List of Publications by Year
in descending order

41 papers	**2,736** citations	257101 **24** h-index	288905 **40** g-index
45 all docs	**45** docs citations	**45** times ranked	**3125** citing authors

#	Article	IF	Citations
1	A powerful tool for genome analysis in maize: development and evaluation of the high density 600 k SNP genotyping array. BMC Genomics, 2014, 15, 823.	1.2	242
2	Towards a whole–genome sequence for rye (*Secale cereale* L.). Plant Journal, 2017, 89, 853-869.	2.8	238
3	Reticulate Evolution of the Rye Genome. Plant Cell, 2013, 25, 3685-3698.	3.1	194
4	Genome Properties and Prospects of Genomic Prediction of Hybrid Performance in a Breeding Program of Maize. Genetics, 2014, 197, 1343-1355.	1.2	192
5	Intraspecific variation of recombination rate in maize. Genome Biology, 2013, 14, R103.	13.9	176
6	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13343-13346.	3.3	173
7	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nature Genetics, 2021, 53, 564-573.	9.4	138
8	Usefulness of Multiparental Populations of Maize (*Zea mays* L.) for Genome-Based Prediction. Genetics, 2014, 198, 3-16.	1.2	114
9	From RNA-seq to large-scale genotyping - genomics resources for rye (Secale cereale L.). BMC Plant Biology, 2011, 11, 131.	1.6	109
10	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. Genetics, 2014, 198, 1717-1734.	1.2	89
11	Model training across multiple breeding cycles significantly improves genomic prediction accuracy in rye (Secale cereale L.). Theoretical and Applied Genetics, 2016, 129, 2043-2053.	1.8	84
12	European maize genomes highlight intraspecies variation in repeat and gene content. Nature Genetics, 2020, 52, 950-957.	9.4	84
13	Association mapping for cold tolerance in two large maize inbred panels. BMC Plant Biology, 2016, 16, 127.	1.6	73
14	Genetic architecture of complex agronomic traits examined in two testcross populations of rye (Secale cereale L.). BMC Genomics, 2012, 13, 706.	1.2	66
15	DroughtDB: an expert-curated compilation of plant drought stress genes and their homologs in nine species. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav046.	1.4	62
16	High levels of nucleotide diversity and fast decline of linkage disequilibrium in rye (Secale cerealeL.) genes involved in frost response. BMC Plant Biology, 2011, 11, 6.	1.6	55
17	European maize landraces made accessible for plant breeding and genome-based studies. Theoretical and Applied Genetics, 2019, 132, 3333-3345.	1.8	52
18	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. Genome Biology, 2016, 17, 137.	3.8	51

#	Article	IF	Citations
19	Genetic mapping reveals a single major QTL for bacterial wilt resistance in Italian ryegrass (Lolium) Tj ETQq1 1 0.784314 rgBT /Overlo	1.8	50
20	Consistent detection of QTLs for crown rust resistance in Italian ryegrass (Lolium multiflorum Lam.) across environments and phenotyping methods. Theoretical and Applied Genetics, 2007, 115, 9-17.	1.8	48
21	Association analysis of frost tolerance in rye using candidate genes and phenotypic data from controlled, semi-controlled, and field phenotyping platforms. BMC Plant Biology, 2011, 11, 146.	1.6	47
22	BSTA: a targeted approach combines bulked segregant analysis with next- generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. BMC Genomics, 2013, 14, 628.	1.2	43
23	Discovery of beneficial haplotypes for complex traits in maize landraces. Nature Communications, 2020, 11, 4954.	5.8	38
24	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. Crop Science, 2014, 54, 1981-1991.	0.8	30
25	Choice of models for QTL mapping with multiple families and design of the training set for prediction of Fusarium resistance traits in maize. Theoretical and Applied Genetics, 2016, 129, 431-444.	1.8	30
26	Testcross performance of doubled haploid lines from European flint maize landraces is promising for broadening the genetic base of elite germplasm. Theoretical and Applied Genetics, 2019, 132, 1897-1908.	1.8	28
27	Carbon isotope composition, water use efficiency, and drought sensitivity are controlled by a common genomic segment in maize. Theoretical and Applied Genetics, 2019, 132, 53-63.	1.8	26
28	Is there an optimum level of diversity in utilization of genetic resources?. Theoretical and Applied Genetics, 2017, 130, 2283-2295.	1.8	25
29	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. Genetics, 2017, 206, 1611-1619.	1.2	24
30	Fine mapping of the restorer gene Rfp3 from an Iranian primitive rye (Secale cereale L.). Theoretical and Applied Genetics, 2017, 130, 1179-1189.	1.8	23
31	Exploring new alleles for frost tolerance in winter rye. Theoretical and Applied Genetics, 2017, 130, 2151-2164.	1.8	20
32	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. Genetics, 2018, 210, 1185-1196.	1.2	18
33	Geography and end use drive the diversification of worldwide winter rye populations. Molecular Ecology, 2016, 25, 500-514.	2.0	17
34	Evolutionarily conserved partial gene duplication in the Triticeae tribe of grasses confers pathogen resistance. Genome Biology, 2018, 19, 116.	3.8	9
35	Genomics-Based Hybrid Rye Breeding. , 2019, , 329-348.		8
36	Detection of donor effects in a rye introgression population with genome‑wide prediction. Plant Breeding, 2015, 134, 406-415.	1.0	7

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37	Oligogenic control of resistance to soil‐borne viruses <scp>SBCMV</scp> and <scp>WSSMV</scp> in rye (<i>Secale cereale</i>ÂL.). Plant Breeding, 2016, 135, 552-559.	1.0	6
38	Natural alleles of the abscisic acid catabolism gene<i>ZmAbh4</i>modulate water use efficiency and carbon isotope discrimination in maize. Plant Cell, 2022, 34, 3860-3872.	3.1	5
39	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	1.2	4
40	Theoretical and experimental assessment of genome-based prediction in landraces of allogamous crops. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2121797119.	3.3	4
41	Genome-wide prediction methods for detecting genetic effects of donor chromosome segments in introgression populations. BMC Genomics, 2014, 15, 782.	1.2	3