

Jean-Luc Jannink

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

181
papers

12,584
citations

53
h-index

110
g-index

205
ext. papers

15,894
ext. citations

3.7
avg, IF

6.77
L-index

#	Paper	IF	Citations
181	Generalizable approaches for genomic prediction of metabolites in plants.. <i>Plant Genome</i> , 2022 , e20205	4.4	0
180	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	6	4
179	Genome-wide association mapping and genomic prediction of yield-related traits and starch pasting properties in cassava. <i>Theoretical and Applied Genetics</i> , 2021 , 135, 145	6	1
178	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	2.5	1
177	Multi-Species Genomics-Enabled Selection for Improving Agroecosystems Across Space and Time. <i>Frontiers in Plant Science</i> , 2021 , 12, 665349	6.2	4
176	Outlook of Cassava Brown Streak Disease Assessment: Perspectives of the Screening Methods of Breeders and Pathologists. <i>Frontiers in Plant Science</i> , 2021 , 12, 648436	6.2	
175	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,	4	7
174	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	4.5	3
173	Data-driven decentralized breeding increases prediction accuracy in a challenging crop production environment. <i>Communications Biology</i> , 2021 , 4, 944	6.7	7
172	RNA polymerase mapping in plants identifies intergenic regulatory elements enriched in causal variants. <i>G3: Genes, Genomes, Genetics</i> , 2021 , 11,	3.2	2
171	A population based expression atlas provides insights into disease resistance and other physiological traits in cassava (<i>Manihot esculenta</i> Crantz). <i>Scientific Reports</i> , 2021 , 11, 23520	4.9	
170	Selection for seed size has uneven effects on specialized metabolite abundance in oat (<i>Avena sativa</i> L.). <i>G3: Genes, Genomes, Genetics</i> , 2021 ,	3.2	1
169	Using public databases for genomic prediction of tropical maize lines. <i>Plant Breeding</i> , 2020 , 139, 697-707	2.4	3
168	Improving root characterisation for genomic prediction in cassava. <i>Scientific Reports</i> , 2020 , 10, 8003	4.9	8
167	Genomic prediction and quantitative trait locus discovery in a cassava training population constructed from multiple breeding stages. <i>Crop Science</i> , 2020 , 60, 896-913	2.4	6
166	Heritable temporal gene expression patterns correlate with metabolomic seed content in developing hexaploid oat seed. <i>Plant Biotechnology Journal</i> , 2020 , 18, 1211-1222	11.6	8
165	Recurrent genomic selection for wheat grain fructans. <i>Crop Science</i> , 2020 , 60, 1499-1512	2.4	11

164	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> , 2020 , 1	4.6	12
163	Population Genetics of Sugar Kelp Throughout the Northeastern United States Using Genome-Wide Markers. <i>Frontiers in Marine Science</i> , 2020 , 7,	4.5	8
162	Homeologous Epistasis in Wheat: The Search for an Immortal Hybrid. <i>Genetics</i> , 2019 , 211, 1105-1122	4	9
161	Genetic Variation and Trait Correlations in an East African Cassava Breeding Population for Genomic Selection. <i>Crop Science</i> , 2019 , 59, 460-473	2.4	9
160	A framework for genomics-informed ecophysiological modeling in plants. <i>Journal of Experimental Botany</i> , 2019 , 70, 2561-2574	7	9
159	Association mapping in common bean revealed regions associated with Anthracnose and Angular Leaf Spot resistance. <i>Scientia Agricola</i> , 2019 , 76, 321-327	2.5	10
158	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	6	42
157	GrainGenes: centralized small grain resources and digital platform for geneticists and breeders. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	27
156	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (L.). <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 2963-2975	3.2	20
155	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	4	16
154	Genome wide association study of 5 agronomic traits in olive (<i>Olea europaea</i> L.). <i>Scientific Reports</i> , 2019 , 9, 18764	4.9	9
153	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	6.2	12
152	Influence of Genotype and Environment on Wheat Grain Fructan Content. <i>Crop Science</i> , 2019 , 59, 190-198.	4	12
151	Prediction of Subgenome Additive and Interaction Effects in Allohexaploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 685-698	3.2	7
150	A Low Resolution Epistasis Mapping Approach To Identify Chromosome Arm Interactions in Allohexaploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 675-684	3.2	9
149	Genome-wide association mapping and genomic prediction for CBSD resistance in <i>Manihot esculenta</i> . <i>Scientific Reports</i> , 2018 , 8, 1549	4.9	45
148	Accuracy of genomic selection to predict maize single-crosses obtained through different mating designs. <i>Theoretical and Applied Genetics</i> , 2018 , 131, 1153-1162	6	34
147	Improving Genomic Prediction in Cassava Field Experiments by Accounting for Interplot Competition. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 933-944	3.2	4

146	Genome-Wide Association Studies and Heritability Estimation in the Functional Genomics Era. <i>Population Genomics</i> , 2018 , 361-425	1.4	4
145	Improving Genomic Prediction in Cassava Field Experiments Using Spatial Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 53-62	3.2	15
144	Genome-Wide Association Study of Resistance to Cassava Green Mite Pest and Related Traits in Cassava. <i>Crop Science</i> , 2018 , 58, 1907-1918	2.4	11
143	Whole-genome prediction of reaction norms to environmental stress in bread wheat (<i>Triticum aestivum</i> L.) by genomic random regression. <i>Field Crops Research</i> , 2018 , 216, 32-41	5.5	31
142	Resistance to Multiple Temperate and Tropical Stem and Sheath Diseases of Rice. <i>Plant Genome</i> , 2018 , 11, 170029	4.4	5
141	A Low-Cost Automated System for High-Throughput Phenotyping of Single Oat Seeds. <i>The Plant Phenome Journal</i> , 2018 , 1, 1-13	5	5
140	A statistical framework for detecting mislabeled and contaminated samples using shallow-depth sequence data. <i>BMC Bioinformatics</i> , 2018 , 19, 478	3.6	5
139	Impact of Mislabeled on Genomic Selection in Cassava Breeding. <i>Crop Science</i> , 2018 , 58, 1470-1480	2.4	6
138	Regional Heritability Mapping Provides Insights into Dry Matter Content in African White and Yellow Cassava Populations. <i>Plant Genome</i> , 2018 , 11, 170050	4.4	4
137	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	3.2	17
136	Wheat Fructans: A Potential Breeding Target for Nutritionally Improved, Climate-Resilient Varieties. <i>Crop Science</i> , 2017 , 57, 1624-1640	2.4	16
135	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	4.4	84
134	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	3.7	24
133	Locally epistatic models for genome-wide prediction and association by importance sampling. <i>Genetics Selection Evolution</i> , 2017 , 49, 74	4.9	14
132	Prospects for Genomic Selection in Cassava Breeding. <i>Plant Genome</i> , 2017 , 10, plantgenome2017.03.0014	4.4	63
131	A Simple Package to Script and Simulate Breeding Schemes: The Breeding Scheme Language. <i>Crop Science</i> , 2017 , 57, 1347-1354	2.4	20
130	Genomic Prediction in a Large African Maize Population. <i>Crop Science</i> , 2017 , 57, 2361-2371	2.4	17
129	Accuracies of univariate and multivariate genomic prediction models in African cassava. <i>Genetics Selection Evolution</i> , 2017 , 49, 88	4.9	31

128	Genome-Wide Association Mapping of Correlated Traits in Cassava: Dry Matter and Total Carotenoid Content. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.09.0094	4.4	40
127	Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. <i>Heredity</i> , 2016 , 116, 395-408	3.6	173
126	Evaluating Imputation Algorithms for Low-Depth Genotyping-By-Sequencing (GBS) Data. <i>PLoS ONE</i> , 2016 , 11, e0160733	3.7	22
125	Genomic Prediction using Phenotypes from Pedigreed Lines with No Marker Data. <i>Crop Science</i> , 2016 , 56, 957-964	2.4	14
124	Comparison of Phenotyping Methods for Resistance to Stem Rot and Aggregated Sheath Spot in Rice. <i>Crop Science</i> , 2016 , 56, 1619-1627	2.4	5
123	Marker-Based Estimates Reveal Significant Nonadditive Effects in Clonally Propagated Cassava (): Implications for the Prediction of Total Genetic Value and the Selection of Varieties. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3497-3506	3.2	21
122	The Triticeae Toolbox: Combining Phenotype and Genotype Data to Advance Small-Grains Breeding. <i>Plant Genome</i> , 2016 , 9, plantgenome2014.12.0099	4.4	52
121	Population Genomics Related to Adaptation in Elite Oat Germplasm. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.10.0101	4.4	35
120	Introduction to a Special Issue on Genotype by Environment Interaction. <i>Crop Science</i> , 2016 , 56, 2081-2089	4.4	51
119	Breeding Value of Primary Synthetic Wheat Genotypes for Grain Yield. <i>PLoS ONE</i> , 2016 , 11, e0162860	3.7	33
118	Genome-Enabled Prediction Models for Yield Related Traits in Chickpea. <i>Frontiers in Plant Science</i> , 2016 , 7, 1666	6.2	80
117	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	4.4	74
116	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. <i>PLoS Genetics</i> , 2015 , 11, e1004982	6	277
115	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, 291-9	3.6	131
114	Training set optimization under population structure in genomic selection. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 145-58	6	207
113	Perspectives for Genomic Selection Applications and Research in Plants. <i>Crop Science</i> , 2015 , 55, 1-12	2.4	179
112	Optimization of genomic selection training populations with a genetic algorithm. <i>Genetics Selection Evolution</i> , 2015 , 47, 38	4.9	84
111	Increased prediction accuracy in wheat breeding trials using a marker \times environment interaction genomic selection model. <i>G3: Genes, Genomes, Genetics</i> , 2015 , 5, 569-82	3.2	155

110	An alternative covariance estimator to investigate genetic heterogeneity in populations. <i>Genetics Selection Evolution</i> , 2015 , 47, 93	4.9	10
109	Locally epistatic genomic relationship matrices for genomic association and prediction. <i>Genetics</i> , 2015 , 199, 857-71	4	29
108	Identification and distribution of the NBS-LRR gene family in the Cassava genome. <i>BMC Genomics</i> , 2015 , 16, 360	4.5	96
107	Integrating environmental covariates and crop modeling into the genomic selection framework to predict genotype by environment interactions. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 463-80	6	213
106	Genomic selection in plant breeding. <i>Methods in Molecular Biology</i> , 2014 , 1145, 117-30	1.4	26
105	Genetic Mapping Using Genotyping-by-Sequencing in the Clonally Propagated Cassava. <i>Crop Science</i> , 2014 , 54, 1384-1396	2.4	41
104	Optimal Design of Preliminary Yield Trials with Genome-Wide Markers. <i>Crop Science</i> , 2014 , 54, 48-59	2.4	74
103	Genomic Selection for Quantitative Adult Plant Stem Rust Resistance in Wheat. <i>Plant Genome</i> , 2014 , 7, plantgenome2014.02.0006	4.4	98
102	Ensemble learning with trees and rules: Supervised, semi-supervised, unsupervised. <i>Intelligent Data Analysis</i> , 2014 , 18, 857-872	1.1	4
101	Microenzymatic Evaluation of Oat (<i>Avena sativa</i> L.) β Glucan for High-Throughput Phenotyping. <i>Cereal Chemistry</i> , 2014 , 91, 183-188	2.4	2
100	solGS: a web-based tool for genomic selection. <i>BMC Bioinformatics</i> , 2014 , 15, 398	3.6	12
99	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	6.4	92
98	Genomic predictability of interconnected biparental maize populations. <i>Genetics</i> , 2013 , 194, 493-503	4	142
97	The use of unbalanced historical data for genomic selection in an international wheat breeding program. <i>Field Crops Research</i> , 2013 , 154, 12-22	5.5	76
96	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	3.7	60
95	Imputation of unordered markers and the impact on genomic selection accuracy. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 427-39	3.2	119
94	Genomic prediction in maize breeding populations with genotyping-by-sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 1903-26	3.2	170
93	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,	2.1	12

92	Using Genomic Prediction to Characterize Environments and Optimize Prediction Accuracy in Applied Breeding Data. <i>Crop Science</i> , 2013 , 53, 921-933	2.4	53
91	Genome-wide Association Study for Beta-glucan Concentration in Elite North American Oat. <i>Crop Science</i> , 2013 , 53, 542-553	2.4	17
90	Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods for β -Glucan Concentration in Elite Oat. <i>Crop Science</i> , 2013 , 53, 1894-1906	2.4	67
89	Relatedness and Genotype \times Environment Interaction Affect Prediction Accuracies in Genomic Selection: A Study in Cassava. <i>Crop Science</i> , 2013 , 53, 1312-1325	2.4	84
88	Impact of marker ascertainment bias on genomic selection accuracy and estimates of genetic diversity. <i>PLoS ONE</i> , 2013 , 8, e74612	3.7	104
87	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, 1687-96	6	48
86	Multiple-trait genomic selection methods increase genetic value prediction accuracy. <i>Genetics</i> , 2012 , 192, 1513-22	4	254
85	The Hordeum Toolbox: The Barley Coordinated Agricultural Project Genotype and Phenotype Resource. <i>Plant Genome</i> , 2012 , 5, 81-91	4.4	29
84	Genomic Selection in Plant Breeding: A Comparison of Models. <i>Crop Science</i> , 2012 , 52, 146-160	2.4	402
83	Potential and Optimization of Genomic Selection for Fusarium Head Blight Resistance in Six-Row Barley. <i>Crop Science</i> , 2012 , 52, 1609-1621	2.4	165
82	Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. <i>PLoS ONE</i> , 2012 , 7, e32253	3.7	1147
81	Shrinkage estimation of the realized relationship matrix. <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 1405-13	3.2	257
80	Effectiveness of genomic prediction of maize hybrid performance in different breeding populations and environments. <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 1427-36	3.2	166
79	Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. <i>Plant Genome</i> , 2012 , 5,	4.4	411
78	Evaluation of Genomic Prediction Methods for Fusarium Head Blight Resistance in Wheat. <i>Plant Genome</i> , 2012 , 5, 51-61	4.4	166
77	Genomic Selection in Plant Breeding: A Comparison of Models 2012 , 52, 146		17
76	Genomic Selection in Plant Breeding. <i>Advances in Agronomy</i> , 2011 , 110, 77-123	7.7	291
75	Factors Affecting the Power of Haplotype Markers in Association Studies. <i>Plant Genome</i> , 2011 , 4, 145-153	4.4	29

74	Assessment of Power and False Discovery Rate in Genome-Wide Association Studies using the BarleyCAP Germplasm. <i>Crop Science</i> , 2011 , 51, 52-59	2.4	41
73	Accuracy and Training Population Design for Genomic Selection on Quantitative Traits in Elite North American Oats. <i>Plant Genome</i> , 2011 , 4,	4.4	171
72	Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011 , 4,	4.4	152
71	Population genetics of genomics-based crop improvement methods. <i>Trends in Genetics</i> , 2011 , 27, 98-106	3.5	181
70	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, 623-32	6	54
69	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	2.4	58
68	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	2.4	7
67	Genomic Selection Accuracy for Grain Quality Traits in Biparental Wheat Populations. <i>Crop Science</i> , 2011 , 51, 2597-2606	2.4	193
66	Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011 , 4, 65	4.4	148
65	Genomic selection in plant breeding: from theory to practice. <i>Briefings in Functional Genomics</i> , 2010 , 9, 166-77	4.9	736
64	Population Structure and Linkage Disequilibrium in U.S. Barley Germplasm: Implications for Association Mapping. <i>Crop Science</i> , 2010 , 50, 556-566	2.4	88
63	Plant Breeding with Genomic Selection: Gain per Unit Time and Cost. <i>Crop Science</i> , 2010 , 50, 1681-1690	2.4	415
62	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	2.4	19
61	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	3.4	41
60	Dynamics of long-term genomic selection. <i>Genetics Selection Evolution</i> , 2010 , 42, 35	4.9	134
59	Performance of single nucleotide polymorphisms versus haplotypes for genome-wide association analysis in barley. <i>PLoS ONE</i> , 2010 , 5, e14079	3.7	90
58	Factors affecting accuracy from genomic selection in populations derived from multiple inbred lines: a Barley case study. <i>Genetics</i> , 2009 , 182, 355-64	4	292
57	The emergence of whole genome association scans in barley. <i>Current Opinion in Plant Biology</i> , 2009 , 12, 218-22	9.9	123

56	New DArT markers for oat provide enhanced map coverage and global germplasm characterization. <i>BMC Genomics</i> , 2009 , 10, 39	4.5	109
55	Overview of QTL detection in plants and tests for synergistic epistatic interactions. <i>Genetica</i> , 2009 , 136, 225-36	1.5	24
54	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, 865-80	6	21
53	Genomic Selection for Crop Improvement. <i>Crop Science</i> , 2009 , 49, 1-12	2.4	939
52	Diversity and Mega-Targets of Selection from the Characterization of a Barley Collection. <i>Crop Science</i> , 2009 , 49, 483-497	2.4	3
51	Selective Advance for Accelerated Development of Recombinant Inbred QTL Mapping Populations. <i>Crop Science</i> , 2009 , 49, 1284-1294	2.4	4
50	Marker Imputation in Barley Association Studies. <i>Plant Genome</i> , 2009 , 2,	4.4	10
49	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, 8672-9	5.7	10
48	Size Distributions of Different Orders of Kernels within the Oat Spikelet. <i>Crop Science</i> , 2008 , 48, 298-304	2.4	5
47	QTL \times genetic background interaction: predicting inbred progeny value. <i>Euphytica</i> , 2008 , 161, 61-69	2.1	13
46	Digestion residues of typical and high-beta-glucan oat flours provide substrates for in vitro fermentation. <i>Journal of Agricultural and Food Chemistry</i> , 2007 , 55, 5306-11	5.7	25
45	Comparison of Transcript Profiles in Wild-Type and $\alpha 2$ Maize Endosperm in Different Genetic Backgrounds. <i>Crop Science</i> , 2007 , 47, S-45	2.4	12
44	Selection for Nutritional Function and Agronomic Performance in Oat. <i>Crop Science</i> , 2007 , 47, 2330-2339	2.4	15
43	Molecular Weight Distribution of (1- β)-(1- α)- 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	2.4	30
42	Identifying quantitative trait locus by genetic background interactions in association studies. <i>Genetics</i> , 2007 , 176, 553-61	4	51
41	Using quantitative trait loci results to discriminate among crosses on the basis of their progeny mean and variance. <i>Genetics</i> , 2007 , 177, 567-76	4	43
40	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	2.4	29
39	In vitro bile acid binding activity within flour fractions from oat lines with typical and high beta-glucan amounts. <i>Journal of Agricultural and Food Chemistry</i> , 2006 , 54, 5142-8	5.7	30

38	Optimizing Seeding Rates for Winter Cereal Grains and Frost-Seeded Red Clover Intercrops. <i>Agronomy Journal</i> , 2006 , 98, 1041-1049	2.2	40
37	Kernel Size Variation in Naked Oat. <i>Crop Science</i> , 2006 , 46, 1117	2.4	2
36	Responses to Selection for Partial Resistance to Crown Rust in Oat. <i>Crop Science</i> , 2006 , 46, 1260-1265	2.4	12
35	Planting Date Effects on Winter Triticale Grain Yield and Yield Components. <i>Crop Science</i> , 2006 , 46, 1218-1224	2.4	8
34	Bayesian Modeling of Heterogeneous Error and Genotype \times Environment Interaction Variances. <i>Crop Science</i> , 2006 , 46, 820-833	2.4	35
33	Using mating designs to uncover QTL and the genetic architecture of complex traits. <i>Heredity</i> , 2006 , 96, 139-49	3.6	72
32	In vitro bile acid binding of flours from oat lines varying in percentage and molecular weight distribution of beta-glucan. <i>Journal of Agricultural and Food Chemistry</i> , 2005 , 53, 8797-803	5.7	37
31	Selective Phenotyping to Accurately Map Quantitative Trait Loci. <i>Crop Science</i> , 2005 , 45, 901-908	2.4	39
30	Registration of NIE426GT Winter Triticale. <i>Crop Science</i> , 2005 , 45, 796-797	2.4	3
29	Expanding the Pool of PCR-Based Markers for Oat. <i>Crop Science</i> , 2005 , 45, 2383-2387	2.4	22
28	Planting Date Effects on Winter Triticale Dry Matter and Nitrogen Accumulation. <i>Agronomy Journal</i> , 2005 , 97, 1333-1341	2.2	36
27	Evaluation of Oat Kernel Size Uniformity. <i>Crop Science</i> , 2004 , 44, 1178-1186	2.4	34
26	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, 641-3	4	15
25	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	2.4	18
24	Optimal sampling of a population to determine QTL location, variance, and allelic number. <i>Theoretical and Applied Genetics</i> , 2004 , 108, 1434-42	6	21
23	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	2.4	17
22	Influence of Oat Kernel Size and Size Distributions on Test Weight. <i>Cereal Research Communications</i> , 2004 , 32, 135-142	1.1	4
21	Estimating allelic number and identity in state of QTLs in interconnected families. <i>Genetical Research</i> , 2003 , 81, 133-44	1.1	35

20	Mapping Quantitative Trait Loci in Plant Breeding Populations. <i>Crop Science</i> , 2003 , 43, 829-834	2.4	69
19	Mapping Quantitative Trait Loci in Plant Breeding Populations. <i>Crop Science</i> , 2003 , 43, 829	2.4	35
18	Feasibility of selection for high weed suppressive ability in soybean: Absence of tradeoffs between rapid initial growth and sustained later growth. <i>Euphytica</i> , 2001 , 120, 291-300	2.1	21
17	Mapping epistatic quantitative trait loci with one-dimensional genome searches. <i>Genetics</i> , 2001 , 157, 445-54	4	95
16	Assessing the practical importance of weed evolution: a research agenda. <i>Weed Research</i> , 1997 , 37, 237-246	2.4	37
15	Biomass Production and Nitrogen Accumulation in Pea, Oat, and Vetch Green Manure Mixtures. <i>Agronomy Journal</i> , 1996 , 88, 231-240	2.2	22
14	Prediction of subgenome additive and interaction effects in allohexaploid wheat		2
13	A low resolution epistasis mapping approach to identify chromosome arm interactions in allohexaploid wheat		1
12	Introgressed <i>Manihot glaziovii</i> Alleles in Modern Cassava Germplasm Benefit Important Traits and Are Under Balancing Selection		1
11	Marker-based estimates reveal significant non-additive effects in clonally propagated cassava (<i>Manihot esculenta</i>): implications for the prediction of total genetic value and the selection of varieties		2
10	Genome-wide association mapping of correlated traits in cassava: dry matter and total carotenoid content		1
9	Prospects for genomic selection in cassava breeding		2
8	Population genetics of sugar kelp in the Northwest Atlantic region using genome-wide markers		1
7	Leveraging Transcriptomics Data for Genomic Prediction Models in Cassava		4
6	RNA polymerase mapping in plants identifies enhancers enriched in causal variants		4
5	A subfunctionalization epistasis model to evaluate homeologous gene interactions in allopolyploid wheat		3
4	Multivariate Genome-wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (<i>Avena sativa</i> L.)		1
3	Sexual dimorphism and the effect of wild introgressions on recombination in <i>Manihot esculenta</i>		1

2	Genome-wide association mapping and genomic prediction unravels CBS resistance in a <i>Manihot esculenta</i> breeding population	1
1	Genomic mating in outbred species: predicting cross usefulness with additive and total genetic covariance matrices	1