

Mark E Sorrells

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5921139/mark-e-sorrells-publications-by-citations.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

204
papers

21,319
citations

74
h-index

145
g-index

213
ext. papers

25,057
ext. citations

4.4
avg, IF

6.85
L-index

#	Paper	IF	Citations
204	Genic microsatellite markers in plants: features and applications. <i>Trends in Biotechnology</i> , 2005 , 23, 48-55	5.1	1315
203	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
202	Optimizing parental selection for genetic linkage maps. <i>Genome</i> , 1993 , 36, 181-6	2.4	955
201	Genomic Selection for Crop Improvement. <i>Crop Science</i> , 2009 , 49, 1-12	2.4	939
200	Association mapping of kernel size and milling quality in wheat (<i>Triticum aestivum</i> L.) cultivars. <i>Genetics</i> , 2006 , 172, 1165-77	4	756
199	Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 8057-62	11.5	719
198	Data mining for simple sequence repeats in expressed sequence tags from barley, maize, rice, sorghum and wheat. <i>Plant Molecular Biology</i> , 2002 , 48, 501-10	4.6	490
197	Genomics-assisted breeding for crop improvement. <i>Trends in Plant Science</i> , 2005 , 10, 621-30	13.1	454
196	Plant Breeding with Genomic Selection: Gain per Unit Time and Cost. <i>Crop Science</i> , 2010 , 50, 1681-1690	2.4	415
195	Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. <i>Plant Genome</i> , 2012 , 5,	4.4	411
194	Genomic Selection in Plant Breeding: A Comparison of Models. <i>Crop Science</i> , 2012 , 52, 146-160	2.4	402
193	Construction of a restriction fragment length polymorphism map for barley (<i>Hordeum vulgare</i>). <i>Genome</i> , 1991 , 34, 437-447	2.4	387
192	A chromosome bin map of 16,000 expressed sequence tag loci and distribution of genes among the three genomes of polyploid wheat. <i>Genetics</i> , 2004 , 168, 701-12	4	346
191	Comparative DNA sequence analysis of wheat and rice genomes. <i>Genome Research</i> , 2003 , 13, 1818-27	9.7	328
190	Isolation of EST-derived microsatellite markers for genotyping the A and B genomes of wheat. <i>Theoretical and Applied Genetics</i> , 2002 , 104, 399-407	6	327
189	Genomic Selection in Plant Breeding. <i>Advances in Agronomy</i> , 2011 , 110, 77-123	7.7	291
188	Homoeologous relationships of rice, wheat and maize chromosomes. <i>Molecular Genetics and Genomics</i> , 1993 , 241, 483-90		285

187	Molecular-genetic maps for group 1 chromosomes of Triticeae species and their relation to chromosomes in rice and oat. <i>Genome</i> , 1995 , 38, 45-59	2.4	268
186	The organization and rate of evolution of wheat genomes are correlated with recombination rates along chromosome arms. <i>Genome Research</i> , 2003 , 13, 753-63	9.7	261
185	Molecular mapping of wheat: major genes and rearrangements in homoeologous groups 4, 5, and 7. <i>Genetics</i> , 1995 , 141, 721-31	4	253
184	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. <i>Plant Science</i> , 2005 , 168, 195-202	5.3	235
183	Linkage between RFLP markers and genes affecting kernel hardness in wheat. <i>Theoretical and Applied Genetics</i> , 1996 , 93, 580-6	6	224
182	Nonrandom distribution and frequencies of genomic and EST-derived microsatellite markers in rice, wheat, and barley. <i>BMC Genomics</i> , 2005 , 6, 23	4.5	217
181	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
180	Training set optimization under population structure in genomic selection. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 145-58	6	207
179	Development and mapping of EST-derived simple sequence repeat markers for hexaploid wheat. <i>Genome</i> , 2004 , 47, 805-18	2.4	206
178	RFLP Analysis of Genomic Regions Associated with Resistance to Preharvest Sprouting in Wheat. <i>Crop Science</i> , 1993 , 33, 453-459	2.4	197
177	Quantitative Trait Loci Associated with Kernel Traits in a Soft × Hard Wheat Cross. <i>Crop Science</i> , 1999 , 39, 1184-1195	2.4	195
176	Genomic Selection Accuracy for Grain Quality Traits in Biparental Wheat Populations. <i>Crop Science</i> , 2011 , 51, 2597-2606	2.4	193
175	Association Analysis as a Strategy for Improvement of Quantitative Traits in Plants. <i>Crop Science</i> , 2006 , 46, 1323-1330	2.4	187
174	Development of a chromosomal arm map for wheat based on RFLP markers. <i>Theoretical and Applied Genetics</i> , 1992 , 83, 1035-43	6	185
173	Phytochemical content and antioxidant activity of six diverse varieties of whole wheat. <i>Food Chemistry</i> , 2010 , 119, 249-257	8.5	184
172	Mapping Yr28 and Other Genes for Resistance to Stripe Rust in Wheat. <i>Crop Science</i> , 2000 , 40, 1148-1155.4	2.4	181
171	Perspectives for Genomic Selection Applications and Research in Plants. <i>Crop Science</i> , 2015 , 55, 1-12	2.4	179
170	Molecular mapping of wheat. Homoeologous group 2. <i>Genome</i> , 1995 , 38, 516-24	2.4	177

169	Population- and genome-specific patterns of linkage disequilibrium and SNP variation in spring and winter wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2010 , 11, 727	4.5	170
168	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
167	Evaluation of Genomic Prediction Methods for Fusarium Head Blight Resistance in Wheat. <i>Plant Genome</i> , 2012 , 5, 51-61	4.4	166
166	Comparative mapping in grasses. Wheat relationships. <i>Molecular Genetics and Genomics</i> , 1995 , 248, 744-54		166
165	Molecular mapping of wheat. Homoeologous group 3. <i>Genome</i> , 1995 , 38, 525-33	2.4	153
164	Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011 , 4,	4.4	152
163	Evaluation of Genetic Diversity and Genome-wide Linkage Disequilibrium among U.S. Wheat (<i>Triticum aestivum</i> L.) Germplasm Representing Different Market Classes. <i>Crop Science</i> , 2007 , 47, 1018-1030	2.4	149
162	Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011 , 4, 65	4.4	148
161	EST derived SSR markers for comparative mapping in wheat and rice. <i>Molecular Genetics and Genomics</i> , 2004 , 271, 742-51	3.1	144
160	Genomic predictability of interconnected biparental maize populations. <i>Genetics</i> , 2013 , 194, 493-503	4	142
159	Synthetic Hexaploids: Harnessing Species of the Primary Gene Pool for Wheat Improvement 2013 , 35-122		136
158	Molecular genetic maps of the group 6 chromosomes of hexaploid wheat (<i>Triticum aestivum</i> L. em. Thell.). <i>Genome</i> , 1996 , 39, 359-66	2.4	136
157	Comparative DNA sequence analysis of mapped wheat ESTs reveals the complexity of genome relationships between rice and wheat. <i>Functional and Integrative Genomics</i> , 2004 , 4, 34-46	3.8	134
156	Mapping Genes Conferring and Suppressing Leaf Rust Resistance in Wheat. <i>Crop Science</i> , 1997 , 37, 1928-1935	2.4	133
155	Inferences on the genome structure of progenitor maize through comparative analysis of rice, maize and the domesticated panicoids. <i>Genetics</i> , 1999 , 153, 453-73	4	131
154	Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 10836-41	11.5	128
153	A molecular linkage map of cultivated oat. <i>Genome</i> , 1995 , 38, 368-80	2.4	126
152	Identification of drought-inducible genes and differentially expressed sequence tags in barley. <i>Theoretical and Applied Genetics</i> , 2004 , 109, 1417-25	6	120

151	Imputation of unordered markers and the impact on genomic selection accuracy. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 427-39	3.2	119
150	Association mapping and gene-gene interaction for stem rust resistance in CIMMYT spring wheat germplasm. <i>Theoretical and Applied Genetics</i> , 2011 , 123, 1257-68	6	117
149	Anchor probes for comparative mapping of grass genera. <i>Theoretical and Applied Genetics</i> , 1998 , 97, 356-69	6	115
148	New DArT markers for oat provide enhanced map coverage and global germplasm characterization. <i>BMC Genomics</i> , 2009 , 10, 39	4.5	109
147	QTL analysis of kernel size and shape in two hexaploid wheat mapping populations. <i>Field Crops Research</i> , 2007 , 101, 172-179	5.5	109
146	Impact of marker ascertainment bias on genomic selection accuracy and estimates of genetic diversity. <i>PLoS ONE</i> , 2013 , 8, e74612	3.7	104
145	Genomic selection for durable stem rust resistance in wheat. <i>Euphytica</i> , 2011 , 179, 161-173	2.1	100
144	Genomic Selection for Quantitative Adult Plant Stem Rust Resistance in Wheat. <i>Plant Genome</i> , 2014 , 7, plantgenome2014.02.0006	4.4	98
143	A consensus map for Ug99 stem rust resistance loci in wheat. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 1561-81	6	97
142	Quantitative Trait Loci Associated with Milling and Baking Quality in a Soft × Hard Wheat Cross. <i>Crop Science</i> , 2001 , 41, 1275-1285	2.4	96
141	Molecular markers for four leaf rust resistance genes introgressed into wheat from wild relatives. <i>Genome</i> , 1995 , 38, 75-83	2.4	96
140	Molecular linkage map for an intraspecific recombinant inbred population of durum wheat (<i>Triticum turgidum</i> L. var. durum). <i>Theoretical and Applied Genetics</i> , 2001 , 102, 177-186	6	94
139	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
138	Mapping quantitative trait loci for preharvest sprouting resistance in white wheat. <i>Theoretical and Applied Genetics</i> , 2009 , 119, 1223-35	6	84
137	Analysis of expressed sequence tag loci on wheat chromosome group 4. <i>Genetics</i> , 2004 , 168, 651-63	4	83
136	Quantitative trait locus analysis of wheat quality traits. <i>Euphytica</i> , 2006 , 149, 145-159	2.1	81
135	Development of an expressed sequence tag (EST) resource for wheat (<i>Triticum aestivum</i> L.): EST generation, unigene analysis, probe selection and bioinformatics for a 16,000-locus bin-delineated map. <i>Genetics</i> , 2004 , 168, 585-93	4	81
134	Genetic Gain from Phenotypic and Genomic Selection for Quantitative Resistance to Stem Rust of Wheat. <i>Plant Genome</i> , 2015 , 8, eplantgenome2014.10.0074	4.4	79

133	Comparative mapping in grasses. Oat relationships. <i>Molecular Genetics and Genomics</i> , 1995 , 249, 349-56		77
132	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
131	Group 3 chromosome bin maps of wheat and their relationship to rice chromosome 1. <i>Genetics</i> , 2004 , 168, 639-50	4	76
130	Optimal Design of Preliminary Yield Trials with Genome-Wide Markers. <i>Crop Science</i> , 2014 , 54, 48-59	2.4	74
129	Association mapping for pre-harvest sprouting resistance in white winter wheat. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 793-805	6	74
128	Chromosome bin map of expressed sequence tags in homoeologous group 1 of hexaploid wheat and homoeology with rice and Arabidopsis. <i>Genetics</i> , 2004 , 168, 609-23	4	73
127	A 2600-locus chromosome bin map of wheat homoeologous group 2 reveals interstitial gene-rich islands and colinearity with rice. <i>Genetics</i> , 2004 , 168, 625-37	4	73
126	Reconstruction of the synthetic W7984 x Opata M85 wheat reference population. <i>Genome</i> , 2011 , 54, 875-82	2.4	69
125	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021 , 26, 631-649	13.1	68
124	Association of a Lipoxxygenase Locus, Lpx-B1, with Variation in Lipoxxygenase Activity in Durum Wheat Seeds. <i>Crop Science</i> , 2002 , 42, 1695-1700	2.4	65
123	A chromosome bin map of 2148 expressed sequence tag loci of wheat homoeologous group 7. <i>Genetics</i> , 2004 , 168, 687-99	4	64
122	Efficient Use of Historical Data for Genomic Selection: A Case Study of Stem Rust Resistance in Wheat. <i>Plant Genome</i> , 2015 , 8, eplantgenome2014.09.0046	4.4	63
121	A 2500-locus bin map of wheat homoeologous group 5 provides insights on gene distribution and colinearity with rice. <i>Genetics</i> , 2004 , 168, 665-76	4	63
120	Comparison of digital image analysis using elliptic Fourier descriptors and major dimensions to phenotype seed shape in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Euphytica</i> , 2013 , 190, 99-116	2.1	62
119	Identification of Ug99 stem rust resistance loci in winter wheat germplasm using genome-wide association analysis. <i>Theoretical and Applied Genetics</i> , 2012 , 125, 749-58	6	60
118	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
117	Diagnostic and co-dominant PCR markers for wheat stem rust resistance genes Sr25 and Sr26. <i>Theoretical and Applied Genetics</i> , 2010 , 120, 691-7	6	60
116	RELp markers linked to two Hessian fly-resistance genes in wheat (<i>Triticum aestivum</i> L.) from <i>Triticum tauschii</i> (coss.) Schmal. <i>Theoretical and Applied Genetics</i> , 1993 , 85, 750-4	6	60

115	Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes. <i>Theoretical and Applied Genetics</i> , 2018 , 131, 1405-1422	6	58
114	A Grounded Guide to Gluten: How Modern Genotypes and Processing Impact Wheat Sensitivity. <i>Comprehensive Reviews in Food Science and Food Safety</i> , 2015 , 14, 285-302	16.4	58
113	Breeding tef [<i>Eragrostis tef</i> (Zucc.) trotter]: conventional and molecular approaches. <i>Plant Breeding</i> , 2011 , 130, 1-9	2.4	57
112	Direct Classification and Selection of Superior Alleles for Crop Improvement. <i>Crop Science</i> , 1997 , 37, 691-697	2.4	57
111	Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1415-1430	6	56
110	Three-Dimensional Seed Size and Shape QTL in Hexaploid Wheat (<i>Triticum aestivum</i> L.) Populations. <i>Crop Science</i> , 2014 , 54, 98-110	2.4	55
109	Genetic mapping of two powdery mildew resistance genes in einkorn (<i>Triticum monococcum</i> L.) accessions. <i>Theoretical and Applied Genetics</i> , 2007 , 114, 351-8	6	55
108	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
107	Genetic Loci Related to Kernel Quality Differences between a Soft and a Hard Wheat Cultivar. <i>Crop Science</i> , 2005 , 45, 1685-1695	2.4	52
106	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. <i>Nature Communications</i> , 2020 , 11, 884	17.4	51
105	Construction and evaluation of cDNA libraries for large-scale expressed sequence tag sequencing in wheat (<i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004 , 168, 595-608	4	50
104	Development and Application of RFLPs in Polyploids. <i>Crop Science</i> , 1992 , 32, 1086-1091	2.4	45
103	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1231-1247	3.2	44
102	Transferability of cereal EST-SSR markers to ryegrass. <i>Genome</i> , 2009 , 52, 431-7	2.4	44
101	Haplotype diversity of stem rust resistance loci in uncharacterized wheat lines. <i>Molecular Breeding</i> , 2010 , 26, 667-680	3.4	44
100	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
99	Development and validation of KASP markers for the greenbug resistance gene Gb7 and the Hessian fly resistance gene H32 in wheat. <i>Theoretical and Applied Genetics</i> , 2017 , 130, 1867-1884	6	42
98	Dispersal of durum wheat [<i>Triticum turgidum</i> L. ssp. <i>turgidum</i> convar. <i>durum</i> (Desf.) MacKey] landraces across the Mediterranean basin assessed by AFLPs and microsatellites. <i>Genetic Resources and Crop Evolution</i> , 2007 , 54, 1133-1144	2	41

97	Deletion mapping of homoeologous group 6-specific wheat expressed sequence tags. <i>Genetics</i> , 2004 , 168, 677-86	4	39
96	Quncho: the first popular tef variety in Ethiopia. <i>International Journal of Agricultural Sustainability</i> , 2011 , 9, 25-34	2.2	38
95	Chromosomal Location of Genes for Resistance to Karnal Bunt in Wheat. <i>Crop Science</i> , 1998 , 38, 231-236	2.4	37
94	Population Genomics Related to Adaptation in Elite Oat Germplasm. <i>Plant Genome</i> , 2016 , 9, plantgenome2015.10.010	4.4	35
93	Comparison of Models and Whole-Genome Profiling Approaches for Genomic-Enabled Prediction of Septoria Tritici Blotch, Stagonospora Nodorum Blotch, and Tan Spot Resistance in Wheat. <i>Plant Genome</i> , 2017 , 10, plantgenome2016.08.0082	4.4	34
92	Counting on Crossovers: Controlled Recombination for Plant Breeding. <i>Trends in Plant Science</i> , 2020 , 25, 455-465	13.1	33
91	Overexpression of BrCIPK1 Gene Enhances Abiotic Stress Tolerance by Increasing Proline Biosynthesis in Rice. <i>Plant Molecular Biology Reporter</i> , 2016 , 34, 501-511	1.7	33
90	Breeding Value of Primary Synthetic Wheat Genotypes for Grain Yield. <i>PLoS ONE</i> , 2016 , 11, e0162860	3.7	33
89	Quantitative Trait Loci for Flour Viscosity in Winter Wheat. <i>Crop Science</i> , 1999 , 39, 238-242	2.4	31
88	Identification and Validation of QTL for Grain Quality Traits in a Cross of Soft Wheat Cultivars Pioneer Brand 25R26 and Foster. <i>Crop Science</i> , 2011 , 51, 1424-1436	2.4	30
87	A genetic linkage map for tef [<i>Eragrostis tef</i> (Zucc.) Trotter]. <i>Theoretical and Applied Genetics</i> , 2006 , 113, 1093-102	6	30
86	Expressed sequence tag analysis in tef (<i>Eragrostis tef</i> (Zucc) Trotter). <i>Genome</i> , 2006 , 49, 365-72	2.4	28
85	Distribution of microsatellite alleles linked to Rht8 dwarfing gene in wheat. <i>Euphytica</i> , 2002 , 123, 235-240	2.1	28
84	Fine mapping of a preharvest sprouting QTL interval on chromosome 2B in white wheat. <i>Theoretical and Applied Genetics</i> , 2014 , 127, 1843-55	6	27
83	Two New Strategies for Detecting and Understanding QTL [Environment Interactions. <i>Crop Science</i> , 2011 , 51, 96-113	2.4	27
82	QTL mapping for yield and lodging resistance in an enhanced SSR-based map for tef. <i>Theoretical and Applied Genetics</i> , 2011 , 122, 77-93	6	27
81	Durum Wheat Landraces from East and West Regions of the Mediterranean Basin Are Genetically Distinct for Yield Components and Phenology. <i>Frontiers in Plant Science</i> , 2018 , 9, 80	6.2	26
80	QTL mapping of agronomic traits in tef [<i>Eragrostis tef</i> (Zucc) Trotter]. <i>BMC Plant Biology</i> , 2007 , 7, 30	5.3	25

79	Genome-Wide Association Mapping for Leaf Tip Necrosis and Pseudo-black Chaff in Relation to Durable Rust Resistance in Wheat. <i>Plant Genome</i> , 2015 , 8, eplantgenome2015.01.0002	4.4	23
78	Use of a large-scale Triticeae expressed sequence tag resource to reveal gene expression profiles in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Genome</i> , 2006 , 49, 531-44	2.4	23
77	Comparative genetic analysis of a wheat seed dormancy QTL with rice and <i>Brachypodium</i> identifies candidate genes for ABA perception and calcium signaling. <i>Functional and Integrative Genomics</i> , 2011 , 11, 479-90	3.8	21
76	Basis for Selecting Soft Wheat for End-Use Quality. <i>Crop Science</i> , 2012 , 52, 21-31	2.4	20
75	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
74	Evaluation of wheat and emmer varieties for artisanal baking, pasta making, and sensory quality. <i>Journal of Cereal Science</i> , 2017 , 74, 19-27	3.8	19
73	Genetic diversity in tef (<i>Eragrostis tef</i>) germplasm using SSR markers. <i>Field Crops Research</i> , 2012 , 127, 64-70	5.5	19
72	Identification of milling and baking quality QTL in multiple soft wheat mapping populations. <i>Theoretical and Applied Genetics</i> , 2015 , 128, 2227-42	6	18
71	Identification and validation of single nucleotide polymorphic markers linked to Ug99 stem rust resistance in spring wheat. <i>PLoS ONE</i> , 2017 , 12, e0171963	3.7	18
70	Characterizing Croatian Wheat Germplasm Diversity and Structure in a European Context by DArT Markers. <i>Frontiers in Plant Science</i> , 2016 , 7, 184	6.2	18
69	Identification of Chromosome Locations of Genes Affecting Preharvest Sprouting and Seed Dormancy Using Chromosome Substitution Lines in Tetraploid Wheat (<i>Triticum turgidum</i> L.). <i>Crop Science</i> , 2010 , 50, 1180-1187	2.4	17
68	Genomic Selection in Plant Breeding: A Comparison of Models 2012 , 52, 146		17
67	Wheat Fructans: A Potential Breeding Target for Nutritionally Improved, Climate-Resilient Varieties. <i>Crop Science</i> , 2017 , 57, 1624-1640	2.4	16
66	Application of new knowledge, technologies, and strategies to wheat improvement. <i>Euphytica</i> , 2007 , 157, 299-306	2.1	15
65	Systems genetics of environmental response in the mature wheat embryo. <i>Genetics</i> , 2013 , 194, 265-77	4	14
64	Aerial high-throughput phenotyping enables indirect selection for grain yield at the early generation, seed-limited stages in breeding programs. <i>Crop Science</i> , 2020 , 60, 3096-3114	2.4	14
63	Linkage Disequilibrium and Association Mapping in the Triticeae 2009 , 655-683		14
62	Genomic Selection in Plants: Empirical Results and Implications for Wheat Breeding 2015 , 401-409		13

61	Genomic Selection for Small Grain Improvement 2017 , 99-130		12
60	Wheat ATIs: Characteristics and Role in Human Disease. <i>Frontiers in Nutrition</i> , 2021 , 8, 667370	6.2	12
59	Influence of Genotype and Environment on Wheat Grain Fructan Content. <i>Crop Science</i> , 2019 , 59, 190-198.4	2.4	12
58	Identification of Small Grains Genotypes Resistant to Soilborne wheat mosaic virus. <i>Plant Disease</i> , 2006 , 90, 1039-1044	1.5	11
57	Recurrent genomic selection for wheat grain fructans. <i>Crop Science</i> , 2020 , 60, 1499-1512	2.4	11
56	KERNEL MORPHOLOGY VARIATION IN A POPULATION DERIVED FROM A SOFT BY HARD WHEAT CROSS AND ASSOCIATIONS WITH END-USE QUALITY TRAITS ¹ . <i>Journal of Food Quality</i> , 2000 , 23, 391-407.7	2.7	10
55	Homeologous Epistasis in Wheat: The Search for an Immortal Hybrid. <i>Genetics</i> , 2019 , 211, 1105-1122	4	9
54	Reduced response diversity does not negatively impact wheat climate resilience. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 10623-10624	11.5	9
53	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
52	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
51	Registration of Clayuga Wheat. <i>Crop Science</i> , 1998 , 38, 551-552	2.4	7
50	Prediction of Subgenome Additive and Interaction Effects in Allohexaploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 685-698	3.2	7
49	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
48	Identification of Small Grains Genotypes Resistant to Wheat spindle streak mosaic virus. <i>Plant Disease</i> , 2006 , 90, 1045-1050	1.5	6
47	Registration of the S2MET Barley Mapping Population for Multi-Environment Genomewide Selection. <i>Journal of Plant Registrations</i> , 2019 , 13, 270-280	0.7	6
46	Genomic Selection of Forage Quality Traits in Winter Wheat. <i>Crop Science</i> , 2019 , 59, 2473-2483	2.4	6
45	Genomic Selection in Wheat 2019 , 273-302		5
44	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat		5

43	Genetic Mapping of Major-Effect Seed Dormancy Quantitative Trait Loci on Chromosome 2B using Recombinant Substitution Lines in Tetraploid Wheat. <i>Crop Science</i> , 2016 , 56, 59-72	2.4	5
42	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
41	Malting of Fusarium Head Blight-Infected Rye (): Growth of , Trichothecene Production, and the Impact on Malt Quality. <i>Toxins</i> , 2018 , 10,	4.9	5
40	Economic Responses of Maize, Soybean, and Wheat in Three Rotations under Conventional and Organic Systems. <i>Agronomy</i> , 2019 , 9, 424	3.6	4
39	A connected half-sib family training population for genomic prediction in barley. <i>Crop Science</i> , 2020 , 60, 262-281	2.4	4
38	Genomic Selection for Crop Improvement: An Introduction 2017 , 1-6		4
37	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
36	Multiple-Race Stem Rust Resistance Loci Identified in Durum Wheat Using Genome-Wide Association Mapping. <i>Frontiers in Plant Science</i> , 2020 , 11, 598509	6.2	4
35	Genotype ×Environment Interactions and Stability in Organic Wheat. <i>Crop Science</i> , 2019 , 59, 25-32	2.4	4
34	Genomic selection of forage agronomic traits in winter wheat. <i>Crop Science</i> , 2021 , 61, 410-421	2.4	4
33	Organic Compared with Conventional Wheat Had Competitive Yields during the Early Years of Organic Production in the Northeast USA. <i>Agronomy</i> , 2019 , 9, 380	3.6	3
32	Eragrostis 2011 , 135-151		3
31	Response to Early Generation Genomic Selection for Yield in Wheat.. <i>Frontiers in Plant Science</i> , 2021 , 12, 718611	6.2	3
30	Chromatographic Methods to Evaluate Nutritional Quality in Oat. <i>Methods in Molecular Biology</i> , 2017 , 1536, 115-125	1.4	3
29	A subfunctionalization epistasis model to evaluate homeologous gene interactions in allopolyploid wheat		3
28	Selection signatures across seven decades of hard winter wheat breeding in the Great Plains of the United States. <i>Plant Genome</i> , 2020 , 13, e20032	4.4	3
27	A SNP-based genetic dissection of versatile traits in bread wheat (<i>Triticum aestivum</i> L.). <i>Plant Journal</i> , 2021 , 108, 960-976	6.9	3
26	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

25	Wheat amylase/trypsin inhibitors (ATIs): occurrence, function and health aspects.. <i>European Journal of Nutrition</i> , 2022 , 1	5.2	3
24	Prediction of subgenome additive and interaction effects in allohexaploid wheat		2
23	Designing Plants To Meet Feedstock Needs. <i>Biotechnology in Agriculture and Forestry</i> , 2010 , 57-84		2
22	Genome-wide association mapping of seedling and adult plant response to stem rust in a durum wheat panel. <i>Plant Genome</i> , 2021 , 14, e20105	4.4	2
21	The Evolution of Comparative Plant Genetics. <i>Stadler Genetics Symposia Series</i> , 2000 , 183-195		2
20	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat.. <i>Nature Communications</i> , 2022 , 13, 826	17.4	1
19	Registration of Corral Oat. <i>Journal of Plant Registrations</i> , 2012 , 6, 273-276	0.7	1
18	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
17	Multivariate Genome-wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (<i>Avena sativa</i> L.)		1
16	Positional-based cloning 'fail-safe' approach is overpowered by wheat chromosome structural variation. <i>Plant Genome</i> , 2021 , 14, e20106	4.4	1
15	Genetic trends in Fusarium head blight resistance due to 20 years of winter wheat breeding and cooperative testing in the Northern US. <i>Plant Disease</i> , 2021 ,	1.5	1
14	Registration of Lightning Barley. <i>Journal of Plant Registrations</i> , 2021 , 15, 407-414	0.7	1
13	Interactions of the barley SD1 and SD2 seed dormancy loci influence preharvest sprouting, seed dormancy, and malting quality. <i>Crop Science</i> ,	2.4	1
12	Cereal Genomics Research in the Post-genomic Era 2004 , 559-584		1
11	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
10	Achieving Controlled Recombination with Targeted Cleavage and Epigenetic Modifiers. <i>Trends in Plant Science</i> , 2020 , 25, 513-514	13.1	0
9	Agronomic Comparisons of Organic and Conventional Soybean with Recommended and High Inputs during the First 4 Years of Organic Management. <i>Agronomy</i> , 2019 , 9, 602	3.6	0
8	Gain from genomic selection for a selection index in two-row spring barley. <i>Plant Genome</i> , 2021 , 14, e20103	1.3	0

7	Genetic characterization of agronomic traits and grain threshability for organic naked barley in the northern United States. <i>Crop Science</i> , 2022 , 62, 690-703	2.4	○
6	Mapping pre-harvest sprouting resistance loci in AAC Innova × AAC Tenacious spring wheat population.. <i>BMC Genomics</i> , 2021 , 22, 900	4.5	○
5	Cold Conditioned: Discovery of Novel Alleles for Low-Temperature Tolerance in the Vavilov Barley Collection.. <i>Frontiers in Plant Science</i> , 2021 , 12, 800284	6.2	○
4	Generalizable approaches for genomic prediction of metabolites in plants.. <i>Plant Genome</i> , 2022 , e202054.4	4.4	○
3	Registration of NYBatavia Wheat. <i>Crop Science</i> , 1998 , 38, 551-551	2.4	
2	QTL x environment modeling of malting barley preharvest sprouting. <i>Theoretical and Applied Genetics</i> , 2021 , 1	6	
1	Breeding Methods: Population Improvement and Selection Methods 2022 , 83-96		