

Eva Bauer

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

2,577
citations

257450
24
h-index

315739
38
g-index

39
all docs

39
docs citations

39
times ranked

3064
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	7.1	4
2	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.	6.6	5
3	Joint analysis of days to flowering reveals independent temperate adaptations in maize. Heredity, 2021, 126, 929-941.	2.6	4
4	Discovery of beneficial haplotypes for complex traits in maize landraces. Nature Communications, 2020, 11, 4954.	12.8	38
5	European maize genomes highlight intraspecies variation in repeat and gene content. Nature Genetics, 2020, 52, 950-957.	21.4	84
6	European maize landraces made accessible for plant breeding and genome-based studies. Theoretical and Applied Genetics, 2019, 132, 3333-3345.	3.6	52
7	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.	3.6	26
8	Genomic Prediction Within and Among Doubled-Haploid Libraries from Maize Landraces. Genetics, 2018, 210, 1185-1196.	2.9	18
9	Safeguarding Our Genetic Resources with Libraries of Doubled-Haploid Lines. Genetics, 2017, 206, 1611-1619.	2.9	24
10	Fine mapping of the restorer gene Rfp3 from an Iranian primitive rye (<i>Secale cereale</i> L.). Theoretical and Applied Genetics, 2017, 130, 1179-1189.	3.6	23
11	Exploring new alleles for frost tolerance in winter rye. Theoretical and Applied Genetics, 2017, 130, 2151-2164.	3.6	20
12	Is there an optimum level of diversity in utilization of genetic resources?. Theoretical and Applied Genetics, 2017, 130, 2283-2295.	3.6	25
13	Towards a whole-genome sequence for rye (<i>Secale cereale</i> L.). Plant Journal, 2017, 89, 853-869.	5.7	238
14	Geography and end use drive the diversification of worldwide winter rye populations. Molecular Ecology, 2016, 25, 500-514.	3.9	17
15	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. Genome Biology, 2016, 17, 137.	8.8	51
16	Association mapping for cold tolerance in two large maize inbred panels. BMC Plant Biology, 2016, 16, 127.	3.6	73
17	Model training across multiple breeding cycles significantly improves genomic prediction accuracy in rye (<i>Secale cereale</i> L.). Theoretical and Applied Genetics, 2016, 129, 2043-2053.	3.6	84
18	Oligogenic control of resistance to soil-borne viruses <i>SBCMV</i> and <i>WSSMV</i> in rye (<i>Secale cereale</i> L.). Plant Breeding, 2016, 135, 552-559.	1.9	6

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19	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.	3.6	30
20	Detection of donor effects in a rye introgression population with genome-wide prediction. Plant Breeding, 2015, 134, 406-415.	1.9	7
21	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.	3.0	62
22	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.	4.8	53
23	Cold Tolerance in Two Large Maize Inbred Panels Adapted to European Climates. Crop Science, 2014, 54, 1981-1991.	1.8	30
24	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.	2.9	89
25	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.	2.8	242
26	Genome-wide prediction methods for detecting genetic effects of donor chromosome segments in introgression populations. BMC Genomics, 2014, 15, 782.	2.8	3
27	Genome Properties and Prospects of Genomic Prediction of Hybrid Performance in a Breeding Program of Maize. Genetics, 2014, 197, 1343-1355.	2.9	192
28	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. Genetics, 2014, 198, 3-16.	2.9	114
29	Intraspecific variation of recombination rate in maize. Genome Biology, 2013, 14, R103.	9.6	176
30	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.	2.8	43
31	Reticulate Evolution of the Rye Genome. Plant Cell, 2013, 25, 3685-3698.	6.6	194
32	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.	7.1	173
33	Genetic architecture of complex agronomic traits examined in two testcross populations of rye (<i>Secale cereale</i> L.). BMC Genomics, 2012, 13, 706.	2.8	66
34	From RNA-seq to large-scale genotyping - genomics resources for rye (<i>Secale cereale</i> L.). BMC Plant Biology, 2011, 11, 131.	3.6	109
35	High levels of nucleotide diversity and fast decline of linkage disequilibrium in rye (<i>Secale cereale</i> L.) genes involved in frost response. BMC Plant Biology, 2011, 11, 6.	3.6	55
36	Consistent detection of QTLs for crown rust resistance in Italian ryegrass (<i>Lolium multiflorum</i> Lam.) across environments and phenotyping methods. Theoretical and Applied Genetics, 2007, 115, 9-17.	3.6	48

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37	Genetic mapping reveals a single major QTL for bacterial wilt resistance in Italian ryegrass (<i>Lolium</i>) Tj ETQq1 1 0.784314 rgBT_/_Overlook	3.6	50
38	High-resolution mapping of the Rym4/Rym5 locus conferring resistance to the barley yellow mosaic virus complex (BaMMV, BaYMV, BaYMV-2) in barley (<i>Hordeum vulgare</i> ssp. <i>vulgare</i> L.). Theoretical and Applied Genetics, 2005, 110, 283-293.	3.6	48