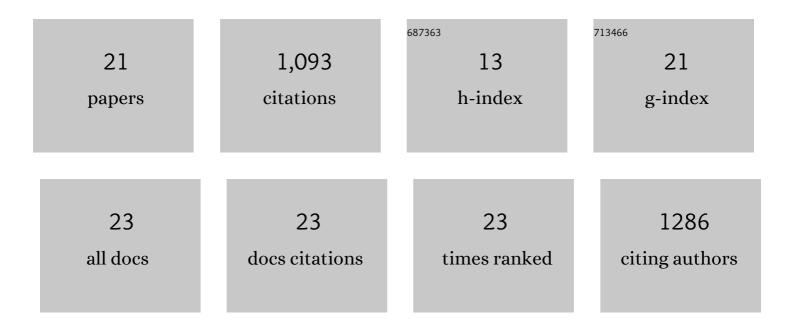
## William D Beavis

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7559116/publications.pdf Version: 2024-02-01



WILLIAM D REAVIS

#	Article	IF	CITATIONS
1	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
2	Dynamic Programming for Resource Allocation in Multi-Allelic Trait Introgression. Frontiers in Plant Science, 2021, 12, 544854.	3.6	2
3	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
4	Estimation of genetic variance contributed by a quantitative trait locus: correcting the bias associated with significance tests. Genetics, 2021, 219, .	2.9	4
5	Technological advances in maize breeding: past, present and future. Theoretical and Applied Genetics, 2019, 132, 817-849.	3.6	97
6	GWASpro: a high-performance genome-wide association analysis server. Bioinformatics, 2019, 35, 2512-2514.	4.1	18
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	Genetic Architecture of Soybean Yield and Agronomic Traits. G3: Genes, Genomes, Genetics, 2018, 8, 3367-3375.	1.8	98
10	The Predicted Cross Value for Genetic Introgression of Multiple Alleles. Genetics, 2017, 205, 1409-1423.	2.9	39
11	Application of Response Surface Methods To Determine Conditions for Optimal Genomic Prediction. G3: Genes, Genomes, Genetics, 2017, 7, 3103-3113.	1.8	5
12	Systematic design for trait introgression projects. Theoretical and Applied Genetics, 2017, 130, 1993-2004.	3.6	16
13	Numericware i: Identical by State Matrix Calculator. Evolutionary Bioinformatics, 2017, 13, 117693431668866.	1.2	6
14	Genetic Characterization of the Soybean Nested Association Mapping Population. Plant Genome, 2017, 10, plantgenome2016.10.0109.	2.8	114
15	Leveraging genomic prediction to scan germplasm collection for crop improvement. PLoS ONE, 2017, 12, e0179191.	2.5	35
16	Numericware N: Numerator Relationship Matrix Calculator. Journal of Heredity, 2016, 107, 686-690.	2.4	4
17	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
18	Family-based association mapping in crop species. Theoretical and Applied Genetics, 2013, 126, 1419-1430.	3.6	22

#	Article	IF	CITATIONS
19	Genomeâ€wide Association Study for Betaâ€glucan Concentration in Elite North American Oat. Crop Science, 2013, 53, 542-553.	1.8	23
20	Genomic, Markerâ€Assisted, and Pedigreeâ€BLUP Selection Methods for βâ€Glucan Concentration in Elite Oat. Crop Science, 2013, 53, 1894-1906.	1.8	84
21	Accuracy and Training Population Design for Genomic Selection on Quantitative Traits in Elite North American Oats. Plant Genome, 2011, 4, .	2.8	214