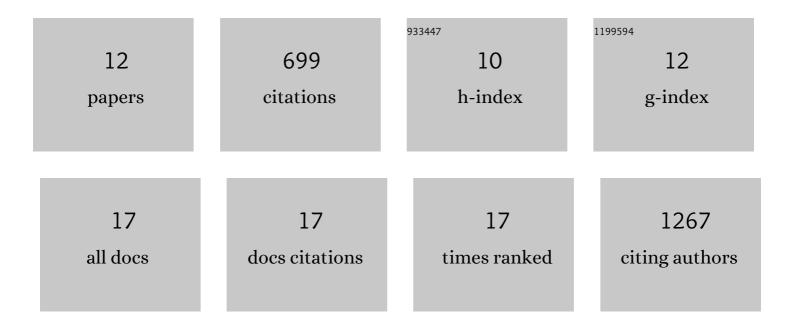
Joseph L Gage

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/452842/publications.pdf Version: 2024-02-01



LOSEDH L CACE

#	Article	IF	CITATIONS
1	Variation in upstream open reading frames contributes to allelic diversity in maize protein abundance. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2112516119.	7.1	10
2	Images carried before the fire: The power, promise, and responsibility of latent phenotyping in plants. The Plant Phenome Journal, 2021, 4, e20023.	2.0	6
3	Ten Years of the Maize Nested Association Mapping Population: Impact, Limitations, and Future Directions. Plant Cell, 2020, 32, 2083-2093.	6.6	81
4	Maize genomes to fields (G2F): 2014–2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. BMC Research Notes, 2020, 13, 71.	1.4	38
5	Multiple Maize Reference Genomes Impact the Identification of Variants by Genomeâ€Wide Association Study in a Diverse Inbred Panel. Plant Genome, 2019, 12, 180069.	2.8	37
6	Residual Heterozygosity and Epistatic Interactions Underlie the Complex Genetic Architecture of Yield in Diploid Potato. Genetics, 2019, 212, 317-332.	2.9	20
7	Inâ€Field Wholeâ€Plant Maize Architecture Characterized by Subcanopy Rovers and Latent Space Phenotyping. The Plant Phenome Journal, 2019, 2, 1-11.	2.0	23
8	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. Genetics, 2018, 210, 1125-1138.	2.9	45
9	Comparing Genome-Wide Association Study Results from Different Measurements of an Underlying Phenotype. G3: Genes, Genomes, Genetics, 2018, 8, 3715-3722.	1.8	16
10	The effect of artificial selection on phenotypic plasticity in maize. Nature Communications, 2017, 8, 1348.	12.8	105
11	TIPS: a system for automated image-based phenotyping of maize tassels. Plant Methods, 2017, 13, 21.	4.3	62
12	Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. Theoretical and Applied Genetics, 2013, 126, 2699-2716.	3.6	228