

# Robert J Elshire

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8020659/publications.pdf>

Version: 2024-02-01

16  
papers

11,158  
citations

567144

15  
h-index

940416

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16  
all docs

16  
docs citations

16  
times ranked

11250  
citing authors

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