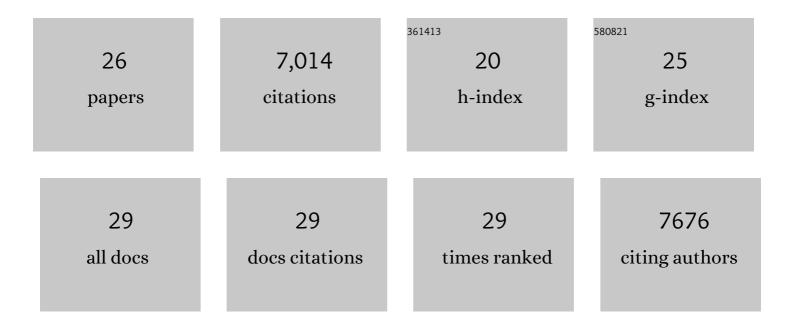
Jessica A Schlueter

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Implementing building-level SARS-CoV-2 wastewater surveillance on a university campus. Science of the Total Environment, 2021, 782, 146749.	8.0	203
2	Performance evaluation of virus concentration methods for implementing SARS-CoV-2 wastewater based epidemiology emphasizing quick data turnaround. Science of the Total Environment, 2021, 801, 149656.	8.0	37
3	Paralog analyses reveal gene duplication events and genes under positive selection in Ixodes scapularis and other ixodid ticks. BMC Genomics, 2016, 17, 241.	2.8	18
4	CONTRAILS: A tool for rapid identification of transgene integration sites in complex, repetitive genomes using low-coverage paired-end sequencing. Genomics Data, 2015, 6, 175-181.	1.3	19
5	Statistical issues associated with modeling of synonymous mutation data. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 361-74.	0.6	0
6	The fate of duplicated genes in a polyploid plant genome. Plant Journal, 2013, 73, 143-153.	5.7	243
7	Large-Scale Development of Cost-Effective Single-Nucleotide Polymorphism Marker Assays for Genetic Mapping in Pigeonpea and Comparative Mapping in Legumes. DNA Research, 2012, 19, 449-461.	3.4	99
8	Co-expression of soybean Dicer-like genes in response to stress and development. Functional and Integrative Genomics, 2012, 12, 671-682.	3.5	19
9	Applications of nextâ€generation sequencing in plant biology. American Journal of Botany, 2012, 99, 175-185.	1.7	249
10	Draft genome sequence of pigeonpea (Cajanus cajan), an orphan legume crop of resource-poor farmers. Nature Biotechnology, 2012, 30, 83-89.	17.5	788
11	Largeâ€scale development of costâ€effective SNP marker assays for diversity assessment and genetic mapping in chickpea and comparative mapping in legumes. Plant Biotechnology Journal, 2012, 10, 716-732.	8.3	221
12	Defining the Transcriptome Assembly and Its Use for Genome Dynamics and Transcriptome Profiling Studies in Pigeonpea (Cajanus cajan L.). DNA Research, 2011, 18, 153-164.	3.4	85
13	Comparative Evolution of Photosynthetic Genes in Response to Polyploid and Nonpolyploid Duplication Â. Plant Physiology, 2011, 155, 2081-2095.	4.8	54
14	Integration of physical and genetic maps of common bean through BAC-derived microsatellite markers. BMC Genomics, 2010, 11, 436.	2.8	59
15	Genome sequence of the palaeopolyploid soybean. Nature, 2010, 463, 178-183.	27.8	3,854
16	Retrotransposons within Syntenic Regions between Soybean and Medicago truncatula and Their Contribution to Local Genome Evolution. Plant Genome, 2009, 2, .	2.8	4
17	BAC-end Sequence Analysis and a Draft Physical Map of the Common Bean (Phaseolus vulgaris L.) Genome. Tropical Plant Biology, 2008, 1, 40-48.	1.9	70

18 Soybean Genome Structure and Organization. , 2008, , 91-99.

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#	Article	IF	CITATIONS
19	<i>Arabidopsis SCAR</i> s Function Interchangeably to Meet Actin-Related Protein 2/3 Activation Thresholds during Morphogenesis. Plant Cell, 2008, 20, 995-1011.	6.6	73
20	Fractionation of Synteny in a Genomic Region Containing Tandemly Duplicated Genes across Glycine max, Medicago truncatula, and Arabidopsis thaliana. Journal of Heredity, 2008, 99, 390-395.	2.4	32
21	The FAD2 Gene Family of Soybean: Insights into the Structural and Functional Divergence of a Paleopolyploid Genome. Crop Science, 2007, 47, S-14.	1.8	108
22	Gene duplication and paleopolyploidy in soybean and the implications for whole genome sequencing. BMC Genomics, 2007, 8, 330.	2.8	132
23	Paleopolyploidy and gene duplication in soybean and other legumes. Current Opinion in Plant Biology, 2006, 9, 104-109.	7.1	230
24	Sequence Conservation of Homeologous Bacterial Artificial Chromosomes and Transcription of Homeologous Genes in Soybean (Glycine max L. Merr.). Genetics, 2006, 174, 1017-1028.	2.9	45
25	Soybean FGAM synthase promoters direct ectopic nematode feeding site activity. Genome, 2004, 47, 404-413.	2.0	18
26	Mining EST databases to resolve evolutionary events in major crop species. Genome, 2004, 47, 868-876.	2.0	310

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