Eva Bauer

List of Publications by Year
in descending order

38 papers	2,577 citations

257357

24 h-index

315616

38 g-index

39 all docs	39 docs citations
39 times ranked	3064 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	Usefulness of Multiparental Populations of Maize (*Zea mays* L.) for Genome-Based Prediction. Genetics, 2014, 198, 3-16.	1.2	114
8	From RNA-seq to large-scale genotyping - genomics resources for rye (Secale cereale L.). BMC Plant Biology, 2011, 11, 131.	1.6	109
9	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
10	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
11	European maize genomes highlight intraspecies variation in repeat and gene content. Nature Genetics, 2020, 52, 950-957.	9.4	84
12	Association mapping for cold tolerance in two large maize inbred panels. BMC Plant Biology, 2016, 16, 127.	1.6	73
13	Genetic architecture of complex agronomic traits examined in two testcross populations of rye (Secale cereale L.). BMC Genomics, 2012, 13, 706.	1.2	66
14	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
15	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
16	Prolonged expression of the BX1 signature enzyme is associated with a recombination hotspot in the benzoxazinoid gene cluster in Zea mays. Journal of Experimental Botany, 2015, 66, 3917-3930.	2.4	53
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	High-resolution mapping of the Rym4/Rym5 locus conferring resistance to the barley yellow mosaic virus complex (BaMMV, BaYMV, BaYMV-2) in barley (Hordeum vulgare ssp. vulgare L.). Theoretical and Applied Genetics, 2005, 110, 283-293.	1.8	48
21	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
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	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
27	Is there an optimum level of diversity in utilization of genetic resources?. Theoretical and Applied Genetics, 2017, 130, 2283-2295.	1.8	25
28	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. Genetics, 2017, 206, 1611-1619.	1.2	24
29	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
30	Exploring new alleles for frost tolerance in winter rye. Theoretical and Applied Genetics, 2017, 130, 2151-2164.	1.8	20
31	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. Genetics, 2018, 210, 1185-1196.	1.2	18
32	Geography and end use drive the diversification of worldwide winter rye populations. Molecular Ecology, 2016, 25, 500-514.	2.0	17
33	Detection of donor effects in a rye introgression population with genome‐wide prediction. Plant Breeding, 2015, 134, 406-415.	1.0	7
34	Oligogenic control of resistance to soil‐borne viruses SBCMV and WSSMV in rye (*Secale cereale* L.). Plant Breeding, 2016, 135, 552-559.	1.0	6
35	Natural alleles of the abscisic acid catabolism gene *ZmAbh4* modulate water use efficiency and carbon isotope discrimination in maize. Plant Cell, 2022, 34, 3860-3872.	3.1	5
36	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	1.2	4

#	Article	IF	Citations
37	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
38	Genome-wide prediction methods for detecting genetic effects of donor chromosome segments in introgression populations. BMC Genomics, 2014, 15, 782.	1.2	3