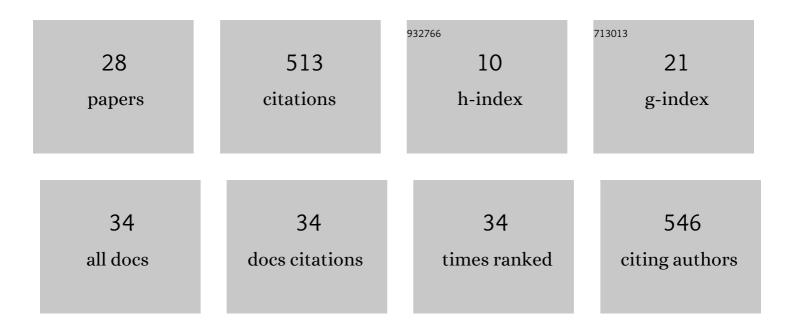
Sarah Z Agapito-Tenfen

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Alterations in genetically modified crops assessed by omics studies: Systematic review and meta-analysis. Trends in Food Science and Technology, 2022, 120, 325-337.	7.8	11
2	Untargeted Proteomics-Based Approach to Investigate Unintended Changes in Genetically Modified Maize for Environmental Risk Assessment Purpose. Frontiers in Toxicology, 2021, 3, 655968.	1.6	0
3	Proteomic Profile of Glyphosate-Resistant Soybean under Combined Herbicide and Drought Stress Conditions. Plants, 2021, 10, 2381.	1.6	7
4	Challenges for monitoring (trans)gene-flow in the environment , 2021, , 39-55.		0
5	PEG-Delivered CRISPR-Cas9 Ribonucleoproteins System for Gene-Editing Screening of Maize Protoplasts. Genes, 2020, 11, 1029.	1.0	36
6	Stacked genetically modified soybean harboring herbicide resistance and insecticide rCry1Ac shows strong defense and redox homeostasis disturbance after glyphosate-based herbicide application. Environmental Sciences Europe, 2020, 32, .	2.6	11
7	Analysis of transcriptomic differences between NK603 maize and near-isogenic varieties using RNA sequencing and RT-qPCR. Environmental Sciences Europe, 2020, 32, .	2.6	2
8	Challenges for transgene detection in landraces and wild relatives: learning from 15Âyears of debate over GM maize in Mexico. Biodiversity and Conservation, 2018, 27, 539-566.	1.2	8
9	Systematic miRNome profiling reveals differential microRNAs in transgenic maize metabolism. Environmental Sciences Europe, 2018, 30, 37.	2.6	0
10	Revisiting Risk Governance of GM Plants: The Need to Consider New and Emerging Gene-Editing Techniques. Frontiers in Plant Science, 2018, 9, 1874.	1.7	56
11	Reply to â€~Comments on two recent publications on GM maize and Roundup'. Scientific Reports, 2018, 8, 13339.	1.6	1
12	Genetic and epigenetic characterization of the cry1Ab coding region and its 3′ flanking genomic region in MON810 maize using next-generation sequencing. European Food Research and Technology, 2018, 244, 1473-1485.	1.6	5
13	Proteome of Plasmopara viticola -infected Vitis vinifera provides insights into grapevine Rpv1 / Rpv3 pyramided resistance to downy mildew. Journal of Proteomics, 2017, 151, 264-274.	1.2	18
14	Transgene flow in Mexican maize revisited: Socioâ€biological analysis across two contrasting farmer communities and seed management systems. Ecology and Evolution, 2017, 7, 9461-9472.	0.8	12
15	Molecular responses of genetically modified maize to abiotic stresses as determined through proteomic and metabolomic analyses. PLoS ONE, 2017, 12, e0173069.	1.1	43
16	An integrated multi-omics analysis of the NK603 Roundup-tolerant GM maize reveals metabolism disturbances caused by the transformation process. Scientific Reports, 2016, 6, 37855.	1.6	58
17	Levels of DNA methylation and transcript accumulation in leaves of transgenic maize varieties. Environmental Sciences Europe, 2016, 28, 29.	2.6	11
18	Response to "A 28-day oral toxicity evaluation of small interfering RNAs and a long double-stranded RNA targeting vacuolar ATPase in mice.― Regulatory Toxicology and Pharmacology, 2015, 71, 599-600.	1.3	2

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#	Article	IF	CITATIONS
19	Identification of the Er1 resistence gene and RNase S-alleles in Malus prunifolia var. ringo rootstock. Scientia Agricola, 2015, 72, 62-68.	0.6	4
20	Reply to comment on sustainability and innovation in staple crop production in the US Midwest. International Journal of Agricultural Sustainability, 2014, 12, 387-390.	1.3	0
21	Sustainability and innovation in staple crop production in the US Midwest. International Journal of Agricultural Sustainability, 2014, 12, 71-88.	1.3	67
22	Effect of stacking insecticidal cry and herbicide tolerance epsps transgenes on transgenic maize proteome. BMC Plant Biology, 2014, 14, 346.	1.6	48
23	Comparative proteomic analysis of genetically modified maize grown under different agroecosystems conditions in Brazil. Proteome Science, 2013, 11, 46.	0.7	32
24	A comparative evaluation of the regulation of GM crops or products containing dsRNA and suggested improvements to risk assessments. Environment International, 2013, 55, 43-55.	4.8	56
25	Comparative proteomic analysis of off-type and normal phenotype somatic plantlets derived from somatic embryos of Feijoa (Acca sellowiana (O. Berg) Burret). Plant Science, 2013, 210, 224-231.	1.7	8
26	Patterns of polyembryony and frequency of surviving multiple embryos of the Brazilian pine Araucaria angustifolia. Australian Journal of Botany, 2011, 59, 749.	0.3	8
27	Detection, Quantification and Identification of Genome-Edited Crops. SSRN Electronic Journal, 0, , .	0.4	0
28	A DNA-Free Editing Platform for Genetic Screens in Soybean via CRISPR/Cas9 Ribonucleoprotein Delivery. Frontiers in Plant Science, 0, 13, .	1.7	7