

Laurence Moreau

List of Publications by Year in descending order

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44
papers

2,576
citations

201385

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docs citations

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times ranked

2285
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Architecture of Flowering Time in Maize As Inferred From Quantitative Trait Loci Meta-analysis and Synteny Conservation With the Rice Genome. <i>Genetics</i> , 2004, 168, 2169-2185.	1.2	353
2	Maximizing the Reliability of Genomic Selection by Optimizing the Calibration Set of Reference Individuals: Comparison of Methods in Two Diverse Groups of Maize Inbreds (<i>Zea mays</i> L.). <i>Genetics</i> , 2012, 192, 715-728.	1.2	258
3	Connected populations for detecting quantitative trait loci and testing for epistasis: an application in maize. <i>Theoretical and Applied Genetics</i> , 2006, 113, 206-224.	1.8	229
4	The Genetic Basis of Heterosis: Multiparental Quantitative Trait Loci Mapping Reveals Contrasted Levels of Apparent Overdominance Among Traits of Agronomical Interest in Maize (<i>Zea mays</i> L.). <i>Genetics</i> , 2012, 190, 795-811.	1.2	146
5	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. <i>Genetics</i> , 2014, 198, 3-16.	1.2	114
6	Genetic Analysis and QTL Mapping of Cell Wall Digestibility and Lignification in Silage Maize. <i>Crop Science</i> , 2001, 41, 690-697.	0.8	97
7	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. <i>Genetics</i> , 2014, 198, 1717-1734.	1.2	89
8	Recovering Power in Association Mapping Panels with Variable Levels of Linkage Disequilibrium. <i>Genetics</i> , 2014, 197, 375-387.	1.2	89
9	Economic Efficiency of One Cycle of Marker-Assisted Selection. <i>Crop Science</i> , 2000, 40, 329-337.	0.8	85
10	Meta-analysis of QTL involved in silage quality of maize and comparison with the position of candidate genes. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1465-1482.	1.8	83
11	Use of trial clustering to study QTL \times environment effects for grain yield and related traits in maize. <i>Theoretical and Applied Genetics</i> , 2004, 110, 92-105.	1.8	61
12	Fine Mapping and Haplotype Structure Analysis of a Major Flowering Time Quantitative Trait Locus on Maize Chromosome 10. <i>Genetics</i> , 2009, 183, 1555-1563.	1.2	60
13	Reciprocal Genetics: Identifying QTL for General and Specific Combining Abilities in Hybrids Between Multiparental Populations from Two Maize (<i>Zea mays</i> L.) Heterotic Groups. <i>Genetics</i> , 2017, 207, 1167-1180.	1.2	53
14	Predicting genomic selection efficiency to optimize calibration set and to assess prediction accuracy in highly structured populations. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2231-2247.	1.8	49
15	Genetic basis of phenotypic plasticity and genotype \times environment interactions in a multi-parental tomato population. <i>Journal of Experimental Botany</i> , 2020, 71, 5365-5376.	2.4	49
16	Usefulness Criterion and Post-selection Parental Contributions in Multi-parental Crosses: Application to Polygenic Trait Introgression. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1469-1479.	0.8	45
17	Disentangling group specific QTL allele effects from genetic background epistasis using admixed individuals in GWAS: An application to maize flowering. <i>PLoS Genetics</i> , 2020, 16, e1008241.	1.5	44
18	Detection of marker-QTL associations by studying change in marker frequencies with selection. <i>Theoretical and Applied Genetics</i> , 2007, 114, 669-681.	1.8	43

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19	General and specific combining abilities in a maize (<i>Zea mays</i> L.) test-cross hybrid panel: relative importance of population structure and genetic divergence between parents. <i>Theoretical and Applied Genetics</i> , 2017, 130, 403-417.	1.8	43
20	Genomic selection efficiency and a priori estimation of accuracy in a structured dent maize panel. <i>Theoretical and Applied Genetics</i> , 2019, 132, 81-96.	1.8	42
21	Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2313-2331.	1.8	41
22	Combined linkage and linkage disequilibrium QTL mapping in multiple families of maize (<i>Zea mays</i> L.) line crosses highlights complementarities between models based on parental haplotype and single locus polymorphism. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2717-2736.	1.8	40
23	Improving Short- and Long-Term Genetic Gain by Accounting for Within-Family Variance in Optimal Cross-Selection. <i>Frontiers in Genetics</i> , 2019, 10, 1006.	1.1	40
24	Genotyping-by-sequencing highlights original diversity patterns within a European collection of 1191 maize flint lines, as compared to the maize USDA genebank. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2165-2189.	1.8	39
25	Number and Fitness of Selected Individuals in Marker-Assisted and Phenotypic Recurrent Selection. <i>Crop Science</i> , 2006, 46, 1972-1980.	0.8	38
26	Optimized breeding strategies to harness genetic resources with different performance levels. <i>BMC Genomics</i> , 2020, 21, 349.	1.2	38
27	A method to optimize selection on multiple identified quantitative trait loci. <i>Genetics Selection Evolution</i> , 2002, 34, 145-70.	1.2	30
28	Training set optimization of genomic prediction by means of EthAcc. <i>PLoS ONE</i> , 2019, 14, e0205629.	1.1	29
29	Assessment of breeding programs sustainability: application of phenotypic and genomic indicators to a North European grain maize program. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1321-1334.	1.8	26
30	Marker-assisted selection efficiency in multiple connected populations: a simulation study based on the results of a QTL detection experiment in maize. <i>Euphytica</i> , 2008, 161, 71-84.	0.6	24
31	Genomic prediction with a maize collaborative panel: identification of genetic resources to enrich elite breeding programs. <i>Theoretical and Applied Genetics</i> , 2020, 133, 201-215.	1.8	23
32	Common gardens in teosintes reveal the establishment of a syndrome of adaptation to altitude. <i>PLoS Genetics</i> , 2019, 15, e1008512.	1.5	22
33	Revisiting hybrid breeding designs using genomic predictions: simulations highlight the superiority of incomplete factorials between segregating families over topcross designs. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1995-2010.	1.8	20
34	Genomic prediction of hybrid crops allows disentangling dominance and epistasis. <i>Genetics</i> , 2021, 218, .	1.2	20
35	Clusthaplo: a plug-in for MCQTL to enhance QTL detection using ancestral alleles in multi-cross design. <i>Theoretical and Applied Genetics</i> , 2014, 127, 921-933.	1.8	19
36	Accounting for Group-Specific Allele Effects and Admixture in Genomic Predictions: Theory and Experimental Evaluation in Maize. <i>Genetics</i> , 2020, 216, 27-41.	1.2	15

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37	Diversity and linkage disequilibrium features in a composite public/private dent maize panel: consequences for association genetics as evaluated from a case study using flowering time. <i>Theoretical and Applied Genetics</i> , 2012, 125, 731-747.	1.8	13
38	Quantitative trait loci mapping in hybrids between Dent and Flint maize multiparental populations reveals group-specific QTL for silage quality traits with variable pleiotropic effects on yield. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1523-1542.	1.8	12
39	Deciphering the Genetic Architecture of Plant Virus Resistance by GWAS, State of the Art and Potential Advances. <i>Cells</i> , 2021, 10, 3080.	1.8	12
40	Linkage Analysis and Association Mapping QTL Detection Models for Hybrids Between Multiparental Populations from Two Heterotic Groups: Application to Biomass Production in Maize (<i>Zea mays</i>) <i>Tj ETQq0 00sgBT /Overlock 10</i>		
41	Quantitative trait loci involved in the reproductive success of a parasitoid wasp. <i>Molecular Ecology</i> , 2020, 29, 3476-3493.	2.0	9
42	X-chromosome meiotic drive in <i>Drosophila simulans</i> : a QTL approach reveals the complex polygenic determinism of Paris drive suppression. <i>Heredity</i> , 2019, 122, 906-915.	1.2	8
43	Building a Calibration Set for Genomic Prediction, Characteristics to Be Considered, and Optimization Approaches. <i>Methods in Molecular Biology</i> , 2022, 2467, 77-112.	0.4	8
44	Improving genomic predictions with inbreeding and nonadditive effects in two admixed maize hybrid populations in single and multienvironment contexts. <i>Genetics</i> , 2022, 220, .	1.2	5