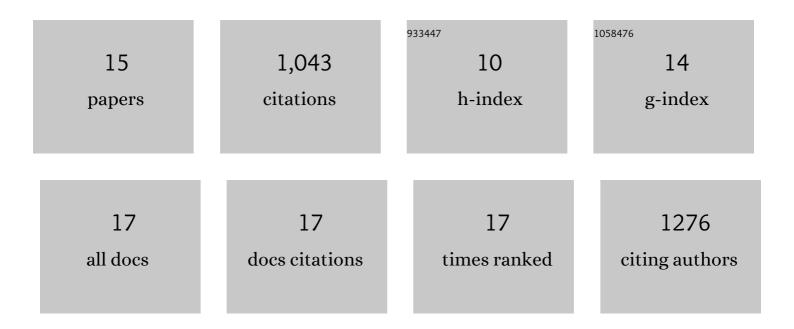
Valentin Wimmer

List of Publications by Year in descending order

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VALENTIN WIMMED

#	Article	IF	CITATIONS
1	synbreed: a framework for the analysis of genomic prediction data using R. Bioinformatics, 2012, 28, 2086-2087.	4.1	296
2	Genome-based prediction of testcross values in maize. Theoretical and Applied Genetics, 2011, 123, 339-350.	3.6	268
3	Genome-Wide Prediction of Traits with Different Genetic Architecture Through Efficient Variable Selection. Genetics, 2013, 195, 573-587.	2.9	129
4	Genome-based prediction of maize hybrid performance across genetic groups, testers, locations, and years. Theoretical and Applied Genetics, 2014, 127, 1375-1386.	3.6	90
5	Genomic prediction with epistasis models: on the marker-coding-dependent performance of the extended GBLUP and properties of the categorical epistasis model (CE). BMC Bioinformatics, 2017, 18, 3.	2.6	60
6	Epistasis and covariance: how gene interaction translates into genomic relationship. Theoretical and Applied Genetics, 2016, 129, 963-976.	3.6	58
7	Improving resistance to the European corn borer: a comprehensive study in elite maize using QTL mapping and genome-wide prediction. Theoretical and Applied Genetics, 2015, 128, 875-891.	3.6	37
8	How do the type of QTL effect and the form of the residual term influence QTL detection in multi-parent populations? A case study in the maize EU-NAM population. Theoretical and Applied Genetics, 2017, 130, 1753-1764.	3.6	32
9	Sensitivity to prior specification in Bayesian genome-based prediction models. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 375-91.	0.6	27
10	A heuristic method for fast and accurate phasing and imputation of single-nucleotide polymorphism data in bi-parental plant populations. Theoretical and Applied Genetics, 2018, 131, 2345-2357.	3.6	20
11	Lost in Translation: On the Problem of Data Coding in Penalized Whole Genome Regression with Interactions. G3: Genes, Genomes, Genetics, 2019, 9, 1117-1129.	1.8	8
12	The influence of QTL allelic diversity on QTL detection in multi-parent populations: a simulation study in sugar beet. BMC Genomic Data, 2021, 22, 4.	1.7	7
13	Phasing and imputation of single nucleotide polymorphism data of missing parents of biparental plant populations. Crop Science, 2021, 61, 2243-2253.	1.8	5
14	A Comparison of the Adoption of Genomic Selection Across Different Breeding Institutions. Frontiers in Plant Science, 2021, 12, 728567.	3.6	4
15	Statistical Models for the Prediction of Genetic Values. , 2014, , 183-205.		0