

Jesse A Poland

List of Publications by Year in descending order

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Version: 2024-02-01

180
papers

26,141
citations

17405

63
h-index

7496

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. | 1.1 | 5,470 |
| 2 | Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, . | 6.0 | 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. | 1.1 | 1,685 |
| 4 | A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. Science, 2014, 345, 1251788. | 6.0 | 1,479 |
| 5 | A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433. | 13.7 | 1,365 |
| 6 | Genotyping-by-Sequencing for Plant Breeding and Genetics. Plant Genome, 2012, 5, . | 1.6 | 703 |
| 7 | Shades of gray: the world of quantitative disease resistance. Trends in Plant Science, 2009, 14, 21-29. | 4.3 | 588 |
| 8 | Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics, 2012, 44, 803-807. | 9.4 | 577 |
| 9 | Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. Plant Genome, 2012, 5, . | 1.6 | 556 |
| 10 | Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283. | 13.7 | 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. | 3.3 | 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. | 0.8 | 336 |
| 13 | Training set optimization under population structure in genomic selection. Theoretical and Applied Genetics, 2015, 128, 145-158. | 1.8 | 284 |
| 14 | Resistance gene cloning from a wild crop relative by sequence capture and association genetics. Nature Biotechnology, 2019, 37, 139-143. | 9.4 | 280 |
| 15 | Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker × Environment Interaction Genomic Selection Model. G3: Genes, Genomes, Genetics, 2015, 5, 569-582. | 0.8 | 266 |
| 16 | Anchoring and ordering <i>NGS</i> contig assemblies by population sequencing (<i>POPSEQ</i>). Plant Journal, 2013, 76, 718-727. | 2.8 | 264 |
| 17 | A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. Genome Biology, 2015, 16, 26. | 3.8 | 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. | 3.3 | 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.. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1187-1209. | 0.8 | 226 |
| 20 | Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. <i>Nature Genetics</i> , 2019, 51, 1530-1539. | 9.4 | 216 |
| 21 | Application of unmanned aerial systems for high throughput phenotyping of large wheat breeding nurseries. <i>Plant Methods</i> , 2016, 12, 35. | 1.9 | 200 |
| 22 | Application of Genotyping-by-Sequencing on Semiconductor Sequencing Platforms: A Comparison of Genetic and Reference-Based Marker Ordering in Barley. <i>PLoS ONE</i> , 2013, 8, e76925. | 1.1 | 186 |
| 23 | Genetic Diversity and Population Structure of F3:6 Nebraska Winter Wheat Genotypes Using Genotyping-By-Sequencing. <i>Frontiers in Genetics</i> , 2018, 9, 76. | 1.1 | 183 |
| 24 | Combining High-Throughput Phenotyping and Genomic Information to Increase Prediction and Selection Accuracy in Wheat Breeding. <i>Plant Genome</i> , 2018, 11, 170043. | 1.6 | 175 |
| 25 | Imputation of Unordered Markers and the Impact on Genomic Selection Accuracy. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 427-439. | 0.8 | 172 |
| 26 | Genomic Selection for Processing and End-Use Quality Traits in the CIMMYT Spring Bread Wheat Breeding Program. <i>Plant Genome</i> , 2016, 9, plantgenome2016.01.0005. | 1.6 | 161 |
| 27 | Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. <i>PLoS ONE</i> , 2014, 9, e102448. | 1.1 | 147 |
| 28 | An evaluation of genotyping by sequencing (GBS) to map the <i>Breviaristatum-e</i> (<i>ari-e</i>) locus in cultivated barley. <i>BMC Genomics</i> , 2014, 15, 104. | 1.2 | 145 |
| 29 | Genomic Selection for Quantitative Adult Plant Stem Rust Resistance in Wheat. <i>Plant Genome</i> , 2014, 7, plantgenome2014.02.0006. | 1.6 | 143 |
| 30 | Advances and Challenges in Genomic Selection for Disease Resistance. <i>Annual Review of Phytopathology</i> , 2016, 54, 79-98. | 3.5 | 143 |
| 31 | 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 |
| 32 | Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573. | 9.4 | 138 |
| 33 | Breeder friendly phenotyping. <i>Plant Science</i> , 2020, 295, 110396. | 1.7 | 135 |
| 34 | Mapping QTL for the traits associated with heat tolerance in wheat (<i>Triticum aestivum</i> L.). <i>BMC Genetics</i> , 2014, 15, 97. | 2.7 | 133 |
| 35 | Two gap-free reference genomes and a global view of the centromere architecture in rice. <i>Molecular Plant</i> , 2021, 14, 1757-1767. | 3.9 | 133 |
| 36 | Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044. | 2.4 | 130 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Impact of Marker Ascertainment Bias on Genomic Selection Accuracy and Estimates of Genetic Diversity. <i>PLoS ONE</i> , 2013, 8, e74612. | 1.1 | 129 |
| 38 | Genome-Wide Association Study of Grain Architecture in Wild Wheat <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 886. | 1.7 | 114 |
| 39 | Increasing Genomic-Enabled Prediction Accuracy by Modeling Genotype × Environment Interactions in Kansas Wheat. <i>Plant Genome</i> , 2017, 10, plantgenome2016.12.0130. | 1.6 | 107 |
| 40 | High-Throughput Phenotyping Enabled Genetic Dissection of Crop Lodging in Wheat. <i>Frontiers in Plant Science</i> , 2019, 10, 394. | 1.7 | 104 |
| 41 | Genotyping-by-Sequencing Derived High-Density Linkage Map and its Application to QTL Mapping of Flag Leaf Traits in Bread Wheat. <i>Scientific Reports</i> , 2017, 7, 16394. | 1.6 | 103 |
| 42 | Population genomic analysis of <i>Aegilops tauschii</i> identifies targets for bread wheat improvement. <i>Nature Biotechnology</i> , 2022, 40, 422-431. | 9.4 | 102 |
| 43 | A Pipeline Strategy for Grain Crop Domestication. <i>Crop Science</i> , 2016, 56, 917-930. | 0.8 | 101 |
| 44 | 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 |
| 45 | 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 |
| 46 | The quest for understanding phenotypic variation via integrated approaches in the field environment. <i>Plant Physiology</i> , 2016, 172, pp.00592.2016. | 2.3 | 99 |
| 47 | 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 |
| 48 | 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 |
| 49 | Field Book: An Open-Source Application for Field Data Collection on Android. <i>Crop Science</i> , 2014, 54, 1624-1627. | 0.8 | 94 |
| 50 | Field-based high-throughput phenotyping of plant height in sorghum using different sensing technologies. <i>Plant Methods</i> , 2018, 14, 53. | 1.9 | 93 |
| 51 | Development of a field-based high-throughput mobile phenotyping platform. <i>Computers and Electronics in Agriculture</i> , 2016, 122, 74-85. | 3.7 | 89 |
| 52 | Development and Evolution of an Intermediate Wheatgrass Domestication Program. <i>Sustainability</i> , 2018, 10, 1499. | 1.6 | 89 |
| 53 | Resistance to Gray Leaf Spot of Maize: Genetic Architecture and Mechanisms Elucidated through Nested Association Mapping and Near-Isogenic Line Analysis. <i>PLoS Genetics</i> , 2015, 11, e1005045. | 1.5 | 86 |
| 54 | Establishment and Optimization of Genomic Selection to Accelerate the Domestication and Improvement of Intermediate Wheatgrass. <i>Plant Genome</i> , 2016, 9, plantgenome2015.07.0059. | 1.6 | 86 |

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|----|---|-----|-----------|
| 55 | A Consensus Map in Cultivated Hexaploid Oat Reveals Conserved Grass Synteny with Substantial Subgenome Rearrangement. <i>Plant Genome</i> , 2016, 9, plantgenome2015.10.0102. | 1.6 | 85 |
| 56 | Increased Genomic Prediction Accuracy in Wheat Breeding Through Spatial Adjustment of Field Trial Data. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2105-2114. | 0.8 | 80 |
| 57 | In the Eye of the Beholder: The Effect of Rater Variability and Different Rating Scales on QTL Mapping. <i>Phytopathology</i> , 2011, 101, 290-298. | 1.1 | 79 |
| 58 | Wheat quality improvement at CIMMYT and the use of genomic selection on it. <i>Applied & Translational Genomics</i> , 2016, 11, 3-8. | 2.1 | 79 |
| 59 | Efficient curation of genebanks using next generation sequencing reveals substantial duplication of germplasm accessions. <i>Scientific Reports</i> , 2019, 9, 650. | 1.6 | 79 |
| 60 | Integrating genomic-enabled prediction and high-throughput phenotyping in breeding for climate-resilient bread wheat. <i>Theoretical and Applied Genetics</i> , 2019, 132, 177-194. | 1.8 | 78 |
| 61 | Incorporating Genome-Wide Association Mapping Results Into Genomic Prediction Models for Grain Yield and Yield Stability in CIMMYT Spring Bread Wheat. <i>Frontiers in Plant Science</i> , 2020, 11, 197. | 1.7 | 78 |
| 62 | Development and Deployment of a Portable Field Phenotyping Platform. <i>Crop Science</i> , 2016, 56, 965-975. | 0.8 | 77 |
| 63 | Unlocking the novel genetic diversity and population structure of synthetic Hexaploid wheat. <i>BMC Genomics</i> , 2018, 19, 591. | 1.2 | 76 |
| 64 | Field-based high throughput phenotyping rapidly identifies genomic regions controlling yield components in rice. <i>Scientific Reports</i> , 2017, 7, 42839. | 1.6 | 74 |
| 65 | Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2735-2747. | 0.8 | 74 |
| 66 | Genome-Wide Association Study Reveals Novel Genomic Regions Associated with 10 Grain Minerals in Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3237. | 1.8 | 72 |
| 67 | 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 |
| 68 | Breeding-assisted genomics. <i>Current Opinion in Plant Biology</i> , 2015, 24, 119-124. | 3.5 | 69 |
| 69 | Genome-Wide Association Study for Identification and Validation of Novel SNP Markers for Sr6 Stem Rust Resistance Gene in Bread Wheat. <i>Frontiers in Plant Science</i> , 2018, 9, 380. | 1.7 | 68 |
| 70 | Single-Step Genomic and Pedigree Genotype × Environment Interaction Models for Predicting Wheat Lines in International Environments. <i>Plant Genome</i> , 2017, 10, plantgenome2016.09.0089. | 1.6 | 66 |
| 71 | Introgression of stem rust resistance genes SrTA10187 and SrTA10171 from <i>Aegilops tauschii</i> to wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2477-2484. | 1.8 | 65 |
| 72 | Prospects and Challenges of Applied Genomic Selection—A New Paradigm in Breeding for Grain Yield in Bread Wheat. <i>Plant Genome</i> , 2018, 11, 180017. | 1.6 | 65 |

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|----|---|-----|-----------|
| 73 | A SNP Genotyping Array for Hexaploid Oat. <i>Plant Genome</i> , 2014, 7, plantgenome2014.03.0010. | 1.6 | 63 |
| 74 | Construction of a SNP and SSR linkage map in autotetraploid blueberry using genotyping by sequencing. <i>Molecular Breeding</i> , 2016, 36, 1. | 1.0 | 63 |
| 75 | Linkage Map Construction and Quantitative Trait Locus Analysis of Agronomic and Fiber Quality Traits in Cotton. <i>Plant Genome</i> , 2014, 7, plantgenome2013.07.0023. | 1.6 | 62 |
| 76 | Simultaneous transfer, introgression, and genomic localization of genes for resistance to stem rust race TTKSK (Ug99) from <i>Aegilops tauschii</i> to wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1179-1188. | 1.8 | 61 |
| 77 | Global Wheat Head Detection 2021: An Improved Dataset for Benchmarking Wheat Head Detection Methods. <i>Plant Phenomics</i> , 2021, 2021, 9846158. | 2.5 | 60 |
| 78 | Unraveling Genomic Complexity at a Quantitative Disease Resistance Locus in Maize. <i>Genetics</i> , 2014, 198, 333-344. | 1.2 | 51 |
| 79 | Multivariate Genomic Selection and Potential of Rapid Indirect Selection with Speed Breeding in Spring Wheat. <i>Crop Science</i> , 2019, 59, 1945-1959. | 0.8 | 51 |
| 80 | Breeding-assisted genomics: Applying meta-GWAS for milling and baking quality in CIMMYT wheat breeding program. <i>PLoS ONE</i> , 2018, 13, e0204757. | 1.1 | 50 |
| 81 | Exploring the tertiary gene pool of bread wheat: sequence assembly and analysis of chromosome 5M ^g of <i>Aegilops geniculata</i> . <i>Plant Journal</i> , 2015, 84, 733-746. | 2.8 | 48 |
| 82 | 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 |
| 83 | The <i>Aegilops ventricosa</i> 2NvS segment in bread wheat: cytology, genomics and breeding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 529-542. | 1.8 | 48 |
| 84 | <i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607. | 5.8 | 48 |
| 85 | Genomic Analysis Confirms Population Structure and Identifies Inter-Lineage Hybrids in <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 9. | 1.7 | 47 |
| 86 | Targeted discovery of quantitative trait loci for resistance to northern leaf blight and other diseases of maize. <i>Theoretical and Applied Genetics</i> , 2011, 123, 307-326. | 1.8 | 45 |
| 87 | Genome-Wide Association Mapping of Grain Micronutrients Concentration in <i>Aegilops tauschii</i> . <i>Frontiers in Plant Science</i> , 2019, 10, 54. | 1.7 | 45 |
| 88 | 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 |
| 89 | Genome-wide association mapping of agronomic traits and carbon isotope discrimination in a worldwide germplasm collection of spring wheat using SNP markers. <i>Molecular Breeding</i> , 2015, 35, 1. | 1.0 | 43 |
| 90 | Development of the first consensus genetic map of intermediate wheatgrass (<i>Thinopyrum</i>) Tj ETQq0 0 0 rgBT /Overclock 10 Tf 50 62 Td | 1.8 | 43 |

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|-----|--|-----|-----------|
| 91 | Application of Population Sequencing (POPSEQ) for Ordering and Imputing Genotyping-by-Sequencing Markers in Hexaploid Wheat. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2547-2553. | 0.8 | 40 |
| 92 | Genotype-by-sequencing facilitates genetic mapping of a stem rust resistance locus in <i>Aegilops umbellulata</i> , a wild relative of cultivated wheat. <i>BMC Genomics</i> , 2016, 17, 1039. | 1.2 | 39 |
| 93 | Strategies for Selecting Crosses Using Genomic Prediction in Two Wheat Breeding Programs. <i>Plant Genome</i> , 2017, 10, plantgenome2016.12.0128. | 1.6 | 37 |
| 94 | Reference Genome Anchoring of High-Density Markers for Association Mapping and Genomic Prediction in European Winter Wheat. <i>Frontiers in Plant Science</i> , 2019, 10, 1278. | 1.7 | 37 |
| 95 | Precisely mapping a major gene conferring resistance to Hessian fly in bread wheat using genotyping-by-sequencing. <i>BMC Genomics</i> , 2015, 16, 108. | 1.2 | 36 |
| 96 | 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 |
| 97 | Utilizing High-Throughput Phenotypic Data for Improved Phenotypic Selection of Stress-Adaptive Traits in Wheat. <i>Crop Science</i> , 2017, 57, 648-659. | 0.8 | 34 |
| 98 | QTL mapping for yield and lodging resistance in an enhanced SSR-based map for <i>tef</i> . <i>Theoretical and Applied Genetics</i> , 2011, 122, 77-93. | 1.8 | 32 |
| 99 | QTL mapping of pre-harvest sprouting resistance in a white wheat cultivar Danby. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1683-1697. | 1.8 | 32 |
| 100 | Genome-Wide Association Study for Multiple Biotic Stress Resistance in Synthetic Hexaploid Wheat. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3667. | 1.8 | 31 |
| 101 | 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 |
| 102 | Genetic Mapping of Race-Specific Stem Rust Resistance in the Synthetic Hexaploid W7984 Å— Opatá M85 Mapping Population. <i>Crop Science</i> , 2015, 55, 2580-2588. | 0.8 | 30 |
| 103 | Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass (<i>Thinopyrum intermedium</i>). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2325-2351. | 1.8 | 30 |
| 104 | Haplotype-Based, Genome-Wide Association Study Reveals Stable Genomic Regions for Grain Yield in CIMMYT Spring Bread Wheat. <i>Frontiers in Genetics</i> , 2020, 11, 589490. | 1.1 | 29 |
| 105 | Cloning of the broadly effective wheat leaf rust resistance gene <i>Lr42</i> transferred from <i>Aegilops tauschii</i> . <i>Nature Communications</i> , 2022, 13, . | 5.8 | 29 |
| 106 | Dense genotyping-by-sequencing linkage maps of two Synthetic W7984 Å— Opatá reference populations provide insights into wheat structural diversity. <i>Scientific Reports</i> , 2019, 9, 1793. | 1.6 | 28 |
| 107 | Enhancing Crop Domestication Through Genomic Selection, a Case Study of Intermediate Wheatgrass. <i>Frontiers in Plant Science</i> , 2020, 11, 319. | 1.7 | 28 |
| 108 | High-throughput phenotyping with deep learning gives insight into the genetic architecture of flowering time in wheat. <i>GigaScience</i> , 2019, 8, . | 3.3 | 28 |

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|-----|--|-----|-----------|
| 109 | Application of Geographically Weighted Regression to Improve Grain Yield Prediction from Unmanned Aerial System Imagery. <i>Crop Science</i> , 2017, 57, 2478-2489. | 0.8 | 27 |
| 110 | Genome-wide association mapping for wheat blast resistance in CIMMYT's international screening nurseries evaluated in Bolivia and Bangladesh. <i>Scientific Reports</i> , 2020, 10, 15972. | 1.6 | 27 |
| 111 | Genomic Selection for Grain Yield in the CIMMYT Wheat Breeding Program—Status and Perspectives. <i>Frontiers in Plant Science</i> , 2020, 11, 564183. | 1.7 | 27 |
| 112 | Uncovering the Genetic Architecture of Seed Weight and Size in Intermediate Wheatgrass through Linkage and Association Mapping. <i>Plant Genome</i> , 2017, 10, plantgenome2017.03.0022. | 1.6 | 26 |
| 113 | Molecular diversity and landscape genomics of the crop wild relative <i>Triticum urartu</i> across the Fertile Crescent. <i>Plant Journal</i> , 2018, 94, 670-684. | 2.8 | 26 |
| 114 | A Field-Based Analysis of Genetic Improvement for Grain Yield in Winter Wheat Cultivars Developed in the US Central Plains from 1992 to 2014. <i>Crop Science</i> , 2019, 59, 905-910. | 0.8 | 26 |
| 115 | Genome-based prediction of multiple wheat quality traits in multiple years. <i>Plant Genome</i> , 2020, 13, e20034. | 1.6 | 25 |
| 116 | Local adaptation, genetic divergence, and experimental selection in a foundation grass across the US Great Plains climate gradient. <i>Global Change Biology</i> , 2019, 25, 850-868. | 4.2 | 24 |
| 117 | New QTLs for Spot Blotch Disease Resistance in Wheat (<i>Triticum aestivum</i> L.) Using Genome-Wide Association Mapping. <i>Frontiers in Genetics</i> , 2020, 11, 613217. | 1.1 | 24 |
| 118 | A whole-genome, radiation hybrid mapping resource of hexaploid wheat. <i>Plant Journal</i> , 2016, 86, 195-207. | 2.8 | 23 |
| 119 | Improving Genomic Prediction for Pre-Harvest Sprouting Tolerance in Wheat by Weighting Large-Effect Quantitative Trait Loci. <i>Crop Science</i> , 2017, 57, 1315-1324. | 0.8 | 22 |
| 120 | Genomic prediction enables rapid selection of high-performing genets in an intermediate wheatgrass breeding program. <i>Plant Genome</i> , 2021, 14, e20080. | 1.6 | 21 |
| 121 | Quantifying variety-specific heat resistance and the potential for adaptation to climate change. <i>Global Change Biology</i> , 2016, 22, 2904-2912. | 4.2 | 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. <i>Communications Biology</i> , 2021, 4, 944. | 2.0 | 20 |
| 124 | Spiked GBS: a unified, open platform for single marker genotyping and whole-genome profiling. <i>BMC Genomics</i> , 2015, 16, 248. | 1.2 | 19 |
| 125 | Development of a complete set of wheat-barley group-7 Robertsonian translocation chromosomes conferring an increased content of β -glucan. <i>Theoretical and Applied Genetics</i> , 2018, 131, 377-388. | 1.8 | 19 |
| 126 | Production of a complete set of wheat-barley group-7 chromosome recombinants with increased grain β -glucan content. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3129-3141. | 1.8 | 18 |

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|-----|--|-----|-----------|
| 127 | A TILLING Resource for Hard Red Winter Wheat Variety Jagger. <i>Crop Science</i> , 2019, 59, 1666-1671. | 0.8 | 17 |
| 128 | Breedbase: a digital ecosystem for modern plant breeding. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, . | 0.8 | 17 |
| 129 | Genomic Selection for Increased Yield in Syntheticâ€Derived Wheat. <i>Crop Science</i> , 2017, 57, 713-725. | 0.8 | 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. <i>Plant and Cell Physiology</i> , 2021, 62, 8-27. | 1.5 | 16 |
| 131 | Accelerated Domestication of New Crops: Yield is Key. <i>Plant and Cell Physiology</i> , 2022, 63, 1624-1640. | 1.5 | 16 |
| 132 | QTL mapping of Fusarium head blight resistance and deoxynivalenol accumulation in the Kansas wheat variety â€Everestâ€™. <i>Molecular Breeding</i> , 2019, 39, 1. | 1.0 | 15 |
| 133 | Recurrent genomic selection for wheat grain fructans. <i>Crop Science</i> , 2020, 60, 1499-1512. | 0.8 | 15 |
| 134 | High molecular weight glutenin gene diversity in <i>Aegilops tauschii</i> demonstrates unique origin of superior wheat quality. <i>Communications Biology</i> , 2021, 4, 1242. | 2.0 | 14 |
| 135 | Joint Use of Genome, Pedigree, and Their Interaction with Environment for Predicting the Performance of Wheat Lines in New Environments. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2925-2934. | 0.8 | 13 |
| 136 | Sequenced-based paternity analysis to improve breeding and identify self-incompatibility loci in intermediate wheatgrass (<i>Thinopyrum intermedium</i>). <i>Theoretical and Applied Genetics</i> , 2020, 133, 3217-3233. | 1.8 | 13 |
| 137 | Genomic Selection for Wheat Blast in a Diversity Panel, Breeding Panel and Full-Sibs Panel. <i>Frontiers in Plant Science</i> , 2021, 12, 745379. | 1.7 | 13 |
| 138 | Genetic characterization and curation of diploid A-genome wheat species. <i>Plant Physiology</i> , 2022, 188, 2101-2114. | 2.3 | 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. <i>Molecular Breeding</i> , 2018, 38, 1. | 1.0 | 12 |
| 140 | Improved Accuracy of High-Throughput Phenotyping From Unmanned Aerial Systems by Extracting Traits Directly From Orthorectified Images. <i>Frontiers in Plant Science</i> , 2020, 11, 587093. | 1.7 | 12 |
| 141 | Adaptive genetic potential and plasticity of trait variation in the foundation prairie grass <i>Andropogon gerardii</i> across the US Great Plainsâ€™ climate gradient: Implications for climate change and restoration. <i>Evolutionary Applications</i> , 2020, 13, 2333-2356. | 1.5 | 12 |
| 142 | Development of wholeâ€genome prediction models to increase the rate of genetic gain in intermediate wheatgrass (<i>Thinopyrum intermedium</i>) breeding. <i>Plant Genome</i> , 2021, 14, e20089. | 1.6 | 12 |
| 143 | Accelerating wheat breeding for endâ€use quality through association mapping and multivariate genomic prediction. <i>Plant Genome</i> , 2021, 14, e20164. | 1.6 | 12 |
| 144 | <sc>SNPM</sc>eta: <sc>SNP</sc> annotation and <sc>SNP</sc> metadata collection without a reference genome. <i>Molecular Ecology Resources</i> , 2014, 14, 419-425. | 2.2 | 11 |

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