

# Roman V Briskine

## List of Publications by Year in Descending Order

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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.

21  
papers

1,394  
citations

18  
h-index

22  
g-index

22  
ext. papers

1,744  
ext. citations

7.7  
avg, IF

3.87  
L-index

#	Paper	IF	Citations
21	Fine-scale empirical data on niche divergence and homeolog expression patterns in an allopolyploid and its diploid progenitor species. <i>New Phytologist</i> , <b>2021</b> , 229, 3587-3601	9.8	2
20	Patterns of polymorphism and selection in the subgenomes of the allopolyploid <i>Arabidopsis kamchatica</i> . <i>Nature Communications</i> , <b>2018</b> , 9, 3909	17.4	26
19	Positional bias in variant calls against draft reference assemblies. <i>BMC Genomics</i> , <b>2017</b> , 18, 263	4.5	5
18	Genome assembly and annotation of <i>Arabidopsis halleri</i> , a model for heavy metal hyperaccumulation and evolutionary ecology. <i>Molecular Ecology Resources</i> , <b>2017</b> , 17, 1025-1036	8.4	64
17	The Cardamine <i>hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , <b>2016</b> , 2, 16167	11.5	56
16	Co-expression network analysis of duplicate genes in maize ( <i>Zea mays</i> L.) reveals no subgenome bias. <i>BMC Genomics</i> , <b>2016</b> , 17, 875	4.5	20
15	Genomic signature of adaptation to climate in <i>Medicago truncatula</i> . <i>Genetics</i> , <b>2014</b> , 196, 1263-75	4	122
14	Discovering functional modules across diverse maize transcriptomes using COB, the Co-expression Browser. <i>PLoS ONE</i> , <b>2014</b> , 9, e99193	3.7	19
13	High-density genome-wide association mapping implicates an F-box encoding gene in <i>Medicago truncatula</i> resistance to <i>Aphanomyces euteiches</i> . <i>New Phytologist</i> , <b>2014</b> , 201, 1328-1342	9.8	62
12	Selection, genome-wide fitness effects and evolutionary rates in the model legume <i>Medicago truncatula</i> . <i>Molecular Ecology</i> , <b>2013</b> , 22, 3525-38	5.7	40
11	Phylogenetic signal variation in the genomes of <i>Medicago</i> (Fabaceae). <i>Systematic Biology</i> , <b>2013</b> , 62, 424- <del>88</del> 4		43
10	Genomic distribution of maize facultative heterochromatin marked by trimethylation of H3K27. <i>Plant Cell</i> , <b>2013</b> , 25, 780-93	11.6	77
9	Estimating heritability using genomic data. <i>Methods in Ecology and Evolution</i> , <b>2013</b> , 4, 1151-1158	7.7	32
8	Epigenetic and genetic influences on DNA methylation variation in maize populations. <i>Plant Cell</i> , <b>2013</b> , 25, 2783-97	11.6	174
7	Maize gene atlas developed by RNA sequencing and comparative evaluation of transcriptomes based on RNA sequencing and microarrays. <i>PLoS ONE</i> , <b>2013</b> , 8, e61005	3.7	125
6	Candidate genes and genetic architecture of symbiotic and agronomic traits revealed by whole-genome, sequence-based association genetics in <i>Medicago truncatula</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e65688	3.7	121
5	Reshaping of the maize transcriptome by domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 11878-83	11.5	113

4	Fine-scale population recombination rates, hotspots, and correlates of recombination in the <i>Medicago truncatula</i> genome. <i>Genome Biology and Evolution</i> , <b>2012</b> , 4, 726-37	3.9	56
3	Population genomics of the facultatively mutualistic bacteria <i>Sinorhizobium meliloti</i> and <i>S. medicae</i> . <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002868	6	56
2	Whole-genome nucleotide diversity, recombination, and linkage disequilibrium in the model legume <i>Medicago truncatula</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, E864-70	11.5	178
1	Fine-scale ecological and transcriptomic data reveal niche differentiation of an allopolyploid from diploid parents in <i>Cardamine</i>		3