Jesse A Poland

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	Population genomic analysis of Aegilops tauschii identifies targets for bread wheat improvement. Nature Biotechnology, 2022, 40, 422-431.	17.5	102
2	Bayesian multitrait kernel methods improve multienvironment genome-based prediction. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	8
3	Intercross: An Android app for plant breeding and genetics cross management. Crop Science, 2022, 62, 820-824.	1.8	1
4	Genetic characterization and curation of diploid A-genome wheat species. Plant Physiology, 2022, 188, 2101-2114.	4.8	13
5	Genome-Wide Association and Genomic Prediction for Stripe Rust Resistance in Synthetic-Derived Wheats. Frontiers in Plant Science, 2022, 13, 788593.	3.6	7
6	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
7	Aegilops sharonensis genome-assisted identification of stem rust resistance gene Sr62. Nature Communications, 2022, 13, 1607.	12.8	48
8	Applied phenomics and genomics for improving barley yellow dwarf resistance in winter wheat. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	1
9	Breedbase: a digital ecosystem for modern plant breeding. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	17
10	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
11	Accelerated Domestication of New Crops: Yield is Key. Plant and Cell Physiology, 2022, 63, 1624-1640.	3.1	16
12	Cloning of the broadly effective wheat leaf rust resistance gene Lr42 transferred from Aegilops tauschii. Nature Communications, 2022, 13, .	12.8	29
13	Evaluation of field‐based single plant phenotyping for wheat breeding. The Plant Phenome Journal, 2022, 5, .	2.0	6
14	Genetic architecture and QTL selection response for Kernza perennial grain domestication traits. Theoretical and Applied Genetics, 2022, 135, 2769-2784.	3.6	4
15	The Aegilops ventricosa 2NvS segment in bread wheat: cytology, genomics and breeding. Theoretical and Applied Genetics, 2021, 134, 529-542.	3.6	48
16	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
17	Prospector: A mobile application for portable, high‐throughput near‐infrared spectroscopy phenotyping. The Plant Phenome Journal, 2021, 4, e20024.	2.0	0
18	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

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19	Population genomics and haplotype analysis in spelt and bread wheat identifies a gene regulating glume color. Communications Biology, 2021, 4, 375.	4.4	11
20	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nature Genetics, 2021, 53, 564-573.	21.4	138
21	Genomic prediction enables rapid selection of high‐performing genets in an intermediate wheatgrass breeding program. Plant Genome, 2021, 14, e20080.	2.8	21
22	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
23	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
24	Elucidating SNP-based genetic diversity and population structure of advanced breeding lines of bread wheat (*Triticum aestivum* L*.*). PeerJ, 2021, 9, e11593.	2.0	5
25	Two gap-free reference genomes and a global view of the centromere architecture in rice. Molecular Plant, 2021, 14, 1757-1767.	8.3	133
26	Data-driven decentralized breeding increases prediction accuracy in a challenging crop production environment. Communications Biology, 2021, 4, 944.	4.4	20
27	Global Wheat Head Detection 2021: An Improved Dataset for Benchmarking Wheat Head Detection Methods. Plant Phenomics, 2021, 2021, 9846158.	5.9	60
28	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
29	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
30	Experiences of Applying Field-Based High-Throughput Phenotyping for Wheat Breeding. Concepts and Strategies in Plant Sciences, 2021, , 71-99.	0.5	0
31	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
32	High molecular weight glutenin gene diversity in Aegilops tauschii demonstrates unique origin of superior wheat quality. Communications Biology, 2021, 4, 1242.	4.4	14
33	Accelerating wheat breeding for end‐use quality through association mapping and multivariate genomic prediction. Plant Genome, 2021, 14, e20164.	2.8	12
34	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
35	Response to Early Generation Genomic Selection for Yield in Wheat. Frontiers in Plant Science, 2021, 12, 718611.	3.6	10
36	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

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37	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
38	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
39	Recurrent genomic selection for wheat grain fructans. Crop Science, 2020, 60, 1499-1512.	1.8	15
40	Multiple wheat genomes reveal global variation in modern breeding. Nature, 2020, 588, 277-283.	27.8	513
41	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
42	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
43	Retrospective Quantitative Genetic Analysis and Genomic Prediction of Global Wheat Yields. Frontiers in Plant Science, 2020, 11, 580136.	3.6	7
44	Genomeâ€based prediction of multiple wheat quality traits in multiple years. Plant Genome, 2020, 13, e20034.	2.8	25
45	Genomic Selection for Grain Yield in the CIMMYT Wheat Breeding Programâ€"Status and Perspectives. Frontiers in Plant Science, 2020, 11, 564183.	3.6	27
46	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
47	Registration of Hessian flyâ€resistant germplasm KS18WGRC65 carrying *H26* in hard red winter wheat â€˜Overleyâ€™ background. Journal of Plant Registrations, 2020, 14, 206-209.	0.5	2
48	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
49	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
50	Implementing withinâ€cross genomic prediction to reduce oat breeding costs. Plant Genome, 2020, 13, e20004.	2.8	11
51	Breeder friendly phenotyping. Plant Science, 2020, 295, 110396.	3.6	135
52	In-silico detection of aneuploidy and chromosomal deletions in wheat using genotyping-by-sequencing. Plant Methods, 2020, 16, 45.	4.3	2
53	Enhancing Crop Domestication Through Genomic Selection, a Case Study of Intermediate Wheatgrass. Frontiers in Plant Science, 2020, 11, 319.	3.6	28
54	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

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55	Multivariate Genomic Selection and Potential of Rapid Indirect Selection with Speed Breeding in Spring Wheat. Crop Science, 2019, 59, 1945-1959.	1.8	51
56	QTL Mapping of Fusarium Head Blight Resistance in Winter Wheat Cultivars â€˜Artâ€™ and â€˜Everestâ€™. Crop Science, 2019, 59, 911-924.	1.8	8
57	Genome-Wide Association Study for Multiple Biotic Stress Resistance in Synthetic Hexaploid Wheat. International Journal of Molecular Sciences, 2019, 20, 3667.	4.1	31
58	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
59	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
60	Efficient curation of genebanks using next generation sequencing reveals substantial duplication of germplasm accessions. Scientific Reports, 2019, 9, 650.	3.3	79
61	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
62	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
63	A TILLING Resource for Hard Red Winter Wheat Variety Jagger. Crop Science, 2019, 59, 1666-1671.	1.8	17
64	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
65	Hyperspectral Reflectance-Derived Relationship Matrices for Genomic Prediction of Grain Yield in Wheat. G3: Genes, Genomes, Genetics, 2019, 9, 1231-1247.	1.8	96
66	High-Throughput Phenotyping Enabled Genetic Dissection of Crop Lodging in Wheat. Frontiers in Plant Science, 2019, 10, 394.	3.6	104
67	Genomic Analysis Confirms Population Structure and Identifies Inter-Lineage Hybrids in Aegilops tauschii. Frontiers in Plant Science, 2019, 10, 9.	3.6	47
68	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
69	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
70	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
71	Genome-Wide Association Mapping of Grain Micronutrients Concentration in Aegilops tauschii. Frontiers in Plant Science, 2019, 10, 54.	3.6	45
72	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

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73	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
74	Improving grain yield, stress resilience and quality of bread wheat using large-scale genomics. Nature Genetics, 2019, 51, 1530-1539.	21.4	216
75	Local adaptation, genetic divergence, and experimental selection in a foundation grass across the US Great Plains' climate gradient. Global Change Biology, 2019, 25, 850-868.	9.5	24
76	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
77	Resistance gene cloning from a wild crop relative by sequence capture and association genetics. Nature Biotechnology, 2019, 37, 139-143.	17.5	280
78	High-throughput phenotyping with deep learning gives insight into the genetic architecture of flowering time in wheat. GigaScience, 2019, 8, .	6.4	28
79	Small plot identification from video streams for high-throughput phenotyping of large breeding populations with unmanned aerial systems. , 2019, , .		2
80	Molecular diversity and landscape genomics of the crop wild relative *Triticum urartu* across the Fertile Crescent. Plant Journal, 2018, 94, 670-684.	5.7	26
81	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
82	Development of a complete set of wheat–barley group-7 Robertsonian translocation chromosomes conferring an increased content of β-glucan. Theoretical and Applied Genetics, 2018, 131, 377-388.	3.6	19
83	Registration of Two Wheat Germplasm Lines Fixed for Pm58. Journal of Plant Registrations, 2018, 12, 270-273.	0.5	3
84	Development and Evolution of an Intermediate Wheatgrass Domestication Program. Sustainability, 2018, 10, 1499.	3.2	89
85	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
86	Breeding-assisted genomics: Applying meta-GWAS for milling and baking quality in CIMMYT wheat breeding program. PLoS ONE, 2018, 13, e0204757.	2.5	50
87	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
88	Genomic Analysis and Prediction within a US Public Collaborative Winter Wheat Regional Testing Nursery. Plant Genome, 2018, 11, 180004.	2.8	10
89	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
90	Registration of a Bread Wheat Recombinant Inbred Line Mapping Population Derived from a Cross Between 'Harry' and 'Wesley'. Journal of Plant Registrations, 2018, 12, 411-414.	0.5	6

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91	Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. G3: Genes, Genomes, Genetics, 2018, 8, 2735-2747.	1.8	74
92	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
93	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
94	Field-based high-throughput phenotyping of plant height in sorghum using different sensing technologies. Plant Methods, 2018, 14, 53.	4.3	93
95	Combining High‐Throughput Phenotyping and Genomic Information to Increase Prediction and Selection Accuracy in Wheat Breeding. Plant Genome, 2018, 11, 170043.	2.8	175
96	Shifting the limits in wheat research and breeding using a fully annotated reference genome. Science, 2018, 361, .	12.6	2,424
97	Unlocking the novel genetic diversity and population structure of synthetic Hexaploid wheat. BMC Genomics, 2018, 19, 591.	2.8	76
98	QTL mapping of pre-harvest sprouting resistance in a white wheat cultivar Danby. Theoretical and Applied Genetics, 2018, 131, 1683-1697.	3.6	32
99	Field-based high throughput phenotyping rapidly identifies genomic regions controlling yield components in rice. Scientific Reports, 2017, 7, 42839.	3.3	74
100	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
101	A chromosome conformation capture ordered sequence of the barley genome. Nature, 2017, 544, 427-433.	27.8	1,365
102	Construction of a map-based reference genome sequence for barley, Hordeum vulgare L.. Scientific Data, 2017, 4, 170044.	5.3	130
103	Genomic Selection for Increased Yield in Synthetic‐Derived Wheat. Crop Science, 2017, 57, 713-725.	1.8	16
104	Utilizing High‐Throughput Phenotypic Data for Improved Phenotypic Selection of Stress‐Adaptive Traits in Wheat. Crop Science, 2017, 57, 648-659.	1.8	34
105	Single‐Step Genomic and Pedigree Genotype Ã— Environment Interaction Models for Predicting Wheat Lines in International Environments. Plant Genome, 2017, 10, plantgenome2016.09.0089.	2.8	66
106	Strategies for Selecting Crosses Using Genomic Prediction in Two Wheat Breeding Programs. Plant Genome, 2017, 10, plantgenome2016.12.0128.	2.8	37
107	Genomic Selection for Small Grain Improvement. , 2017, , 99-130.		20
108	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

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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	Improving Genomic Prediction for Pre-Harvest Sprouting Tolerance in Wheat by Weighting Large-Effect Quantitative Trait Loci. Crop Science, 2017, 57, 1315-1324.	1.8	22
111	Review Articles: The Black-Market of Scientific Currency. Annals of the Entomological Society of America, 2017, 110, 90-90.	2.5	2
112	Development of the first consensus genetic map of intermediate wheatgrass (Thinopyrum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td	3.6	43
113	Genome-Wide Association Study of Grain Architecture in Wild Wheat Aegilops tauschii. Frontiers in Plant Science, 2017, 8, 886.	3.6	114
114	Increasing Genomic-Enabled Prediction Accuracy by Modeling Genotype Ã— Environment Interactions in Kansas Wheat. Plant Genome, 2017, 10, plantgenome2016.12.0130.	2.8	107
115	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. Plant Genome, 2017, 10, plantgenome2016.08.0082.	2.8	48
116	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
117	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
118	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
119	Mapping Four Quantitative Trait Loci Associated with Type I Fusarium Head Blight Resistance in Winter Wheat â€˜INW0412â€™. Crop Science, 2016, 56, 1163-1172.	1.8	2
120	A Pipeline Strategy for Grain Crop Domestication. Crop Science, 2016, 56, 917-930.	1.8	101
121	Quantifying variety-specific heat resistance and the potential for adaptation to climate change. Global Change Biology, 2016, 22, 2904-2912.	9.5	20
122	A whole-genome, radiation hybrid mapping resource of hexaploid wheat. Plant Journal, 2016, 86, 195-207.	5.7	23
123	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
124	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
125	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
126	The quest for understanding phenotypic variation via integrated approaches in the field environment. Plant Physiology, 2016, 172, pp.00592.2016.	4.8	99

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127	Construction of a SNP and SSR linkage map in autotetraploid blueberryÂusing genotyping by sequencing. Molecular Breeding, 2016, 36, 1.	2.1	63
128	Fine mapping of the stem rust resistance gene SrTA10187. Theoretical and Applied Genetics, 2016, 129, 2369-2378.	3.6	7
129	Advances and Challenges in Genomic Selection for Disease Resistance. Annual Review of Phytopathology, 2016, 54, 79-98.	7.8	143
130	Wheat quality improvement at CIMMYT and the use of genomic selection on it. Applied & Translational Genomics, 2016, 11, 3-8.	2.1	79
131	Application of unmanned aerial systems for high throughput phenotyping of large wheat breeding nurseries. Plant Methods, 2016, 12, 35.	4.3	200
132	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
133	Development and Deployment of a Portable Field Phenotyping Platform. Crop Science, 2016, 56, 965-975.	1.8	77
134	Genotyping-by-sequencing to remap QTL for type II Fusarium head blight and leaf rust resistance in a wheatâ€"tall wheatgrass introgression recombinant inbred population. Molecular Breeding, 2016, 36, 1.	2.1	7
135	Development of a field-based high-throughput mobile phenotyping platform. Computers and Electronics in Agriculture, 2016, 122, 74-85.	7.7	89
136	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
137	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
138	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
139	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
140	Effect of cytoplasmic diversity on post anthesis heat tolerance in wheat. Euphytica, 2015, 204, 383-394.	1.2	11
141	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
142	Development of a 63K SNP Array for Cotton and High-Density Mapping of Intraspecific and Interspecific Populations of *Gossypium* spp.. G3: Genes, Genomes, Genetics, 2015, 5, 1187-1209.	1.8	226
143	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
144	Training set optimization under population structure in genomic selection. Theoretical and Applied Genetics, 2015, 128, 145-158.	3.6	284

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145	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
146	Spiked GBS: a unified, open platform for single marker genotyping and whole-genome profiling. BMC Genomics, 2015, 16, 248.	2.8	19
147	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. Genome Biology, 2015, 16, 26.	8.8	256
148	Breeding-assisted genomics. Current Opinion in Plant Biology, 2015, 24, 119-124.	7.1	69
149	Increased Prediction Accuracy in Wheat Breeding Trials Using a Marker × Environment Interaction Genomic Selection Model. G3: Genes, Genomes, Genetics, 2015, 5, 569-582.	1.8	266
150	Using Genotyping-By-Sequencing (GBS) for Genomic Discovery in Cultivated Oat. PLoS ONE, 2014, 9, e102448.	2.5	147
151	Genomic Selection for Quantitative Adult Plant Stem Rust Resistance in Wheat. Plant Genome, 2014, 7, plantgenome2014.02.0006.	2.8	143
152	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
153	A SNP Genotyping Array for Hexaploid Oat. Plant Genome, 2014, 7, plantgenome2014.03.0010.	2.8	63
154	Mapping QTL for the traits associated with heat tolerance in wheat (Triticum aestivumL.). BMC Genetics, 2014, 15, 97.	2.7	133
155	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
156	Unraveling Genomic Complexity at a Quantitative Disease Resistance Locus in Maize. Genetics, 2014, 198, 333-344.	2.9	51
157	<scp>SNPM</scp>eta: <scp>SNP</scp> annotation and <scp>SNP</scp> metadata collection without a reference genome. Molecular Ecology Resources, 2014, 14, 419-425.	4.8	11
158	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. Science, 2014, 345, 1251788.	12.6	1,479
159	Field Book: An Open–Source Application for Field Data Collection on Android. Crop Science, 2014, 54, 1624-1627.	1.8	94
160	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
161	Anchoring and ordering <scp>NGS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). Plant Journal, 2013, 76, 718-727.	5.7	264
162	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

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163	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
164	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
165	Imputation of Unordered Markers and the Impact on Genomic Selection Accuracy. G3: Genes, Genomes, Genetics, 2013, 3, 427-439.	1.8	172
166	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
167	Impact of Marker Ascertainment Bias on Genomic Selection Accuracy and Estimates of Genetic Diversity. PLoS ONE, 2013, 8, e74612.	2.5	129
168	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
169	Genomic Selection in Wheat Breeding using Genotypingâ€byâ€Sequencing. Plant Genome, 2012, 5, .	2.8	556
170	Genotypingâ€byâ€Sequencing for Plant Breeding and Genetics. Plant Genome, 2012, 5, .	2.8	703
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