Jesse A Poland

List of Publications by Year
in descending order

180 papers	**26,141** citations	17440 **63** h-index	7518 **151** g-index
197 all docs	**197** docs citations	**197** times ranked	**18013** citing authors

#	Article	IF	Citations
1	A Robust, Simple Genotyping-by-Sequencing (GBS) Approach for High Diversity Species. PLoS ONE, 2011, 6, e19379.	2.5	5,470
2	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
3	Development of High-Density Genetic Maps for Barley and Wheat Using a Novel Two-Enzyme Genotyping-by-Sequencing Approach. PLoS ONE, 2012, 7, e32253.	2.5	1,685
4	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. Science, 2014, 345, 1251788.	12.6	1,479
5	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	27.8	1,365
6	Genotypingâ€by–Sequencing for Plant Breeding and Genetics. Plant Genome, 2012, 5, .	2.8	703
7	Shades of gray: the world of quantitative disease resistance. Trends in Plant Science, 2009, 14, 21-29.	8.8	588
8	Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012, 44, 803-807.	21.4	577
9	Genomic Selection in Wheat Breeding using Genotypingâ€by–Sequencing. Plant Genome, 2012, 5, .	2.8	556
10	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	27.8	513
11	Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6893-6898.	7.1	350
12	Canopy Temperature and Vegetation Indices from High-Throughput Phenotyping Improve Accuracy of Pedigree and Genomic Selection for Grain Yield in Wheat. G3: Genes, Genomes, Genetics, 2016, 6, 2799-2808.	1.8	336
13	Training set optimization under population structure in genomic selection. Theoretical and Applied Genetics, 2015, 128, 145-158.	3.6	284
14	Resistance gene cloning from a wild crop relative by sequence capture and association genetics. Nature Biotechnology, 2019, 37, 139-143.	17.5	280
15	Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker Ã— Environment Interaction Genomic Selection Model. G3: Genes, Genomes, Genetics, 2015, 5, 569-582.	1.8	266
16	Anchoring and ordering <scp>NGS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). Plant Journal, 2013, 76, 718-727.	5.7	264
17	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. Genome Biology, 2015, 16, 26.	8.8	256
18	A maize resistance gene functions against bacterial streak disease in rice. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15383-15388.	7.1	243

#	Article	IF	Citations
19	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of <i>Gossypium</i> spp.. G3: Genes, Genomes, Genetics, 2015, 5, 1187-1209.	1.8	226
20	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. Nature Genetics, 2019, 51, 1530-1539.	21.4	216
21	Application of unmanned aerial systems for high throughput phenotyping of large wheat breeding nurseries. Plant Methods, 2016, 12, 35.	4.3	200
22	Application of Genotyping-by-Sequencing on Semiconductor Sequencing Platforms: A Comparison of Genetic and Reference-Based Marker Ordering in Barley. PLoS ONE, 2013, 8, e76925.	2.5	186
23	Genetic Diversity and Population Structure of F3:6 Nebraska Winter Wheat Genotypes Using Genotyping-By-Sequencing. Frontiers in Genetics, 2018, 9, 76.	2.3	183
24	Combining High‐Throughput Phenotyping and Genomic Information to Increase Prediction and Selection Accuracy in Wheat Breeding. Plant Genome, 2018, 11, 170043.	2.8	175
25	Imputation of Unordered Markers and the Impact on Genomic Selection Accuracy. G3: Genes, Genomes, Genetics, 2013, 3, 427-439.	1.8	172
26	Genomic Selection for Processing and End‐Use Quality Traits in the CIMMYT Spring Bread Wheat Breeding Program. Plant Genome, 2016, 9, plantgenome2016.01.0005.	2.8	161
27	Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. PLoS ONE, 2014, 9, e102448.	2.5	147
28	An evaluation of genotyping by sequencing (GBS) to map the Breviaristatum-e (ari-e) locus in cultivated barley. BMC Genomics, 2014, 15, 104.	2.8	145
29	Genomic Selection for Quantitative Adult Plant Stem Rust Resistance in Wheat. Plant Genome, 2014, 7, plantgenome2014.02.0006.	2.8	143
30	Advances and Challenges in Genomic Selection for Disease Resistance. Annual Review of Phytopathology, 2016, 54, 79-98.	7.8	143
31	Multitrait, Random Regression, or Simple Repeatability Model in High‐Throughput Phenotyping Data Improve Genomic Prediction for Wheat Grain Yield. Plant Genome, 2017, 10, plantgenome2016.11.0111.	2.8	138
32	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nature Genetics, 2021, 53, 564-573.	21.4	138
33	Breeder friendly phenotyping. Plant Science, 2020, 295, 110396.	3.6	135
34	Mapping QTL for the traits associated with heat tolerance in wheat (Triticum aestivumL.). BMC Genetics, 2014, 15, 97.	2.7	133
35	Two gap-free reference genomes and a global view of the centromere architecture in rice. Molecular Plant, 2021, 14, 1757-1767.	8.3	133
36	Construction of a map-based reference genome sequence for barley, Hordeum vulgare L.. Scientific Data, 2017, 4, 170044.	5.3	130

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37	Impact of Marker Ascertainment Bias on Genomic Selection Accuracy and Estimates of Genetic Diversity. PLoS ONE, 2013, 8, e74612.	2.5	129
38	Genome-Wide Association Study of Grain Architecture in Wild Wheat Aegilops tauschii. Frontiers in Plant Science, 2017, 8, 886.	3.6	114
39	Increasing Genomic‐Enabled Prediction Accuracy by Modeling Genotype Ã— Environment Interactions in Kansas Wheat. Plant Genome, 2017, 10, plantgenome2016.12.0130.	2.8	107
40	High-Throughput Phenotyping Enabled Genetic Dissection of Crop Lodging in Wheat. Frontiers in Plant Science, 2019, 10, 394.	3.6	104
41	Genotyping-by-Sequencing Derived High-Density Linkage Map and its Application to QTL Mapping of Flag Leaf Traits in Bread Wheat. Scientific Reports, 2017, 7, 16394.	3.3	103
42	Population genomic analysis of Aegilops tauschii identifies targets for bread wheat improvement. Nature Biotechnology, 2022, 40, 422-431.	17.5	102
43	A Pipeline Strategy for Grain Crop Domestication. Crop Science, 2016, 56, 917-930.	1.8	101
44	Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes. Theoretical and Applied Genetics, 2018, 131, 1405-1422.	3.6	101
45	The use of unbalanced historical data for genomic selection in an international wheat breeding program. Field Crops Research, 2013, 154, 12-22.	5.1	100
46	The quest for understanding phenotypic variation via integrated approaches in the field environment. Plant Physiology, 2016, 172, pp.00592.2016.	4.8	99
47	Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. Theoretical and Applied Genetics, 2017, 130, 1415-1430.	3.6	99
48	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. G3: Genes, Genomes, Genetics, 2019, 9, 1231-1247.	1.8	96
49	Field Book: An Open‐Source Application for Field Data Collection on Android. Crop Science, 2014, 54, 1624-1627.	1.8	94
50	Field-based high-throughput phenotyping of plant height in sorghum using different sensing technologies. Plant Methods, 2018, 14, 53.	4.3	93
51	Development of a field-based high-throughput mobile phenotyping platform. Computers and Electronics in Agriculture, 2016, 122, 74-85.	7.7	89
52	Development and Evolution of an Intermediate Wheatgrass Domestication Program. Sustainability, 2018, 10, 1499.	3.2	89
53	Resistance to Gray Leaf Spot of Maize: Genetic Architecture and Mechanisms Elucidated through Nested Association Mapping and Near-Isogenic Line Analysis. PLoS Genetics, 2015, 11, e1005045.	3.5	86
54	Establishment and Optimization of Genomic Selection to Accelerate the Domestication and Improvement of Intermediate Wheatgrass. Plant Genome, 2016, 9, plantgenome2015.07.0059.	2.8	86

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55	A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. Plant Genome, 2016, 9, plantgenome2015.10.0102.	2.8	85
56	Increased Genomic Prediction Accuracy in Wheat Breeding Through Spatial Adjustment of Field Trial Data. G3: Genes, Genomes, Genetics, 2013, 3, 2105-2114.	1.8	80
57	In the Eye of the Beholder: The Effect of Rater Variability and Different Rating Scales on QTL Mapping. Phytopathology, 2011, 101, 290-298.	2.2	79
58	Wheat quality improvement at CIMMYT and the use of genomic selection on it. Applied & Translational Genomics, 2016, 11, 3-8.	2.1	79
59	Efficient curation of genebanks using next generation sequencing reveals substantial duplication of germplasm accessions. Scientific Reports, 2019, 9, 650.	3.3	79
60	Integrating genomic-enabled prediction and high-throughput phenotyping in breeding for climate-resilient bread wheat. Theoretical and Applied Genetics, 2019, 132, 177-194.	3.6	78
61	Incorporating Genome-Wide Association Mapping Results Into Genomic Prediction Models for Grain Yield and Yield Stability in CIMMYT Spring Bread Wheat. Frontiers in Plant Science, 2020, 11, 197.	3.6	78
62	Development and Deployment of a Portable Field Phenotyping Platform. Crop Science, 2016, 56, 965-975.	1.8	77
63	Unlocking the novel genetic diversity and population structure of synthetic Hexaploid wheat. BMC Genomics, 2018, 19, 591.	2.8	76
64	Field-based high throughput phenotyping rapidly identifies genomic regions controlling yield components in rice. Scientific Reports, 2017, 7, 42839.	3.3	74
65	Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. G3: Genes, Genomes, Genetics, 2018, 8, 2735-2747.	1.8	74
66	Genome-Wide Association Study Reveals Novel Genomic Regions Associated with 10 Grain Minerals in Synthetic Hexaploid Wheat. International Journal of Molecular Sciences, 2018, 19, 3237.	4.1	72
67	High-throughput phenotyping platforms enhance genomic selection for wheat grain yield across populations and cycles in early stage. Theoretical and Applied Genetics, 2019, 132, 1705-1720.	3.6	70
68	Breeding-assisted genomics. Current Opinion in Plant Biology, 2015, 24, 119-124.	7.1	69
69	Genome-Wide Association Study for Identification and Validation of Novel SNP Markers for Sr6 Stem Rust Resistance Gene in Bread Wheat. Frontiers in Plant Science, 2018, 9, 380.	3.6	68
70	Single‐Step Genomic and Pedigree Genotype × Environment Interaction Models for Predicting Wheat Lines in International Environments. Plant Genome, 2017, 10, plantgenome2016.09.0089.	2.8	66
71	Introgression of stem rust resistance genes SrTA10187 and SrTA10171 from Aegilops tauschii to wheat. Theoretical and Applied Genetics, 2013, 126, 2477-2484.	3.6	65
72	Prospects and Challenges of Applied Genomic Selection—A New Paradigm in Breeding for Grain Yield in Bread Wheat. Plant Genome, 2018, 11, 180017.	2.8	65

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73	A SNP Genotyping Array for Hexaploid Oat. Plant Genome, 2014, 7, plantgenome2014.03.0010.	2.8	63
74	Construction of a SNP and SSR linkage map in autotetraploid blueberryÂusing genotyping by sequencing. Molecular Breeding, 2016, 36, 1.	2.1	63
75	Linkage Map Construction and Quantitative Trait Locus Analysis of Agronomic and Fiber Quality Traits in Cotton. Plant Genome, 2014, 7, plantgenome2013.07.0023.	2.8	62
76	Simultaneous transfer, introgression, and genomic localization of genes for resistance to stem rust race TTKSK (Ug99) from Aegilops tauschii to wheat. Theoretical and Applied Genetics, 2013, 126, 1179-1188.	3.6	61
77	Global Wheat Head Detection 2021: An Improved Dataset for Benchmarking Wheat Head Detection Methods. Plant Phenomics, 2021, 2021, 9846158.	5.9	60
78	Unraveling Genomic Complexity at a Quantitative Disease Resistance Locus in Maize. Genetics, 2014, 198, 333-344.	2.9	51
79	Multivariate Genomic Selection and Potential of Rapid Indirect Selection with Speed Breeding in Spring Wheat. Crop Science, 2019, 59, 1945-1959.	1.8	51
80	Breeding-assisted genomics: Applying meta-GWAS for milling and baking quality in CIMMYT wheat breeding program. PLoS ONE, 2018, 13, e0204757.	2.5	50
81	Exploring the tertiary gene pool of bread wheat: sequence assembly and analysis of chromosome 5M^g of *Aegilops geniculata*. Plant Journal, 2015, 84, 733-746.	5.7	48
82	Comparison of Models and Wholeâ€Genome Profiling Approaches for Genomicâ€Enabled Prediction of Septoria Tritici Blotch, Stagonospora Nodorum Blotch, and Tan Spot Resistance in Wheat. Plant Genome, 2017, 10, plantgenome2016.08.0082.	2.8	48
83	The Aegilops ventricosa 2NvS segment in bread wheat: cytology, genomics and breeding. Theoretical and Applied Genetics, 2021, 134, 529-542.	3.6	48
84	Aegilops sharonensis genome-assisted identification of stem rust resistance gene Sr62. Nature Communications, 2022, 13, 1607.	12.8	48
85	Genomic Analysis Confirms Population Structure and Identifies Inter-Lineage Hybrids in Aegilops tauschii. Frontiers in Plant Science, 2019, 10, 9.	3.6	47
86	Targeted discovery of quantitative trait loci for resistance to northern leaf blight and other diseases of maize. Theoretical and Applied Genetics, 2011, 123, 307-326.	3.6	45
87	Genome-Wide Association Mapping of Grain Micronutrients Concentration in Aegilops tauschii. Frontiers in Plant Science, 2019, 10, 54.	3.6	45
88	Multivariate Genome-Wide Association Analyses Reveal the Genetic Basis of Seed Fatty Acid Composition in Oat (*Avena sativa* L.). G3: Genes, Genomes, Genetics, 2019, 9, 2963-2975.	1.8	44
89	Genome-wide association mapping of agronomic traits and carbon isotope discrimination in a worldwide germplasm collection of spring wheat using SNP markers. Molecular Breeding, 2015, 35, 1.	2.1	43
90	Development of the first consensus genetic map of intermediate wheatgrass (Thinopyrum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 Td (	3.6	43

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91	Application of Population Sequencing (POPSEQ) for Ordering and Imputing Genotyping-by-Sequencing Markers in Hexaploid Wheat. G3: Genes, Genomes, Genetics, 2015, 5, 2547-2553.	1.8	40
92	Genotype-by-sequencing facilitates genetic mapping of a stem rust resistance locus in Aegilops umbellulata, a wild relative of cultivated wheat. BMC Genomics, 2016, 17, 1039.	2.8	39
93	Strategies for Selecting Crosses Using Genomic Prediction in Two Wheat Breeding Programs. Plant Genome, 2017, 10, plantgenome2016.12.0128.	2.8	37
94	Reference Genome Anchoring of High-Density Markers for Association Mapping and Genomic Prediction in European Winter Wheat. Frontiers in Plant Science, 2019, 10, 1278.	3.6	37
95	Precisely mapping a major gene conferring resistance to Hessian fly in bread wheat using genotyping-by-sequencing. BMC Genomics, 2015, 16, 108.	2.8	36
96	Genomeâ€Wide Association Mapping for Leaf Tip Necrosis and Pseudoâ€black Chaff in Relation to Durable Rust Resistance in Wheat. Plant Genome, 2015, 8, eplantgenome2015.01.0002.	2.8	34
97	Utilizing Highâ€Throughput Phenotypic Data for Improved Phenotypic Selection of Stressâ€Adaptive Traits in Wheat. Crop Science, 2017, 57, 648-659.	1.8	34
98	QTL mapping for yield and lodging resistance in an enhanced SSR-based map for tef. Theoretical and Applied Genetics, 2011, 122, 77-93.	3.6	32
99	QTL mapping of pre-harvest sprouting resistance in a white wheat cultivar Danby. Theoretical and Applied Genetics, 2018, 131, 1683-1697.	3.6	32
100	Genome-Wide Association Study for Multiple Biotic Stress Resistance in Synthetic Hexaploid Wheat. International Journal of Molecular Sciences, 2019, 20, 3667.	4.1	31
101	Aerial highâ€throughput phenotyping enables indirect selection for grain yield at the early generation, seedâ€limited stages in breeding programs. Crop Science, 2020, 60, 3096-3114.	1.8	31
102	Genetic Mapping of Raceâ€Specific Stem Rust Resistance in the Synthetic Hexaploid W7984 Ã— Opata M85 Mapping Population. Crop Science, 2015, 55, 2580-2588.	1.8	30
103	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass (Thinopyrum intermedium). Theoretical and Applied Genetics, 2019, 132, 2325-2351.	3.6	30
104	Haplotype-Based, Genome-Wide Association Study Reveals Stable Genomic Regions for Grain Yield in CIMMYT Spring Bread Wheat. Frontiers in Genetics, 2020, 11, 589490.	2.3	29
105	Cloning of the broadly effective wheat leaf rust resistance gene Lr42 transferred from Aegilops tauschii. Nature Communications, 2022, 13, .	12.8	29
106	Dense genotyping-by-sequencing linkage maps of two Synthetic W7984Ã—Opata reference populations provide insights into wheat structural diversity. Scientific Reports, 2019, 9, 1793.	3.3	28
107	Enhancing Crop Domestication Through Genomic Selection, a Case Study of Intermediate Wheatgrass. Frontiers in Plant Science, 2020, 11, 319.	3.6	28
108	High-throughput phenotyping with deep learning gives insight into the genetic architecture of flowering time in wheat. GigaScience, 2019, 8, .	6.4	28

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109	Application of Geographically Weighted Regression to Improve Grain Yield Prediction from Unmanned Aerial System Imagery. Crop Science, 2017, 57, 2478-2489.	1.8	27
110	Genome-wide association mapping for wheat blast resistance in CIMMYTâ€™s international screening nurseries evaluated in Bolivia and Bangladesh. Scientific Reports, 2020, 10, 15972.	3.3	27
111	Genomic Selection for Grain Yield in the CIMMYT Wheat Breeding Programâ€"Status and Perspectives. Frontiers in Plant Science, 2020, 11, 564183.	3.6	27
112	Uncovering the Genetic Architecture of Seed Weight and Size in Intermediate Wheatgrass through Linkage and Association Mapping. Plant Genome, 2017, 10, plantgenome2017.03.0022.	2.8	26
113	Molecular diversity and landscape genomics of the crop wild relative <i>Triticum urartu</i> across the Fertile Crescent. Plant Journal, 2018, 94, 670-684.	5.7	26
114	A Fieldâ€Based Analysis of Genetic Improvement for Grain Yield in Winter Wheat Cultivars Developed in the US Central Plains from 1992 to 2014. Crop Science, 2019, 59, 905-910.	1.8	26
115	Genomeâ€based prediction of multiple wheat quality traits in multiple years. Plant Genome, 2020, 13, e20034.	2.8	25
116	Local adaptation, genetic divergence, and experimental selection in a foundation grass across the US Great Plainsâ€™ climate gradient. Global Change Biology, 2019, 25, 850-868.	9.5	24
117	New QTLs for Spot Blotch Disease Resistance in Wheat (Triticum aestivum L.) Using Genome-Wide Association Mapping. Frontiers in Genetics, 2020, 11, 613217.	2.3	24
118	A wholeâ€genome, radiation hybrid mapping resource of hexaploid wheat. Plant Journal, 2016, 86, 195-207.	5.7	23
119	Improving Genomic Prediction for Preâ€Harvest Sprouting Tolerance in Wheat by Weighting Largeâ€Effect Quantitative Trait Loci. Crop Science, 2017, 57, 1315-1324.	1.8	22
120	Genomic prediction enables rapid selection of highâ€performing genets in an intermediate wheatgrass breeding program. Plant Genome, 2021, 14, e20080.	2.8	21
121	Quantifying varietyâ€specific heat resistance and the potential for adaptation to climate change. Global Change Biology, 2016, 22, 2904-2912.	9.5	20
122	Genomic Selection for Small Grain Improvement. , 2017, , 99-130.		20
123	Data-driven decentralized breeding increases prediction accuracy in a challenging crop production environment. Communications Biology, 2021, 4, 944.	4.4	20
124	Spiked GBS: a unified, open platform for single marker genotyping and whole-genome profiling. BMC Genomics, 2015, 16, 248.	2.8	19
125	Development of a complete set of wheatâ€"barley group-7 Robertsonian translocation chromosomes conferring an increased content of Î²-glucan. Theoretical and Applied Genetics, 2018, 131, 377-388.	3.6	19
126	Production of a complete set of wheatâ€"barley group-7 chromosome recombinants with increased grain Î²-glucan content. Theoretical and Applied Genetics, 2019, 132, 3129-3141.	3.6	18

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127	A TILLING Resource for Hard Red Winter Wheat Variety Jagger. Crop Science, 2019, 59, 1666-1671.	1.8	17
128	Breedbase: a digital ecosystem for modern plant breeding. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	17
129	Genomic Selection for Increased Yield in Synthetic‐Derived Wheat. Crop Science, 2017, 57, 713-725.	1.8	16
130	De Novo Genome Assembly of the Japanese Wheat Cultivar Norin 61 Highlights Functional Variation in Flowering Time and Fusarium-Resistant Genes in East Asian Genotypes. Plant and Cell Physiology, 2021, 62, 8-27.	3.1	16
131	Accelerated Domestication of New Crops: Yield is Key. Plant and Cell Physiology, 2022, 63, 1624-1640.	3.1	16
132	QTL mapping of Fusarium head blight resistance and deoxynivalenol accumulation in the Kansas wheat variety â€˜Everestâ€™. Molecular Breeding, 2019, 39, 1.	2.1	15
133	Recurrent genomic selection for wheat grain fructans. Crop Science, 2020, 60, 1499-1512.	1.8	15
134	High molecular weight glutenin gene diversity in Aegilops tauschii demonstrates unique origin of superior wheat quality. Communications Biology, 2021, 4, 1242.	4.4	14
135	Joint Use of Genome, Pedigree, and Their Interaction with Environment for Predicting the Performance of Wheat Lines in New Environments. G3: Genes, Genomes, Genetics, 2019, 9, 2925-2934.	1.8	13
136	Sequenced-based paternity analysis to improve breeding and identify self-incompatibility loci in intermediate wheatgrass (Thinopyrum intermedium). Theoretical and Applied Genetics, 2020, 133, 3217-3233.	3.6	13
137	Genomic Selection for Wheat Blast in a Diversity Panel, Breeding Panel and Full-Sibs Panel. Frontiers in Plant Science, 2021, 12, 745379.	3.6	13
138	Genetic characterization and curation of diploid A-genome wheat species. Plant Physiology, 2022, 188, 2101-2114.	4.8	13
139	Identification of quantitative trait loci conferring resistance to tan spot in a biparental population derived from two Nebraska hard red winter wheat cultivars. Molecular Breeding, 2018, 38, 1.	2.1	12
140	Improved Accuracy of High-Throughput Phenotyping From Unmanned Aerial Systems by Extracting Traits Directly From Orthorectified Images. Frontiers in Plant Science, 2020, 11, 587093.	3.6	12
141	Adaptive genetic potential and plasticity of trait variation in the foundation prairie grass *Andropogon gerardii* across the US Great Plainsâ€™ climate gradient: Implications for climate change and restoration. Evolutionary Applications, 2020, 13, 2333-2356.	3.1	12
142	Development of whole‐genome prediction models to increase the rate of genetic gain in intermediate wheatgrass (*Thinopyrum intermedium*) breeding. Plant Genome, 2021, 14, e20089.	2.8	12
143	Accelerating wheat breeding for end‐use quality through association mapping and multivariate genomic prediction. Plant Genome, 2021, 14, e20164.	2.8	12
144	SNPMeta: SNP annotation and SNP metadata collection without a reference genome. Molecular Ecology Resources, 2014, 14, 419-425.	4.8	11

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145	Effect of cytoplasmic diversity on post anthesis heat tolerance in wheat. Euphytica, 2015, 204, 383-394.	1.2	11
146	Reduced response diversity does not negatively impact wheat climate resilience. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10623-10624.	7.1	11
147	Implementing within–cross genomic prediction to reduce oat breeding costs. Plant Genome, 2020, 13, e20004.	2.8	11
148	The Independent Domestication of Timopheev's Wheat: Insights from Haplotype Analysis of the Brittle rachis 1 (BTR1-A) Gene. Genes, 2021, 12, 338.	2.4	11
149	Population genomics and haplotype analysis in spelt and bread wheat identifies a gene regulating glume color. Communications Biology, 2021, 4, 375.	4.4	11
150	Elucidating the genetics of grain yield and stress-resilience in bread wheat using a large-scale genome-wide association mapping study with 55,568 lines. Scientific Reports, 2021, 11, 5254.	3.3	11
151	Genomic Analysis and Prediction within a US Public Collaborative Winter Wheat Regional Testing Nursery. Plant Genome, 2018, 11, 180004.	2.8	10
152	Increased Predictive Accuracy of Multi-Environment Genomic Prediction Model for Yield and Related Traits in Spring Wheat (Triticum aestivum L.). Frontiers in Plant Science, 2021, 12, 720123.	3.6	10
153	Response to Early Generation Genomic Selection for Yield in Wheat. Frontiers in Plant Science, 2021, 12, 718611.	3.6	10
154	Evaluations of Genomic Prediction and Identification of New Loci for Resistance to Stripe Rust Disease in Wheat (Triticum aestivum L.). Frontiers in Genetics, 2021, 12, 710485.	2.3	9
155	Genome-Wide Association Mapping Indicates Quantitative Genetic Control of Spot Blotch Resistance in Bread Wheat and the Favorable Effects of Some Spot Blotch Loci on Grain Yield. Frontiers in Plant Science, 2022, 13, 835095.	3.6	9
156	Genomic selection for spot blotch in bread wheat breeding panels, full-sibs and half-sibs and index-based selection for spot blotch, heading and plant height. Theoretical and Applied Genetics, 2022, , 1.	3.6	9
157	Multivariate Mixed Linear Model Analysis of Longitudinal Data: An Information-Rich Statistical Technique for Analyzing Plant Disease Resistance. Phytopathology, 2012, 102, 1016-1025.	2.2	8
158	QTL Mapping of Fusarium Head Blight Resistance in Winter Wheat Cultivars 'Art' and 'Everest'. Crop Science, 2019, 59, 911-924.	1.8	8
159	Improving Wheat Yield Prediction Using Secondary Traits and High-Density Phenotyping Under Heat-Stressed Environments. Frontiers in Plant Science, 2021, 12, 633651.	3.6	8
160	Bayesian multitrait kernel methods improve multienvironment genome-based prediction. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	8
161	Fine mapping of the stem rust resistance gene SrTA10187. Theoretical and Applied Genetics, 2016, 129, 2369-2378.	3.6	7
162	Genotyping-by-sequencing to remap QTL for type II Fusarium head blight and leaf rust resistance in a wheat–tall wheatgrass introgression recombinant inbred population. Molecular Breeding, 2016, 36, 1.	2.1	7

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163	Retrospective Quantitative Genetic Analysis and Genomic Prediction of Global Wheat Yields. Frontiers in Plant Science, 2020, 11, 580136.	3.6	7
164	Genome-Wide Association and Genomic Prediction for Stripe Rust Resistance in Synthetic-Derived Wheats. Frontiers in Plant Science, 2022, 13, 788593.	3.6	7
165	Registration of a Bread Wheat Recombinant Inbred Line Mapping Population Derived from a Cross Between â€˜Harryâ€™ and â€˜Wesleyâ€™. Journal of Plant Registrations, 2018, 12, 411-414.	0.5	6
166	QTL mapping for stripe rust and powdery mildew resistance in Triticum durumâ€"Aegilops speltoides backcross introgression lines. Plant Genetic Resources: Characterisation and Utilisation, 2020, 18, 211-221.	0.8	6
167	Evaluation of fieldâ€based single plant phenotyping for wheat breeding. The Plant Phenome Journal, 2022, 5, .	2.0	6
168	Elucidating SNP-based genetic diversity and population structure of advanced breeding lines of bread wheat (<i>Triticum aestivum</i> L<i>.</i>). PeerJ, 2021, 9, e11593.	2.0	5
169	Genetic architecture and QTL selection response for Kernza perennial grain domestication traits. Theoretical and Applied Genetics, 2022, 135, 2769-2784.	3.6	4
170	Registration of Two Wheat Germplasm Lines Fixed for Pm58. Journal of Plant Registrations, 2018, 12, 270-273.	0.5	3
171	Genome-Wide Association Mapping Identifies Key Genomic Regions for Grain Zinc and Iron Biofortification in Bread Wheat. Frontiers in Plant Science, 0, 13, .	3.6	3
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