## Sarah Z Agapito-Tenfen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7072347/publications.pdf

Version: 2024-02-01

28 papers 513 citations

932766 10 h-index 21 g-index

34 all docs

34 docs citations

times ranked

34

546 citing authors

#	Article	IF	CITATIONS
1	Sustainability and innovation in staple crop production in the US Midwest. International Journal of Agricultural Sustainability, 2014, 12, 71-88.	1.3	67
2	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
3	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
4	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
5	Effect of stacking insecticidal cry and herbicide tolerance epsps transgenes on transgenic maize proteome. BMC Plant Biology, 2014, 14, 346.	1.6	48
6	Molecular responses of genetically modified maize to abiotic stresses as determined through proteomic and metabolomic analyses. PLoS ONE, 2017, 12, e0173069.	1.1	43
7	PEG-Delivered CRISPR-Cas9 Ribonucleoproteins System for Gene-Editing Screening of Maize Protoplasts. Genes, 2020, 11, 1029.	1.0	36
8	Comparative proteomic analysis of genetically modified maize grown under different agroecosystems conditions in Brazil. Proteome Science, 2013, 11, 46.	0.7	32
9	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
10	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
11	Levels of DNA methylation and transcript accumulation in leaves of transgenic maize varieties. Environmental Sciences Europe, 2016, 28, 29.	2.6	11
12	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
13	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
14	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
15	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
16	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
17	Proteomic Profile of Glyphosate-Resistant Soybean under Combined Herbicide and Drought Stress Conditions. Plants, 2021, 10, 2381.	1.6	7
18	A DNA-Free Editing Platform for Genetic Screens in Soybean via CRISPR/Cas9 Ribonucleoprotein Delivery. Frontiers in Plant Science, 0, 13, .	1.7	7

#	Article	IF	CITATIONS
19	Genetic and epigenetic characterization of the cry1Ab coding region and its $3\hat{a}\in^2$ flanking genomic region in MON810 maize using next-generation sequencing. European Food Research and Technology, 2018, 244, 1473-1485.	1.6	5
20	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
21	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
22	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
23	Reply to â€~Comments on two recent publications on GM maize and Roundup'. Scientific Reports, 2018, 8, 13339.	1.6	1
24	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
25	Systematic miRNome profiling reveals differential microRNAs in transgenic maize metabolism. Environmental Sciences Europe, 2018, 30, 37.	2.6	O
26	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
27	Challenges for monitoring (trans)gene-flow in the environment, 2021, , 39-55.		0
28	Detection, Quantification and Identification of Genome-Edited Crops. SSRN Electronic Journal, 0, , .	0.4	0