

# William D Beavis

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7559116/publications.pdf>

Version: 2024-02-01

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	High-throughput characterization, correlation, and mapping of leaf photosynthetic and functional traits in the soybean ( <i>Glycine max</i> ) nested association mapping population. <i>Genetics</i> , 2022, , .	2.9	8
2	Dynamic Programming for Resource Allocation in Multi-Allelic Trait Introgression. <i>Frontiers in Plant Science</i> , 2021, 12, 544854.	3.6	2
3	Predictions from algorithmic modeling result in better decisions than from data modeling for soybean iron deficiency chlorosis. <i>PLoS ONE</i> , 2021, 16, e0240948.	2.5	2
4	Estimation of genetic variance contributed by a quantitative trait locus: correcting the bias associated with significance tests. <i>Genetics</i> , 2021, 219, .	2.9	4
5	Technological advances in maize breeding: past, present and future. <i>Theoretical and Applied Genetics</i> , 2019, 132, 817-849.	3.6	97
6	GWASpro: a high-performance genome-wide association analysis server. <i>Bioinformatics</i> , 2019, 35, 2512-2514.	4.1	18
7	Multi-objective optimized genomic breeding strategies for sustainable food improvement. <i>Heredity</i> , 2019, 122, 672-683.	2.6	77
8	Genome-Wide Analysis of Grain Yield Stability and Environmental Interactions in a Multiparental Soybean Population. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 519-529.	1.8	75
9	Genetic Architecture of Soybean Yield and Agronomic Traits. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3367-3375.	1.8	98
10	The Predicted Cross Value for Genetic Introgression of Multiple Alleles. <i>Genetics</i> , 2017, 205, 1409-1423.	2.9	39
11	Application of Response Surface Methods To Determine Conditions for Optimal Genomic Prediction. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3103-3113.	1.8	5
12	Systematic design for trait introgression projects. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1993-2004.	3.6	16
13	Numericware i: Identical by State Matrix Calculator. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431668866.	1.2	6
14	Genetic Characterization of the Soybean Nested Association Mapping Population. <i>Plant Genome</i> , 2017, 10, plantgenome2016.10.0109.	2.8	114
15	Leveraging genomic prediction to scan germplasm collection for crop improvement. <i>PLoS ONE</i> , 2017, 12, e0179191.	2.5	35
16	Numericware N: Numerator Relationship Matrix Calculator. <i>Journal of Heredity</i> , 2016, 107, 686-690.	2.4	4
17	Parametric and Nonparametric Statistical Methods for Genomic Selection of Traits with Additive and Epistatic Genetic Architectures. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1027-1046.	1.8	148
18	Family-based association mapping in crop species. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1419-1430.	3.6	22

#	ARTICLE	IF	CITATIONS
19	Genome-wide Association Study for Beta-glucan Concentration in Elite North American Oat. <i>Crop Science</i> , 2013, 53, 542-553.	1.8	23
20	Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods for $\beta$ -glucan Concentration in Elite Oat. <i>Crop Science</i> , 2013, 53, 1894-1906.	1.8	84
21	Accuracy and Training Population Design for Genomic Selection on Quantitative Traits in Elite North American Oats. <i>Plant Genome</i> , 2011, 4, .	2.8	214