

Alain Charcosset

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

4,763
citations

109264

35
h-index

128225

60
g-index

69
all docs

69
docs citations

69
times ranked

4029
citing authors

#	ARTICLE	IF	CITATIONS
1	A Large Maize (<i>Zea mays</i> L.) SNP Genotyping Array: Development and Germplasm Genotyping, and Genetic Mapping to Compare with the B73 Reference Genome. PLoS ONE, 2011, 6, e28334.	1.1	523
2	Genetic Architecture of Flowering Time in Maize As Inferred From Quantitative Trait Loci Meta-analysis and Synteny Conservation With the Rice Genome. Genetics, 2004, 168, 2169-2185.	1.2	353
3	Marker-Assisted Introgression of Quantitative Trait Loci. Genetics, 1997, 147, 1469-1485.	1.2	268
4	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.). Genetics, 2012, 192, 715-728.	1.2	258
5	Maize Adaptation to Temperate Climate: Relationship Between Population Structure and Polymorphism in the Dwarf8 Gene. Genetics, 2006, 172, 2449-2463.	1.2	204
6	Intraspecific variation of recombination rate in maize. Genome Biology, 2013, 14, R103.	13.9	176
7	Maize introduction into Europe: the history reviewed in the light of molecular data. Theoretical and Applied Genetics, 2003, 106, 895-903.	1.8	162
8	Genomic prediction of maize yield across European environmental conditions. Nature Genetics, 2019, 51, 952-956.	9.4	157
9	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.). Genetics, 2012, 190, 795-811.	1.2	146
10	Genome-wide analysis of yield in Europe: allelic effects as functions of drought and heat scenarios. Plant Physiology, 2016, 172, pp.00621.2016.	2.3	140
11	Key Impact of <i>Vgt1</i> on Flowering Time Adaptation in Maize: Evidence From Association Mapping and Ecogeographical Information. Genetics, 2008, 178, 2433-2437.	1.2	129
12	Usefulness of Multiparental Populations of Maize (<i>Zea mays</i> L.) for Genome-Based Prediction. Genetics, 2014, 198, 3-16.	1.2	114
13	A European perspective on maize history. Comptes Rendus - Biologies, 2011, 334, 221-228.	0.1	111
14	Relationship between heterosis and heterozygosity at marker loci: a theoretical computation. Theoretical and Applied Genetics, 1991, 81, 571-575.	1.8	94
15	Linkage Disequilibrium with Linkage Analysis of Multiline Crosses Reveals Different Multiallelic QTL for Hybrid Performance in the Flint and Dent Heterotic Groups of Maize. Genetics, 2014, 198, 1717-1734.	1.2	89
16	Recovering Power in Association Mapping Panels with Variable Levels of Linkage Disequilibrium. Genetics, 2014, 197, 375-387.	1.2	89
17	Adaptation of Maize to Temperate Climates: Mid-Density Genome-Wide Association Genetics and Diversity Patterns Reveal Key Genomic Regions, with a Major Contribution of the <i>Vgt2</i> (ZCN8) Locus. PLoS ONE, 2013, 8, e71377.	1.1	83
18	Genetic diversity within and among maize populations: a comparison between isozyme and nuclear RFLP loci. Theoretical and Applied Genetics, 1998, 96, 577-587.	1.8	76

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19	The effect of population structure on the relationship between heterosis and heterozygosity at marker loci. <i>Theoretical and Applied Genetics</i> , 1994, 89-89, 336-343.	1.8	75
20	Flowering Time in Maize: Linkage and Epistasis at a Major Effect Locus. <i>Genetics</i> , 2012, 190, 1547-1562.	1.2	75
21	Large scale molecular analysis of traditional European maize populations. Relationships with morphological variation. <i>Heredity</i> , 2001, 86, 574-587.	1.2	74
22	Linkage Mapping of 1454 New Maize Candidate Gene Loci. <i>Genetics</i> , 2005, 170, 1957-1966.	1.2	74
23	Association mapping for cold tolerance in two large maize inbred panels. <i>BMC Plant Biology</i> , 2016, 16, 127.	1.6	73
24	Independent introductions and admixtures have contributed to adaptation of European maize and its American counterparts. <i>PLoS Genetics</i> , 2017, 13, e1006666.	1.5	73
25	Out of America: tracing the genetic footprints of the global diffusion of maize. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2671-2682.	1.8	72
26	Relationship between phenotypic and marker distances: theoretical and experimental investigations. <i>Heredity</i> , 1997, 79, 477-483.	1.2	61
27	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
28	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
29	RFLP diversity and relationships among traditional European maize populations. <i>Theoretical and Applied Genetics</i> , 2002, 105, 91-99.	1.8	46
30	Genotyping-by-sequencing and SNP-arrays are complementary for detecting quantitative trait loci by tagging different haplotypes in association studies. <i>BMC Plant Biology</i> , 2019, 19, 318.	1.6	45
31	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
32	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
33	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
34	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
35	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
36	Relationships among maize inbred lines and populations from European and North-American origins as estimated using RFLP markers. <i>Theoretical and Applied Genetics</i> , 1999, 99, 473-480.	1.8	41

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37	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
38	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
39	Evaluation of a DNA pooled-sampling strategy for estimating the RFLP diversity of maize populations. <i>Plant Molecular Biology Reporter</i> , 1999, 17, 123-138.	1.0	39
40	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
41	Number and Fitness of Selected Individuals in Marker-Assisted and Phenotypic Recurrent Selection. <i>Crop Science</i> , 2006, 46, 1972-1980.	0.8	38
42	Optimized breeding strategies to harness genetic resources with different performance levels. <i>BMC Genomics</i> , 2020, 21, 349.	1.2	38
43	Mapping of a spontaneous mutation for early flowering time in maize highlights contrasting allelic series at two-linked QTL on chromosome 8. <i>Theoretical and Applied Genetics</i> , 2005, 112, 1-11.	1.8	35
44	Study on Essential Derivation in Maize: III. Selection and Evaluation of a Panel of Single Nucleotide Polymorphism Loci for Use in European and North American Germplasm. <i>Crop Science</i> , 2015, 55, 1170-1180.	0.8	33
45	Sequence analysis of European maize inbred line F2 provides new insights into molecular and chromosomal characteristics of presence/absence variants. <i>BMC Genomics</i> , 2018, 19, 119.	1.2	27
46	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
47	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
48	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
49	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
50	Genomic prediction of hybrid crops allows disentangling dominance and epistasis. <i>Genetics</i> , 2021, 218, .	1.2	20
51	Physiological adaptive traits are a potential allele reservoir for maize genetic progress under challenging conditions. <i>Nature Communications</i> , 2022, 13, .	5.8	19
52	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
53	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
54	Efficient ReML inference in variance component mixed models using a Min-Max algorithm. <i>PLoS Computational Biology</i> , 2022, 18, e1009659.	1.5	13

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55	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
56	A systems genetics approach reveals environment-dependent associations between SNPs, protein coexpression, and drought-related traits in maize. <i>Genome Research</i> , 2020, 30, 1593-1604.	2.4	10
57	Deciphering the Genetic Diversity of Landraces With High-Throughput SNP Genotyping of DNA Bulks: Methodology and Application to the Maize 50k Array. <i>Frontiers in Plant Science</i> , 2020, 11, 568699.	1.7	9
58	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
59	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
60	Estimation of the Relatedness Coefficients from Biallelic Markers, Application in Plant Mating Designs. <i>Biometrics</i> , 2017, 73, 885-894.	0.8	1