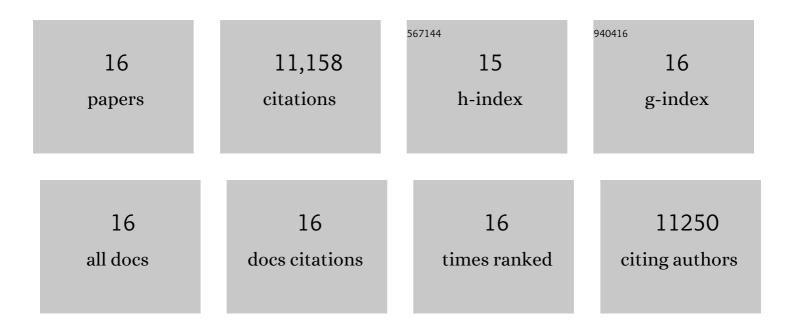
Robert J Elshire

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8020659/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. PLoS ONE, 2011, 6, e19379.	1.1	5,470
2	TASSEL-GBS: A High Capacity Genotyping by Sequencing Analysis Pipeline. PLoS ONE, 2014, 9, e90346.	1.1	1,511
3	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	9.4	816
4	A First-Generation Haplotype Map of Maize. Science, 2009, 326, 1115-1117.	6.0	747
5	Switchgrass Genomic Diversity, Ploidy, and Evolution: Novel Insights from a Network-Based SNP Discovery Protocol. PLoS Genetics, 2013, 9, e1003215.	1.5	608
6	Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012, 44, 803-807.	9.4	577
7	Comprehensive genotyping of the USA national maize inbred seed bank. Genome Biology, 2013, 14, R55.	3.8	458
8	Novel Methods to Optimize Genotypic Imputation for Low overage, Nextâ€Generation Sequence Data in Crop Plants. Plant Genome, 2014, 7, plantgenome2014.05.0023.	1.6	241
9	High-resolution genetic mapping of maize pan-genome sequence anchors. Nature Communications, 2015, 6, 6914.	5.8	213
10	Recombination in diverse maize is stable, predictable, and associated with genetic load. Proceedings of the United States of America, 2015, 112, 3823-3828.	3.3	210
11	Laser Microdissection of Narrow Sheath Mutant Maize Uncovers Novel Gene Expression in the Shoot Apical Meristem. PLoS Genetics, 2007, 3, e101.	1.5	73
12	Microdissection of Shoot Meristem Functional Domains. PLoS Genetics, 2009, 5, e1000476.	1.5	73
13	Independent Molecular Basis of Convergent Highland Adaptation in Maize. Genetics, 2015, 200, 1297-1312.	1.2	67
14	Mining conifers' mega-genome using rapid and efficient multiplexed high-throughput genotyping-by-sequencing (GBS) SNP discovery platform. Tree Genetics and Genomes, 2013, 9, 1537-1544.	0.6	54
15	Cross-amplification of EST-derived markers among 16 grass species. Field Crops Research, 2010, 118, 28-35.	2.3	24
16	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. Molecular Ecology, 2016, 25, 5267-5281.	2.0	16