

Robert J Elshire

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

16
papers

8,012
citations

15
h-index

16
g-index

16
ext. papers

10,236
ext. citations

12.1
avg. IF

5.52
L-index

#	Paper	IF	Citations
16	A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. <i>PLoS ONE</i> , 2011 , 6, e19379	3.7	3791
15	TASSEL-GBS: a high capacity genotyping by sequencing analysis pipeline. <i>PLoS ONE</i> , 2014 , 9, e90346	3.7	994
14	A first-generation haplotype map of maize. <i>Science</i> , 2009 , 326, 1115-7	33.3	613
13	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012 , 44, 808-11	36.3	600
12	Switchgrass genomic diversity, ploidy, and evolution: novel insights from a network-based SNP discovery protocol. <i>PLoS Genetics</i> , 2013 , 9, e1003215	6	481
11	Maize HapMap2 identifies extant variation from a genome in flux. <i>Nature Genetics</i> , 2012 , 44, 803-7	36.3	470
10	Comprehensive genotyping of the USA national maize inbred seed bank. <i>Genome Biology</i> , 2013 , 14, R55	18.3	337
9	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	4.4	184
8	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, 3823-8	11.5	147
7	High-resolution genetic mapping of maize pan-genome sequence anchors. <i>Nature Communications</i> , 2015 , 6, 6914	17.4	142
6	Microdissection of shoot meristem functional domains. <i>PLoS Genetics</i> , 2009 , 5, e1000476	6	64
5	Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. <i>PLoS Genetics</i> , 2007 , 3, e101	6	58
4	Independent Molecular Basis of Convergent Highland Adaptation in Maize. <i>Genetics</i> , 2015 , 200, 1297-312	2.1	50
3	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	2.1	45
2	Cross-amplification of EST-derived markers among 16 grass species. <i>Field Crops Research</i> , 2010 , 118, 28-35	5.5	24
1	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. <i>Molecular Ecology</i> , 2016 , 25, 5267-5281	5.7	12