

Valentin Wimmer

List of Publications by Year in descending order

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15
papers

1,043
citations

933447

10
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

1276
citing authors

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