

## List of Publications by Year in descending order

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41  
papers

2,736  
citations

257101

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288905

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docs citations

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times ranked

3125  
citing authors

#	ARTICLE	IF	CITATIONS
1	Theoretical and experimental assessment of genome-based prediction in landraces of allogamous crops. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2121797119.	3.3	4
2	Natural alleles of the abscisic acid catabolism gene <i>ZmAbh4</i> modulate water use efficiency and carbon isotope discrimination in maize. <i>Plant Cell</i> , 2022, 34, 3860-3872.	3.1	5
3	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
4	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941.	1.2	4
5	Discovery of beneficial haplotypes for complex traits in maize landraces. <i>Nature Communications</i> , 2020, 11, 4954.	5.8	38
6	European maize genomes highlight intraspecies variation in repeat and gene content. <i>Nature Genetics</i> , 2020, 52, 950-957.	9.4	84
7	European maize landraces made accessible for plant breeding and genome-based studies. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3333-3345.	1.8	52
8	Genomics-Based Hybrid Rye Breeding. , 2019, , 329-348.		8
9	Testcross performance of doubled haploid lines from European flint maize landraces is promising for broadening the genetic base of elite germplasm. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1897-1908.	1.8	28
10	Carbon isotope composition, water use efficiency, and drought sensitivity are controlled by a common genomic segment in maize. <i>Theoretical and Applied Genetics</i> , 2019, 132, 53-63.	1.8	26
11	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. <i>Genetics</i> , 2018, 210, 1185-1196.	1.2	18
12	Evolutionarily conserved partial gene duplication in the Triticeae tribe of grasses confers pathogen resistance. <i>Genome Biology</i> , 2018, 19, 116.	3.8	9
13	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. <i>Genetics</i> , 2017, 206, 1611-1619.	1.2	24
14	Fine mapping of the restorer gene <i>Rfp3</i> from an Iranian primitive rye ( <i>Secale cereale</i> L.). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1179-1189.	1.8	23
15	Exploring new alleles for frost tolerance in winter rye. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2151-2164.	1.8	20
16	Is there an optimum level of diversity in utilization of genetic resources?. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2283-2295.	1.8	25
17	Towards a whole-genome sequence for rye ( <i>Secale cereale</i> L.). <i>Plant Journal</i> , 2017, 89, 853-869.	2.8	238
18	Geography and end use drive the diversification of worldwide winter rye populations. <i>Molecular Ecology</i> , 2016, 25, 500-514.	2.0	17

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19	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. <i>Genome Biology</i> , 2016, 17, 137.	3.8	51
20	Association mapping for cold tolerance in two large maize inbred panels. <i>BMC Plant Biology</i> , 2016, 16, 127.	1.6	73
21	Model training across multiple breeding cycles significantly improves genomic prediction accuracy in rye ( <i>Secale cereale</i> L.). <i>Theoretical and Applied Genetics</i> , 2016, 129, 2043-2053.	1.8	84
22	Oligogenic control of resistance to soil-borne viruses <i>SBCMV</i> and <i>WSSMV</i> in rye ( <i>Secale cereale</i> L.). <i>Plant Breeding</i> , 2016, 135, 552-559.	1.0	6
23	Choice of models for QTL mapping with multiple families and design of the training set for prediction of <i>Fusarium</i> resistance traits in maize. <i>Theoretical and Applied Genetics</i> , 2016, 129, 431-444.	1.8	30
24	Detection of donor effects in a rye introgression population with genome-wide prediction. <i>Plant Breeding</i> , 2015, 134, 406-415.	1.0	7
25	DroughtDB: an expert-curated compilation of plant drought stress genes and their homologs in nine species. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav046.	1.4	62
26	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. <i>Crop Science</i> , 2014, 54, 1981-1991.	0.8	30
27	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. <i>Genetics</i> , 2014, 198, 1717-1734.	1.2	89
28	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. <i>BMC Genomics</i> , 2014, 15, 823.	1.2	242
29	Genome-wide prediction methods for detecting genetic effects of donor chromosome segments in introgression populations. <i>BMC Genomics</i> , 2014, 15, 782.	1.2	3
30	Genome Properties and Prospects of Genomic Prediction of Hybrid Performance in a Breeding Program of Maize. <i>Genetics</i> , 2014, 197, 1343-1355.	1.2	192
31	Usefulness of Multiparental Populations of Maize ( <i>Zea mays</i> L.) for Genome-Based Prediction. <i>Genetics</i> , 2014, 198, 3-16.	1.2	114
32	Intraspecific variation of recombination rate in maize. <i>Genome Biology</i> , 2013, 14, R103.	13.9	176
33	BSTA: a targeted approach combines bulked segregant analysis with next-generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. <i>BMC Genomics</i> , 2013, 14, 628.	1.2	43
34	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	3.1	194
35	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	3.3	173
36	Genetic architecture of complex agronomic traits examined in two testcross populations of rye ( <i>Secale cereale</i> L.). <i>BMC Genomics</i> , 2012, 13, 706.	1.2	66

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37	From RNA-seq to large-scale genotyping - genomics resources for rye ( <i>Secale cereale</i> L.). <i>BMC Plant Biology</i> , 2011, 11, 131.	1.6	109
38	Association analysis of frost tolerance in rye using candidate genes and phenotypic data from controlled, semi-controlled, and field phenotyping platforms. <i>BMC Plant Biology</i> , 2011, 11, 146.	1.6	47
39	High levels of nucleotide diversity and fast decline of linkage disequilibrium in rye ( <i>Secale cereale</i> L.) genes involved in frost response. <i>BMC Plant Biology</i> , 2011, 11, 6.	1.6	55
40	Consistent detection of QTLs for crown rust resistance in Italian ryegrass ( <i>Lolium multiflorum</i> Lam.) across environments and phenotyping methods. <i>Theoretical and Applied Genetics</i> , 2007, 115, 9-17.	1.8	48
41	Genetic mapping reveals a single major QTL for bacterial wilt resistance in Italian ryegrass ( <i>Lolium</i> ) Tj ETQq1 1 0.784314 rgBT_/_Overlook	1.8	50