

Jean-Luc Jannink

List of Publications by Year in descending order

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176
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205
docs citations

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9636
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Development of High-Density Genetic Maps for Barley and Wheat Using a Novel Two-Enzyme Genotyping-by-Sequencing Approach. PLoS ONE, 2012, 7, e32253. | 1.1 | 1,685 |
| 2 | Genomic Selection for Crop Improvement. Crop Science, 2009, 49, 1-12. | 0.8 | 1,266 |
| 3 | Genomic selection in plant breeding: from theory to practice. Briefings in Functional Genomics, 2010, 9, 166-177. | 1.3 | 996 |
| 4 | Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. Plant Genome, 2012, 5, . | 1.6 | 556 |
| 5 | Plant Breeding with Genomic Selection: Gain per Unit Time and Cost. Crop Science, 2010, 50, 1681-1690. | 0.8 | 547 |
| 6 | Genomic Selection in Plant Breeding: A Comparison of Models. Crop Science, 2012, 52, 146-160. | 0.8 | 546 |
| 7 | Genomic Selection and Association Mapping in Rice (<i>Oryza sativa</i>): Effect of Trait Genetic Architecture, Training Population Composition, Marker Number and Statistical Model on Accuracy of Rice Genomic Selection in Elite, Tropical Rice Breeding Lines. PLoS Genetics, 2015, 11, e1004982. | 1.5 | 425 |
| 8 | Shrinkage Estimation of the Realized Relationship Matrix. G3: Genes, Genomes, Genetics, 2012, 2, 1405-1413. | 0.8 | 420 |
| 9 | Genomic Selection in Plant Breeding. Advances in Agronomy, 2011, 110, 77-123. | 2.4 | 395 |
| 10 | Multiple-Trait Genomic Selection Methods Increase Genetic Value Prediction Accuracy. Genetics, 2012, 192, 1513-1522. | 1.2 | 372 |
| 11 | Factors Affecting Accuracy From Genomic Selection in Populations Derived From Multiple Inbred Lines: A Barley Case Study. Genetics, 2009, 182, 355-364. | 1.2 | 362 |
| 12 | Integrating environmental covariates and crop modeling into the genomic selection framework to predict genotype by environment interactions. Theoretical and Applied Genetics, 2014, 127, 463-480. | 1.8 | 296 |
| 13 | Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. Heredity, 2016, 116, 395-408. | 1.2 | 296 |
| 14 | Perspectives for Genomic Selection Applications and Research in Plants. Crop Science, 2015, 55, 1-12. | 0.8 | 290 |
| 15 | Training set optimization under population structure in genomic selection. Theoretical and Applied Genetics, 2015, 128, 145-158. | 1.8 | 284 |
| 16 | Genomic Selection in Plant Breeding. Methods in Molecular Biology, 2014, 1145, 117-130. | 0.4 | 275 |
| 17 | Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker \times Environment Interaction Genomic Selection Model. G3: Genes, Genomes, Genetics, 2015, 5, 569-582. | 0.8 | 266 |
| 18 | Genomic Selection Accuracy for Grain Quality Traits in Biparental Wheat Populations. Crop Science, 2011, 51, 2597-2606. | 0.8 | 255 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Effectiveness of Genomic Prediction of Maize Hybrid Performance in Different Breeding Populations and Environments. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1427-1436. | 0.8 | 242 |
| 20 | Genomic Prediction in Maize Breeding Populations with Genotyping-by-Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1903-1926. | 0.8 | 235 |
| 21 | Population genetics of genomics-based crop improvement methods. <i>Trends in Genetics</i> , 2011, 27, 98-106. | 2.9 | 230 |
| 22 | Evaluation of Genomic Prediction Methods for Fusarium Head Blight Resistance in Wheat. <i>Plant Genome</i> , 2012, 5, 51-61. | 1.6 | 220 |
| 23 | Potential and Optimization of Genomic Selection for Fusarium Head Blight Resistance in Six-Row Barley. <i>Crop Science</i> , 2012, 52, 1609-1621. | 0.8 | 216 |
| 24 | Accuracy and Training Population Design for Genomic Selection on Quantitative Traits in Elite North American Oats. <i>Plant Genome</i> , 2011, 4, . | 1.6 | 214 |
| 25 | Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011, 4, 65. | 1.6 | 208 |
| 26 | Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011, 4, . | 1.6 | 206 |
| 27 | Dynamics of long-term genomic selection. <i>Genetics Selection Evolution</i> , 2010, 42, 35. | 1.2 | 193 |
| 28 | Genomic prediction in biparental tropical maize populations in water-stressed and well-watered environments using low-density and GBS SNPs. <i>Heredity</i> , 2015, 114, 291-299. | 1.2 | 187 |
| 29 | Genomic Predictability of Interconnected Biparental Maize Populations. <i>Genetics</i> , 2013, 194, 493-503. | 1.2 | 180 |
| 30 | Imputation of Unordered Markers and the Impact on Genomic Selection Accuracy. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 427-439. | 0.8 | 172 |
| 31 | Using complex plant pedigrees to map valuable genes. <i>Trends in Plant Science</i> , 2001, 6, 337-342. | 4.3 | 147 |
| 32 | Genomic Selection for Quantitative Adult Plant Stem Rust Resistance in Wheat. <i>Plant Genome</i> , 2014, 7, plantgenome2014.02.0006. | 1.6 | 143 |
| 33 | High-resolution mapping of resistance to cassava mosaic geminiviruses in cassava using genotyping-by-sequencing and its implications for breeding. <i>Virus Research</i> , 2014, 186, 87-96. | 1.1 | 143 |
| 34 | The emergence of whole genome association scans in barley. <i>Current Opinion in Plant Biology</i> , 2009, 12, 218-222. | 3.5 | 138 |
| 35 | Multitrait, Random Regression, or Simple Repeatability Model in High-Throughput Phenotyping Data Improve Genomic Prediction for Wheat Grain Yield. <i>Plant Genome</i> , 2017, 10, plantgenome2016.11.0111. | 1.6 | 138 |
| 36 | New DARt markers for oat provide enhanced map coverage and global germplasm characterization. <i>BMC Genomics</i> , 2009, 10, 39. | 1.2 | 135 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Identification and distribution of the NBS-LRR gene family in the Cassava genome. <i>BMC Genomics</i> , 2015, 16, 360. | 1.2 | 130 |
| 38 | Impact of Marker Ascertainment Bias on Genomic Selection Accuracy and Estimates of Genetic Diversity. <i>PLoS ONE</i> , 2013, 8, e74612. | 1.1 | 129 |
| 39 | Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016, 7, 1666. | 1.7 | 127 |
| 40 | Optimization of genomic selection training populations with a genetic algorithm. <i>Genetics Selection Evolution</i> , 2015, 47, 38. | 1.2 | 123 |
| 41 | Genome-Wide Association and Prediction Reveals Genetic Architecture of Cassava Mosaic Disease Resistance and Prospects for Rapid Genetic Improvement. <i>Plant Genome</i> , 2016, 9, plantgenome2015.11.0118. | 1.6 | 120 |
| 42 | Performance of Single Nucleotide Polymorphisms versus Haplotypes for Genome-Wide Association Analysis in Barley. <i>PLoS ONE</i> , 2010, 5, e14079. | 1.1 | 118 |
| 43 | Mapping Epistatic Quantitative Trait Loci With One-Dimensional Genome Searches. <i>Genetics</i> , 2001, 157, 445-454. | 1.2 | 115 |
| 44 | Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. <i>Crop Science</i> , 2010, 50, 556-566. | 0.8 | 106 |
| 45 | The Triticeae Toolbox: Combining Phenotype and Genotype Data to Advance Small-Grains Breeding. <i>Plant Genome</i> , 2016, 9, plantgenome2014.12.0099. | 1.6 | 104 |
| 46 | Relatedness and Genotype \times Environment Interaction Affect Prediction Accuracies in Genomic Selection: A Study in Cassava. <i>Crop Science</i> , 2013, 53, 1312-1325. | 0.8 | 102 |
| 47 | Prospects for Genomic Selection in Cassava Breeding. <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0015. | 1.6 | 101 |
| 48 | The use of unbalanced historical data for genomic selection in an international wheat breeding program. <i>Field Crops Research</i> , 2013, 154, 12-22. | 2.3 | 100 |
| 49 | Optimal Design of Preliminary Yield Trials with Genome-Wide Markers. <i>Crop Science</i> , 2014, 54, 48-59. | 0.8 | 100 |
| 50 | Introduction to a Special Issue on Genotype by Environment Interaction. <i>Crop Science</i> , 2016, 56, 2081-2089. | 0.8 | 92 |
| 51 | Genomic Selection in Plant Breeding: A Comparison of Models. <i>Crop Science</i> , 2012, 52, 146. | 0.8 | 85 |
| 52 | Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods for β -Glucan Concentration in Elite Oat. <i>Crop Science</i> , 2013, 53, 1894-1906. | 0.8 | 84 |
| 53 | Using mating designs to uncover QTL and the genetic architecture of complex traits. <i>Heredity</i> , 2006, 96, 139-149. | 1.2 | 83 |
| 54 | Accuracy of Genomic Selection Prediction in Barley Breeding Programs: A Simulation Study Based On the Real Single Nucleotide Polymorphism Data of Barley Breeding Lines. <i>Crop Science</i> , 2011, 51, 1915-1927. | 0.8 | 80 |

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|----|---|-----|-----------|
| 55 | Population structure and linkage disequilibrium in oat (<i>Avena sativa</i> L.): implications for genome-wide association studies. <i>Theoretical and Applied Genetics</i> , 2011, 122, 623-632. | 1.8 | 79 |
| 56 | SNP Discovery and Chromosome Anchoring Provide the First Physically-Anchored Hexaploid Oat Map and Reveal Synteny with Model Species. <i>PLoS ONE</i> , 2013, 8, e58068. | 1.1 | 73 |
| 57 | Mapping Quantitative Trait Loci in Plant Breeding Populations. <i>Crop Science</i> , 2003, 43, 829-834. | 0.8 | 72 |
| 58 | High-throughput phenotyping platforms enhance genomic selection for wheat grain yield across populations and cycles in early stage. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1705-1720. | 1.8 | 70 |
| 59 | Using Quantitative Trait Loci Results to Discriminate Among Crosses on the Basis of Their Progeny Mean and Variance. <i>Genetics</i> , 2007, 177, 567-576. | 1.2 | 69 |
| 60 | Genome-wide association mapping and genomic prediction for CBSD resistance in <i>Manihot esculenta</i> . <i>Scientific Reports</i> , 2018, 8, 1549. | 1.6 | 66 |
| 61 | Identifying Quantitative Trait Locus by Genetic Background Interactions in Association Studies. <i>Genetics</i> , 2007, 176, 553-561. | 1.2 | 65 |
| 62 | Using Genomic Prediction to Characterize Environments and Optimize Prediction Accuracy in Applied Breeding Data. <i>Crop Science</i> , 2013, 53, 921-933. | 0.8 | 65 |
| 63 | Genome-wide association study for oat (<i>Avena sativa</i> L.) beta-glucan concentration using germplasm of worldwide origin. <i>Theoretical and Applied Genetics</i> , 2012, 125, 1687-1696. | 1.8 | 63 |
| 64 | Genome-wide Association Mapping of Correlated Traits in Cassava: Dry Matter and Total Carotenoid Content. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0094. | 1.6 | 63 |
| 65 | Whole-genome prediction of reaction norms to environmental stress in bread wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314,rgBT /Overlock 10 2.3 62 | 1.7 | 62 |
| 66 | Breeding Value of Primary Synthetic Wheat Genotypes for Grain Yield. <i>PLoS ONE</i> , 2016, 11, e0162860. | 1.1 | 61 |
| 67 | Accuracy of genomic selection to predict maize single-crosses obtained through different mating designs. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1153-1162. | 1.8 | 56 |
| 68 | Population Genomics Related to Adaptation in Elite Oat Germplasm. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0103. | 1.6 | 55 |
| 69 | Genome-wide association study of grain shape variation among <i>Oryza sativa</i> L. germplasms based on elliptic Fourier analysis. <i>Molecular Breeding</i> , 2010, 25, 203-215. | 1.0 | 54 |
| 70 | Accuracies of univariate and multivariate genomic prediction models in African cassava. <i>Genetics Selection Evolution</i> , 2017, 49, 88. | 1.2 | 54 |
| 71 | Mapping Quantitative Trait Loci in Plant Breeding Populations. <i>Crop Science</i> , 2003, 43, 829. | 0.8 | 51 |
| 72 | Genetic Mapping Using Genotyping-by-Sequencing in the Clonally Propagated Cassava. <i>Crop Science</i> , 2014, 54, 1384-1396. | 0.8 | 50 |

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|----|---|-----|-----------|
| 73 | OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, . | 1.4 | 50 |
| 74 | Optimizing Seeding Rates for Winter Cereal Grains and Frost-Seeded Red Clover Intercrops. <i>Agronomy Journal</i> , 2006, 98, 1041-1049. | 0.9 | 49 |
| 75 | Rapid analyses of dry matter content and carotenoids in fresh cassava roots using a portable visible and near infrared spectrometer (Vis/NIRS). <i>PLoS ONE</i> , 2017, 12, e0188918. | 1.1 | 49 |
| 76 | Assessing the practical importance of weed evolution: a research agenda. <i>Weed Research</i> , 1997, 37, 237-246. | 0.8 | 48 |
| 77 | Planting Date Effects on Winter Triticale Dry Matter and Nitrogen Accumulation. <i>Agronomy Journal</i> , 2005, 97, 1333-1341. | 0.9 | 46 |
| 78 | Factors Affecting the Power of Haplotype Markers in Association Studies. <i>Plant Genome</i> , 2011, 4, 145-153. | 1.6 | 46 |
| 79 | Bayesian Modeling of Heterogeneous Error and Genotype \times Environment Interaction Variances. <i>Crop Science</i> , 2006, 46, 820-833. | 0.8 | 45 |
| 80 | Assessment of Power and False Discovery Rate in Genome-Wide Association Studies using the BarleyCAP Germplasm. <i>Crop Science</i> , 2011, 51, 52-59. | 0.8 | 45 |
| 81 | Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (<i>Avena sativa</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2963-2975. | 0.8 | 44 |
| 82 | Estimating allelic number and identity in state of QTLs in interconnected families. <i>Genetical Research</i> , 2003, 81, 133-144. | 0.3 | 43 |
| 83 | Selective Phenotyping to Accurately Map Quantitative Trait Loci. <i>Crop Science</i> , 2005, 45, 901-908. | 0.8 | 42 |
| 84 | Evaluation of Oat Kernel Size Uniformity. <i>Crop Science</i> , 2004, 44, 1178-1186. | 0.8 | 40 |
| 85 | In Vitro Bile Acid Binding of Flours from Oat Lines Varying in Percentage and Molecular Weight Distribution of β -Glucan. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 8797-8803. | 2.4 | 40 |
| 86 | Locally Epistatic Genomic Relationship Matrices for Genomic Association and Prediction. <i>Genetics</i> , 2015, 199, 857-871. | 1.2 | 40 |
| 87 | Molecular Weight Distribution of β -Glucan Affects Pasting Properties of Flour from Oat Lines with High and Typical Amounts of β -Glucan. <i>Cereal Chemistry</i> , 2007, 84, 471-479. | 1.1 | 36 |
| 88 | The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012, 5, 81-91. | 1.6 | 35 |
| 89 | Physical and Sensory Characteristics of Extruded Products Made from Two Oat Lines with Different β -Glucan Concentrations. <i>Cereal Chemistry</i> , 2006, 83, 692-699. | 1.1 | 34 |
| 90 | Marker-Based Estimates Reveal Significant Nonadditive Effects in Clonally Propagated Cassava (<i>Manihot esculenta</i>): Implications for the Prediction of Total Genetic Value and the Selection of Varieties. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3497-3506. | 0.8 | 34 |

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|-----|--|-----|-----------|
| 91 | Genome-wide association analysis reveals new insights into the genetic architecture of defensive, agro-morphological and quality-related traits in cassava. <i>Plant Molecular Biology</i> , 2022, 109, 195-213. | 2.0 | 33 |
| 92 | Evaluating Imputation Algorithms for Low-Depth Genotyping-By-Sequencing (GBS) Data. <i>PLoS ONE</i> , 2016, 11, e0160733. | 1.1 | 33 |
| 93 | Digestion Residues of Typical and High- β -Glucan Oat Flours Provide Substrates for in Vitro Fermentation. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 5306-5311. | 2.4 | 32 |
| 94 | In Vitro Bile Acid Binding Activity within Flour Fractions from Oat Lines with Typical and High β -Glucan Amounts. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 5142-5148. | 2.4 | 31 |
| 95 | A Simple Package to Script and Simulate Breeding Schemes: The Breeding Scheme Language. <i>Crop Science</i> , 2017, 57, 1347-1354. | 0.8 | 29 |
| 96 | Overview of QTL detection in plants and tests for synergistic epistatic interactions. <i>Genetica</i> , 2009, 136, 225-236. | 0.5 | 28 |
| 97 | Bayesian multilocus association mapping on ordinal and censored traits and its application to the analysis of genetic variation among <i>Oryza sativa</i> L. germplasms. <i>Theoretical and Applied Genetics</i> , 2009, 118, 865-880. | 1.8 | 28 |
| 98 | Genome-Wide Association Study of Resistance to Cassava Green Mite Pest and Related Traits in Cassava. <i>Crop Science</i> , 2018, 58, 1907-1918. | 0.8 | 28 |
| 99 | Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. <i>Genetics</i> , 2019, 213, 1237-1253. | 1.2 | 27 |
| 100 | Genomic Prediction in a Large African Maize Population. <i>Crop Science</i> , 2017, 57, 2361-2371. | 0.8 | 25 |
| 101 | Biomass Production and Nitrogen Accumulation in Pea, Oat, and Vetch Green Manure Mixtures. <i>Agronomy Journal</i> , 1996, 88, 231-240. | 0.9 | 24 |
| 102 | Optimal sampling of a population to determine QTL location, variance, and allelic number. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1434-1442. | 1.8 | 24 |
| 103 | Genetic Correlation, Genome-Wide Association and Genomic Prediction of Portable NIRS Predicted Carotenoids in Cassava Roots. <i>Frontiers in Plant Science</i> , 2019, 10, 1570. | 1.7 | 24 |
| 104 | Population Genetics of Sugar Kelp Throughout the Northeastern United States Using Genome-Wide Markers. <i>Frontiers in Marine Science</i> , 2020, 7, . | 1.2 | 24 |
| 105 | Title is missing!. <i>Euphytica</i> , 2001, 120, 291-300. | 0.6 | 23 |
| 106 | Expanding the Pool of PCR-Based Markers for Oat. <i>Crop Science</i> , 2005, 45, 2383-2387. | 0.8 | 23 |
| 107 | Selection for Nutritional Function and Agronomic Performance in Oat. <i>Crop Science</i> , 2007, 47, 2330-2339. | 0.8 | 23 |
| 108 | Marker Genotype Imputation in a Low-Marker-Density Panel with a High-Marker-Density Reference Panel: Accuracy Evaluation in Barley Breeding Lines. <i>Crop Science</i> , 2010, 50, 1269-1278. | 0.8 | 23 |

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|-----|--|-----|-----------|
| 109 | Genome-wide Association Study for Beta-glucan Concentration in Elite North American Oat. <i>Crop Science</i> , 2013, 53, 542-553. | 0.8 | 23 |
| 110 | Training Population Optimization for Prediction of Cassava Brown Streak Disease Resistance in West African Clones. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3903-3913. | 0.8 | 23 |
| 111 | GrainGenes: a data-rich repository for small grains genetics and genomics. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, . | 1.4 | 22 |
| 112 | Prediction of β -Glucan Concentration Based on Viscosity Evaluations of Raw Oat Flours from High β -Glucan and Traditional Oat Lines. <i>Cereal Chemistry</i> , 2004, 81, 434-443. | 1.1 | 21 |
| 113 | Pasting and Thermal Properties of Flours from Oat Lines with High and Typical Amounts of β -Glucan. <i>Cereal Chemistry</i> , 2004, 81, 686-692. | 1.1 | 20 |
| 114 | Improving Genomic Prediction in Cassava Field Experiments Using Spatial Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 53-62. | 0.8 | 20 |
| 115 | Data-driven decentralized breeding increases prediction accuracy in a challenging crop production environment. <i>Communications Biology</i> , 2021, 4, 944. | 2.0 | 20 |
| 116 | Multi-omics prediction of oat agronomic and seed nutritional traits across environments and in distantly related populations. <i>Theoretical and Applied Genetics</i> , 2021, 134, 4043-4054. | 1.8 | 20 |
| 117 | On the Metropolis-Hastings Acceptance Probability to Add or Drop a Quantitative Trait Locus in Markov Chain Monte Carlo-Based Bayesian Analyses. <i>Genetics</i> , 2004, 166, 641-643. | 1.2 | 19 |
| 118 | Genetic Variation and Trait Correlations in an East African Cassava Breeding Population for Genomic Selection. <i>Crop Science</i> , 2019, 59, 460-473. | 0.8 | 19 |
| 119 | Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. <i>Plant Biotechnology Journal</i> , 2020, 18, 1211-1222. | 4.1 | 19 |
| 120 | solGS: a web-based tool for genomic selection. <i>BMC Bioinformatics</i> , 2014, 15, 398. | 1.2 | 18 |
| 121 | Genomic Prediction using Phenotypes from Pedigreed Lines with No Marker Data. <i>Crop Science</i> , 2016, 56, 957-964. | 0.8 | 18 |
| 122 | Locally epistatic models for genome-wide prediction and association by importance sampling. <i>Genetics Selection Evolution</i> , 2017, 49, 74. | 1.2 | 18 |
| 123 | A framework for genomics-informed ecophysiological modeling in plants. <i>Journal of Experimental Botany</i> , 2019, 70, 2561-2574. | 2.4 | 18 |
| 124 | Association mapping in common bean revealed regions associated with Anthracnose and Angular Leaf Spot resistance. <i>Scientia Agricola</i> , 2019, 76, 321-327. | 0.6 | 18 |
| 125 | Genome wide association study of 5 agronomic traits in olive (<i>Olea europaea</i> L.). <i>Scientific Reports</i> , 2019, 9, 18764. | 1.6 | 18 |
| 126 | Influence of Genotype and Environment on Wheat Grain Fructan Content. <i>Crop Science</i> , 2019, 59, 190-198. | 0.8 | 18 |

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|-----|---|-----|-----------|
| 127 | Wheat Fructans: A Potential Breeding Target for Nutritionally Improved, Climate-Resilient Varieties. <i>Crop Science</i> , 2017, 57, 1624-1640. | 0.8 | 17 |
| 128 | Translating insights from the seed metabolome into improved prediction for lipid-composition traits in oat (<i>Avena sativa</i> L.). <i>Genetics</i> , 2021, 217, . | 1.2 | 17 |
| 129 | Breedbase: a digital ecosystem for modern plant breeding. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, . | 0.8 | 17 |
| 130 | A Low Resolution Epistasis Mapping Approach To Identify Chromosome Arm Interactions in Allohexaploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 675-684. | 0.8 | 16 |
| 131 | Responses to Selection for Partial Resistance to Crown Rust in Oat. <i>Crop Science</i> , 2006, 46, 1260-1265. | 0.8 | 15 |
| 132 | Recurrent genomic selection for wheat grain fructans. <i>Crop Science</i> , 2020, 60, 1499-1512. | 0.8 | 15 |
| 133 | Improving root characterisation for genomic prediction in cassava. <i>Scientific Reports</i> , 2020, 10, 8003. | 1.6 | 15 |
| 134 | An algorithm for deciding the number of clusters and validation using simulated data with application to exploring crop population structure. <i>Annals of Applied Statistics</i> , 2013, 7, . | 0.5 | 14 |
| 135 | Improving Genomic Prediction for Seed Quality Traits in Oat (<i>Avena sativa</i> L.) Using Trait-Specific Relationship Matrices. <i>Frontiers in Genetics</i> , 2021, 12, 643733. | 1.1 | 14 |
| 136 | Exploring genotype by environment interaction on cassava yield and yield related traits using classical statistical methods. <i>PLoS ONE</i> , 2022, 17, e0268189. | 1.1 | 14 |
| 137 | QTL-Genetic background interaction: predicting inbred progeny value. <i>Euphytica</i> , 2008, 161, 61-69. | 0.6 | 13 |
| 138 | An alternative covariance estimator to investigate genetic heterogeneity in populations. <i>Genetics Selection Evolution</i> , 2015, 47, 93. | 1.2 | 13 |
| 139 | Comparative analysis of morphometric traits of farmed sugar kelp and skinny kelp, <i>Saccharina</i> spp., strains from the Northwest Atlantic. <i>Journal of the World Aquaculture Society</i> , 2021, 52, 1059-1068. | 1.2 | 13 |
| 140 | Genomic mating in outbred species: predicting cross usefulness with additive and total genetic covariance matrices. <i>Genetics</i> , 2021, 219, . | 1.2 | 13 |
| 141 | Comparison of Transcript Profiles in Wild-Type and $\alpha 2$ Maize Endosperm in Different Genetic Backgrounds. <i>Crop Science</i> , 2007, 47, S-45. | 0.8 | 12 |
| 142 | Impact of Mislabeling on Genomic Selection in Cassava Breeding. <i>Crop Science</i> , 2018, 58, 1470-1480. | 0.8 | 12 |
| 143 | Homeologous Epistasis in Wheat: The Search for an Immortal Hybrid. <i>Genetics</i> , 2019, 211, 1105-1122. | 1.2 | 12 |
| 144 | Genome-wide association mapping and genomic prediction of yield-related traits and starch pasting properties in cassava. <i>Theoretical and Applied Genetics</i> , 2022, 135, 145-171. | 1.8 | 12 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 145 | Planting Date Effects on Winter Triticale Grain Yield and Yield Components. <i>Crop Science</i> , 2006, 46, 1218-1224. | 0.8 | 11 |
| 146 | Impact of Dry Solids and Bile Acid Concentrations on Bile Acid Binding Capacity of Extruded Oat Cereals. <i>Journal of Agricultural and Food Chemistry</i> , 2008, 56, 8672-8679. | 2.4 | 11 |
| 147 | Resistance to Multiple Temperate and Tropical Stem and Sheath Diseases of Rice. <i>Plant Genome</i> , 2018, 11, 170029. | 1.6 | 11 |
| 148 | RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, . | 0.8 | 11 |
| 149 | Textural and Bile Acid Binding Properties of Muffins Impacted by Oat β -Glucan with Different Molecular Weights. <i>Cereal Chemistry</i> , 2011, 88, 564-569. | 1.1 | 10 |
| 150 | A statistical framework for detecting mislabeled and contaminated samples using shallow-depth sequence data. <i>BMC Bioinformatics</i> , 2018, 19, 478. | 1.2 | 10 |
| 151 | Regional Heritability Mapping Provides Insights into Dry Matter Content in African White and Yellow Cassava Populations. <i>Plant Genome</i> , 2018, 11, 170050. | 1.6 | 10 |
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