Kelly L Swarts

List of Publications by Year in descending order

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1040056 1281871 1,579 13 9 11 citations g-index h-index papers 20 20 20 2414 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Heritable and Climatic Sources of Variation in Juvenile Tree Growth in an Austrian Common Garden Experiment of Central European Norway Spruce Populations. Forests, 2022, 13, 809.	2.1	0
2	The Last Trees Standing: Climate modulates tree survival factors during a prolonged bark beetle outbreak in Europe. Agricultural and Forest Meteorology, 2022, 322, 109025.	4.8	10
3	Genome assembly and population genomic analysis provide insights into the evolution of modern sweet corn. Nature Communications, 2021, 12, 1227.	12.8	37
4	An in situ and morphometric study of maize (Zea mays L.) cob rondel phytoliths from Southwestern North American landraces. Journal of Archaeological Science: Reports, 2021, 35, 102732.	0.5	0
5	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	2.6	4
6	Genotypic and phenotypic characterization of a large, diverse population of maize nearâ€isogenic lines. Plant Journal, 2020, 103, 1246-1255.	5.7	12
7	Dysregulation of expression correlates with rare-allele burden and fitness loss in maize. Nature, 2018, 555, 520-523.	27.8	211
8	Parallel altitudinal clines reveal trends in adaptive evolution of genome size in Zea mays. PLoS Genetics, 2018, 14, e1007162.	3.5	97
9	A study of allelic diversity underlying flowering-time adaptation in maize landraces. Nature Genetics, 2017, 49, 476-480.	21.4	254
10	Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. Science, 2017, 357, 512-515.	12.6	169
11	Independent Molecular Basis of Convergent Highland Adaptation in Maize. Genetics, 2015, 200, 1297-1312.	2.9	67
12	Novel Methods to Optimize Genotypic Imputation for Low overage, Nextâ€Generation Sequence Data in Crop Plants. Plant Genome, 2014, 7, plantgenome2014.05.0023.	2.8	241
13	Comprehensive genotyping of the USA national maize inbred seed bank. Genome Biology, 2013, 14, R55.	8.8	458