i>Zea mays</i> . <i>Plant Journal</i> , 2014, 79, 375-384.	5.7	13
15	QTL mapping in an interspecific sorghum population uncovers candidate regulators of salinity tolerance. <i>Plant Stress</i> , 2021, 2, 100024.	5.5	12
16	Evolutionary Dynamics of Transposable Elements Following a Shared Polyploidization Event in the Tribe Andropogoneae. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4387-4398.	1.8	9
17	Phenotypic and physiological responses to salt exposure in <i>Sorghum</i> reveal diversity among domesticated landraces. <i>American Journal of Botany</i> , 2020, 107, 983-992.	1.7	7
18	Tobacco genomes quickly go up in smoke. <i>New Phytologist</i> , 2007, 175, 599-602.	7.3	5

#	ARTICLE	IF	CITATIONS
19	Methods for accurate quantification of LTR-retrotransposon copy number using short-read sequence data: a case study in Sorghum. <i>Molecular Genetics and Genomics</i> , 2016, 291, 1871-1883.	2.1	5
20	Integration of high-density genetic mapping with transcriptome analysis uncovers numerous agronomic QTL and reveals candidate genes for the control of tillering in sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	4