

Mark E Sorrells

List of Publications by Year in descending order

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201
papers

27,942
citations

6233

80
h-index

5806

161
g-index

213
all docs

213
docs citations

213
times ranked

13415
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. <i>PLoS ONE</i> , 2012, 7, e32253.	1.1	1,685
2	Genic microsatellite markers in plants: features and applications. <i>Trends in Biotechnology</i> , 2005, 23, 48-55.	4.9	1,543
3	Genomic Selection for Crop Improvement. <i>Crop Science</i> , 2009, 49, 1-12.	0.8	1,266
4	Optimizing parental selection for genetic linkage maps. <i>Genome</i> , 1993, 36, 181-186.	0.9	1,191
5	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, 8057-8062.	3.3	1,065
6	Association Mapping of Kernel Size and Milling Quality in Wheat (<i>Triticum aestivum</i> L.) Cultivars. <i>Genetics</i> , 2006, 172, 1165-1177.	1.2	1,010
7	Genomics-assisted breeding for crop improvement. <i>Trends in Plant Science</i> , 2005, 10, 621-630.	4.3	579
8	Data mining for simple sequence repeats in expressed sequence tags from barley, maize, rice, sorghum and wheat. <i>Plant Molecular Biology</i> , 2002, 48, 501-510.	2.0	574
9	Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. <i>Plant Genome</i> , 2012, 5, .	1.6	556
10	Plant Breeding with Genomic Selection: Gain per Unit Time and Cost. <i>Crop Science</i> , 2010, 50, 1681-1690.	0.8	547
11	Genomic Selection in Plant Breeding: A Comparison of Models. <i>Crop Science</i> , 2012, 52, 146-160.	0.8	546
12	Construction of a restriction fragment length polymorphism map for barley (<i>Hordeum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 Td	0.9	428
13	Genomic Selection in Plant Breeding. <i>Advances in Agronomy</i> , 2011, 110, 77-123.	2.4	395
14	Homoeologous relationships of rice, wheat and maize chromosomes. <i>Molecular Genetics and Genomics</i> , 1993, 241-241, 483-490.	2.4	387
15	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, 701-712.	1.2	369
16	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. <i>Genome Research</i> , 2003, 13, 1818-1827.	2.4	369
17	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.	1.8	359
18	Molecular mapping of wheat: major genes and rearrangements in homoeologous groups 4, 5, and 7.. <i>Genetics</i> , 1995, 141, 721-731.	1.2	334

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19	The Organization and Rate of Evolution of Wheat Genomes Are Correlated With Recombination Rates Along Chromosome Arms. <i>Genome Research</i> , 2003, 13, 753-763.	2.4	298
20	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.	0.9	297
21	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, 463-480.	1.8	296
22	Perspectives for Genomic Selection Applications and Research in Plants. <i>Crop Science</i> , 2015, 55, 1-12.	0.8	290
23	Training set optimization under population structure in genomic selection. <i>Theoretical and Applied Genetics</i> , 2015, 128, 145-158.	1.8	284
24	Nonrandom distribution and frequencies of genomic and EST-derived microsatellite markers in rice, wheat, and barley. <i>BMC Genomics</i> , 2005, 6, 23.	1.2	271
25	Interspecific transferability and comparative mapping of barley EST-SSR markers in wheat, rye and rice. <i>Plant Science</i> , 2005, 168, 195-202.	1.7	266
26	Linkage between RFLP markers and genes affecting kernel hardness in wheat. <i>Theoretical and Applied Genetics</i> , 1996, 93, 580-586.	1.8	259
27	Genomic Selection Accuracy for Grain Quality Traits in Biparental Wheat Populations. <i>Crop Science</i> , 2011, 51, 2597-2606.	0.8	255
28	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
29	Mapping <i>Yr28</i> and Other Genes for Resistance to Stripe Rust in Wheat. <i>Crop Science</i> , 2000, 40, 1148-1155.	0.8	243
30	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
31	Association Analysis as a Strategy for Improvement of Quantitative Traits in Plants. <i>Crop Science</i> , 2006, 46, 1323-1330.	0.8	237
32	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.	1.2	234
33	Quantitative Trait Loci Associated with Kernel Traits in a Soft $\tilde{\text{A}}$ – Hard Wheat Cross. <i>Crop Science</i> , 1999, 39, 1184-1195.	0.8	231
34	Phytochemical content and antioxidant activity of six diverse varieties of whole wheat. <i>Food Chemistry</i> , 2010, 119, 249-257.	4.2	226
35	RFLP Analysis of Genomic Regions Associated with Resistance to Preharvest Sprouting in Wheat. <i>Crop Science</i> , 1993, 33, 453-459.	0.8	220
36	Evaluation of Genomic Prediction Methods for Fusarium Head Blight Resistance in Wheat. <i>Plant Genome</i> , 2012, 5, 51-61.	1.6	220

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37	Development and mapping of EST-derived simple sequence repeat markers for hexaploid wheat. <i>Genome</i> , 2004, 47, 805-818.	0.9	218
38	Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011, 4, 65.	1.6	208
39	Development of a chromosomal arm map for wheat based on RFLP markers. <i>Theoretical and Applied Genetics</i> , 1992, 83, 1035-1043.	1.8	207
40	Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. <i>Plant Genome</i> , 2011, 4, .	1.6	206
41	Molecular mapping of wheat. Homoeologous group 2. <i>Genome</i> , 1995, 38, 516-524.	0.9	197
42	Molecular mapping of wheat. Homoeologous group 3. <i>Genome</i> , 1995, 38, 525-533.	0.9	192
43	Comparative mapping in grasses. Wheat relationships. <i>Molecular Genetics and Genomics</i> , 1995, 248, 744-754.	2.4	183
44	Comparative mapping in grasses. Oat relationships. <i>Molecular Genetics and Genomics</i> , 1995, 249, 349-356.	2.4	180
45	Genomic Predictability of Interconnected Biparental Maize Populations. <i>Genetics</i> , 2013, 194, 493-503.	1.2	180
46	Imputation of Unordered Markers and the Impact on Genomic Selection Accuracy. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 427-439.	0.8	172
47	Evaluation of Genetic Diversity and Genome-wide Linkage Disequilibrium among U.S. Wheat (Triticum) Tj ETQq1 1 0.784314 rgBT /Ov	0.8	167
48	QTL analysis of kernel size and shape in two hexaploid wheat mapping populations. <i>Field Crops Research</i> , 2007, 101, 172-179.	2.3	162
49	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, 10836-10841.	3.3	159
50	Association mapping and gene-gene interaction for stem rust resistance in CIMMYT spring wheat germplasm. <i>Theoretical and Applied Genetics</i> , 2011, 123, 1257-1268.	1.8	158
51	Molecular genetic maps of the group 6 chromosomes of hexaploid wheat (<i>Triticum aestivum</i> L.) Tj ETQq1 1 0.784314 rgBT /Ov	0.9	156
52	A molecular linkage map of cultivated oat. <i>Genome</i> , 1995, 38, 368-380.	0.9	155
53	EST derived SSR markers for comparative mapping in wheat and rice. <i>Molecular Genetics and Genomics</i> , 2004, 271, 742-751.	1.0	155
54	Inferences on the Genome Structure of Progenitor Maize Through Comparative Analysis of Rice, Maize and the Domesticated Panicoids. <i>Genetics</i> , 1999, 153, 453-473.	1.2	154

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55	Mapping Genes Conferring and Suppressing Leaf Rust Resistance in Wheat. <i>Crop Science</i> , 1997, 37, 1928-1935.	0.8	149
56	A consensus map for Ug99 stem rust resistance loci in wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1561-1581.	1.8	149
57	Genomic Selection for Quantitative Adult Plant Stem Rust Resistance in Wheat. <i>Plant Genome</i> , 2014, 7, plantgenome2014.02.0006.	1.6	143
58	Identification of drought-inducible genes and differentially expressed sequence tags in barley. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1417-1425.	1.8	142
59	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.	1.4	141
60	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
61	New DArT markers for oat provide enhanced map coverage and global germplasm characterization. <i>BMC Genomics</i> , 2009, 10, 39.	1.2	135
62	Impact of Marker Ascertainment Bias on Genomic Selection Accuracy and Estimates of Genetic Diversity. <i>PLoS ONE</i> , 2013, 8, e74612.	1.1	129
63	Anchor probes for comparative mapping of grass genera. <i>Theoretical and Applied Genetics</i> , 1998, 97, 356-369.	1.8	123
64	Genomic selection for durable stem rust resistance in wheat. <i>Euphytica</i> , 2011, 179, 161-173.	0.6	123
65	Identification of Ug99 stem rust resistance loci in winter wheat germplasm using genome-wide association analysis. <i>Theoretical and Applied Genetics</i> , 2012, 125, 749-758.	1.8	119
66	Genetic Gain from Phenotypic and Genomic Selection for Quantitative Resistance to Stem Rust of Wheat. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.10.0074.	1.6	118
67	Quantitative Trait Loci Associated with Milling and Baking Quality in a Soft—Hard Wheat Cross. <i>Crop Science</i> , 2001, 41, 1275-1285.	0.8	114
68	Molecular linkage map for an intraspecific recombinant inbred population of durum wheat (<i>Triticum</i>) Tj ETQq0 0 0 rBT /Overlock 10 Tf	1.8	107
69	Quantitative trait locus analysis of wheat quality traits. <i>Euphytica</i> , 2006, 149, 145-159.	0.6	105
70	Mapping quantitative trait loci for preharvest sprouting resistance in white wheat. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1223-1235.	1.8	105
71	Molecular markers for four leaf rust resistance genes introgressed into wheat from wild relatives. <i>Genome</i> , 1995, 38, 75-83.	0.9	103
72	Association mapping for pre-harvest sprouting resistance in white winter wheat. <i>Theoretical and Applied Genetics</i> , 2012, 125, 793-805.	1.8	101

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73	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.	1.8	101
74	Exceptional subgenome stability and functional divergence in the allotetraploid Ethiopian cereal teff. <i>Nature Communications</i> , 2020, 11, 884.	5.8	101
75	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
76	Optimal Design of Preliminary Yield Trials with Genome-Wide Markers. <i>Crop Science</i> , 2014, 54, 48-59.	0.8	100
77	Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2017, 130, 1415-1430.	1.8	99
78	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.	1.6	96
79	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1231-1247.	0.8	96
80	Reconstruction of the Synthetic W7984 × Opata M85 wheat reference population. <i>Genome</i> , 2011, 54, 875-882.	0.9	94
81	Analysis of Expressed Sequence Tag Loci on Wheat Chromosome Group 4. <i>Genetics</i> , 2004, 168, 651-663.	1.2	90
82	Breeding <i>tef</i> [<i>Eragrostis tef</i> (Zucc.) trotter]: conventional and molecular approaches. <i>Plant Breeding</i> , 2011, 130, 1-9.	1.0	90
83	Development of an Expressed Sequence Tag (EST) Resource for Wheat (<i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 585-593.	1.2	87
84	Genomic Selection in Plant Breeding: A Comparison of Models. <i>Crop Science</i> , 2012, 52, 146.	0.8	85
85	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.	0.6	83
86	Group 3 Chromosome Bin Maps of Wheat and Their Relationship to Rice Chromosome 1. <i>Genetics</i> , 2004, 168, 639-650.	1.2	81
87	REL _P 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, 85-85, 750-754.	1.8	79
88	Association of a Lipxygenase Locus, <i>Lpx-1</i> , with Variation in Lipxygenase Activity in Durum Wheat Seeds. <i>Crop Science</i> , 2002, 42, 1695-1700.	0.8	79
89	Three-Dimensional Seed Size and Shape QTL in Hexaploid Wheat (<i>Triticum aestivum</i> L.) Populations. <i>Crop Science</i> , 2014, 54, 98-110.	0.8	79
90	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.	5.9	79

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91	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, 609-623.	1.2	78
92	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, 625-637.	1.2	78
93	Diagnostic and co-dominant PCR markers for wheat stem rust resistance genes Sr25 and Sr26. <i>Theoretical and Applied Genetics</i> , 2010, 120, 691-697.	1.8	75
94	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
95	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
96	A Chromosome Bin Map of 2148 Expressed Sequence Tag Loci of Wheat Homoeologous Group 7. <i>Genetics</i> , 2004, 168, 687-699.	1.2	68
97	A 2500-Locus Bin Map of Wheat Homoeologous Group 5 Provides Insights on Gene Distribution and Colinearity With Rice. <i>Genetics</i> , 2004, 168, 665-676.	1.2	67
98	Genetic mapping of two powdery mildew resistance genes in einkorn (<i>Triticum monococcum</i> L.) accessions. <i>Theoretical and Applied Genetics</i> , 2006, 114, 351-358.	1.8	66
99	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
100	Counting on Crossovers: Controlled Recombination for Plant Breeding. <i>Trends in Plant Science</i> , 2020, 25, 455-465.	4.3	65
101	Direct Classification and Selection of Superior Alleles for Crop Improvement. <i>Crop Science</i> , 1997, 37, 691-697.	0.8	63
102	Breeding Value of Primary Synthetic Wheat Genotypes for Grain Yield. <i>PLoS ONE</i> , 2016, 11, e0162860.	1.1	61
103	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.	1.8	60
104	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.	1.2	57
105	Population Genomics Related to Adaptation in Elite Oat Germplasm. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0103.	1.6	55
106	Genetic Loci Related to Kernel Quality Differences between a Soft and a Hard Wheat Cultivar. <i>Crop Science</i> , 2005, 45, 1685-1695.	0.8	53
107	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.	0.8	53
108	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.	1.7	51

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109	Haplotype diversity of stem rust resistance loci in uncharacterized wheat lines. <i>Molecular Breeding</i> , 2010, 26, 667-680.	1.0	50
110	<i>Quncho</i> : the first popular tef variety in Ethiopia. <i>International Journal of Agricultural Sustainability</i> , 2011, 9, 25-34.	1.3	50
111	Transferability of cereal EST-SSR markers to ryegrass. <i>Genome</i> , 2009, 52, 431-437.	0.9	49
112	Development and Application of RFLPs in Polyploids. <i>Crop Science</i> , 1992, 32, 1086-1091.	0.8	48
113	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.	1.6	48
114	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.	0.8	45
115	Two New Strategies for Detecting and Understanding QTL × Environment Interactions. <i>Crop Science</i> , 2011, 51, 96-113.	0.8	44
116	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
117	Deletion Mapping of Homoeologous Group 6-Specific Wheat Expressed Sequence Tags. <i>Genetics</i> , 2004, 168, 677-686.	1.2	43
118	Chromosomal Location of Genes for Resistance to Karnal Bunt in Wheat. <i>Crop Science</i> , 1998, 38, 231-236.	0.8	42
119	Wheat ATIs: Characteristics and Role in Human Disease. <i>Frontiers in Nutrition</i> , 2021, 8, 667370.	1.6	42
120	Overexpression of BrCIPK1 Gene Enhances Abiotic Stress Tolerance by Increasing Proline Biosynthesis in Rice. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 501-511.	1.0	41
121	Basis for Selecting Soft Wheat for End-Use Quality. <i>Crop Science</i> , 2012, 52, 21-31.	0.8	38
122	Fine mapping of a preharvest sprouting QTL interval on chromosome 2B in white wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1843-1855.	1.8	38
123	QTL mapping of agronomic traits in tef [<i>Eragrostis tef</i> (Zucc) Trotter]. <i>BMC Plant Biology</i> , 2007, 7, 30.	1.6	35
124	Quantitative Trait Loci for Flour Viscosity in Winter Wheat. <i>Crop Science</i> , 1999, 39, 238-242.	0.8	34
125	Expressed sequence tag analysis in tef (<i>Eragrostis tef</i> (Zucc) Trotter). <i>Genome</i> , 2006, 49, 365-372.	0.9	34
126	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.	1.6	34

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127	Distribution of microsatellite alleles linked to Rht8 dwarfing gene in wheat. <i>Euphytica</i> , 2002, 123, 235-240.	0.6	33
128	A genetic linkage map for tef [<i>Eragrostis tef</i> (Zucc.) Trotter]. <i>Theoretical and Applied Genetics</i> , 2006, 113, 1093-1102.	1.8	33
129	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.	1.8	32
130	Evaluation of wheat and emmer varieties for artisanal baking, pasta making, and sensory quality. <i>Journal of Cereal Science</i> , 2017, 74, 19-27.	1.8	32
131	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.	0.8	31
132	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. <i>Nature Communications</i> , 2022, 13, 826.	5.8	31
133	Characterizing Croatian Wheat Germplasm Diversity and Structure in a European Context by DArT Markers. <i>Frontiers in Plant Science</i> , 2016, 7, 184.	1.7	27
134	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, 531-544.	0.9	26
135	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, 479-490.	1.4	26
136	Identification and validation of single nucleotide polymorphic markers linked to Ug99 stem rust resistance in spring wheat. <i>PLoS ONE</i> , 2017, 12, e0171963.	1.1	25
137	Genetic diversity in tef (<i>Eragrostis tef</i>) germplasm using SSR markers. <i>Field Crops Research</i> , 2012, 127, 64-70.	2.3	24
138	Identification of milling and baking quality QTL in multiple soft wheat mapping populations. <i>Theoretical and Applied Genetics</i> , 2015, 128, 2227-2242.	1.8	22
139	A SNP-based genetic dissection of versatile traits in bread wheat (<i>Triticum aestivum</i> L.). <i>Plant Journal</i> , 2021, 108, 960-976.	2.8	22
140	Application of new knowledge, technologies, and strategies to wheat improvement. <i>Euphytica</i> , 2007, 157, 299-306.	0.6	20
141	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.	0.8	20
142	Genomic Selection for Small Grain Improvement. , 2017, , 99-130.		20
143	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
144	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

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145	Influence of Genotype and Environment on Wheat Grain Fructan Content. <i>Crop Science</i> , 2019, 59, 190-198.	0.8	18
146	Wheat amylase/trypsin inhibitors (ATIs): occurrence, function and health aspects. <i>European Journal of Nutrition</i> , 2022, 61, 2873-2880.	1.8	18
147	Wheat Fructans: A Potential Breeding Target for Nutritionally Improved, Climate-Resilient Varieties. <i>Crop Science</i> , 2017, 57, 1624-1640.	0.8	17
148	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
149	Systems Genetics of Environmental Response in the Mature Wheat Embryo. <i>Genetics</i> , 2013, 194, 265-277.	1.2	16
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.	0.8	16
151	Linkage Disequilibrium and Association Mapping in the Triticeae. , 2009, , 655-683.		16
152	Malting of Fusarium Head Blight-Infected Rye (<i>Secale cereale</i>): Growth of <i>Fusarium graminearum</i> , Trichothecene Production, and the Impact on Malt Quality. <i>Toxins</i> , 2018, 10, 369.	1.5	15
153	Recurrent genomic selection for wheat grain fructans. <i>Crop Science</i> , 2020, 60, 1499-1512.	0.8	15
154	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
155	Multiple-Race Stem Rust Resistance Loci Identified in Durum Wheat Using Genome-Wide Association Mapping. <i>Frontiers in Plant Science</i> , 2020, 11, 598509.	1.7	14
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