William D Beavis

List of Publications by Year
in descending order

21 papers	1,093 citations	687363 13 h-index	713466 21 g-index
23 all docs	23 docs citations	23 times ranked	1286 citing authors

#	Article	IF	Citations
1	Accuracy and Training Population Design for Genomic Selection on Quantitative Traits in Elite North American Oats. Plant Genome, 2011, 4, .	2.8	214
2	Parametric and Nonparametric Statistical Methods for Genomic Selection of Traits with Additive and Epistatic Genetic Architectures. G3: Genes, Genomes, Genetics, 2014, 4, 1027-1046.	1.8	148
3	Genetic Characterization of the Soybean Nested Association Mapping Population. Plant Genome, 2017, 10, plantgenome2016.10.0109.	2.8	114
4	Genetic Architecture of Soybean Yield and Agronomic Traits. G3: Genes, Genomes, Genetics, 2018, 8, 3367-3375.	1.8	98
5	Technological advances in maize breeding: past, present and future. Theoretical and Applied Genetics, 2019, 132, 817-849.	3.6	97
6	Genomic, Marker‐Assisted, and Pedigree‐BLUP Selection Methods for Î²‐Glucan Concentration in Elite Oat. Crop Science, 2013, 53, 1894-1906.	1.8	84
7	Multi-objective optimized genomic breeding strategies for sustainable food improvement. Heredity, 2019, 122, 672-683.	2.6	77
8	Genome-Wide Analysis of Grain Yield Stability and Environmental Interactions in a Multiparental Soybean Population. G3: Genes, Genomes, Genetics, 2018, 8, 519-529.	1.8	75
9	The Predicted Cross Value for Genetic Introgression of Multiple Alleles. Genetics, 2017, 205, 1409-1423.	2.9	39
10	Leveraging genomic prediction to scan germplasm collection for crop improvement. PLoS ONE, 2017, 12, e0179191.	2.5	35
11	Genome‐wide Association Study for Beta‐glucan Concentration in Elite North American Oat. Crop Science, 2013, 53, 542-553.	1.8	23
12	Family-based association mapping in crop species. Theoretical and Applied Genetics, 2013, 126, 1419-1430.	3.6	22
13	GWASpro: a high-performance genome-wide association analysis server. Bioinformatics, 2019, 35, 2512-2514.	4.1	18
14	Systematic design for trait introgression projects. Theoretical and Applied Genetics, 2017, 130, 1993-2004.	3.6	16
15	High-throughput characterization, correlation, and mapping of leaf photosynthetic and functional traits in the soybean (<i>Glycine max</i>) nested association mapping population. Genetics, 2022, , .	2.9	8
16	Numericware i: Identical by State Matrix Calculator. Evolutionary Bioinformatics, 2017, 13, 117693431668866.	1.2	6
17	Application of Response Surface Methods To Determine Conditions for Optimal Genomic Prediction. G3: Genes, Genomes, Genetics, 2017, 7, 3103-3113.	1.8	5
18	Numericware N: Numerator Relationship Matrix Calculator. Journal of Heredity, 2016, 107, 686-690.	2.4	4

#	Article	IF	Citations
19	Estimation of genetic variance contributed by a quantitative trait locus: correcting the bias associated with significance tests. Genetics, 2021, 219, .	2.9	4
20	Dynamic Programming for Resource Allocation in Multi-Allelic Trait Introgression. Frontiers in Plant Science, 2021, 12, 544854.	3.6	2
21	Predictions from algorithmic modeling result in better decisions than from data modeling for soybean iron deficiency chlorosis. PLoS ONE, 2021, 16, e0240948.	2.5	2