

# Jorge Dubcovsky

## List of Publications by Year in descending order

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252  
papers

31,754  
citations

4146

87  
h-index

4885

168  
g-index

272  
all docs

272  
docs citations

272  
times ranked

12594  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. <i>Plant Biotechnology Journal</i> , 2014, 12, 787-796.	8.3	1,828
2	A NAC Gene Regulating Senescence Improves Grain Protein, Zinc, and Iron Content in Wheat. <i>Science</i> , 2006, 314, 1298-1301.	12.6	1,408
3	Positional cloning of the wheat vernalization gene <i>VRN1</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6263-6268.	7.1	1,254
4	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.	7.1	1,065
5	The Wheat <i>VRN2</i> Gene Is a Flowering Repressor Down-Regulated by Vernalization. <i>Science</i> , 2004, 303, 1640-1644.	12.6	999
6	The wheat and barley vernalization gene <i>VRN3</i> is an orthologue of <i>FT</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19581-19586.	7.1	937
7	Genome Plasticity a Key Factor in the Success of Polyploid Wheat Under Domestication. <i>Science</i> , 2007, 316, 1862-1866.	12.6	886
8	A Kinase-START Gene Confers Temperature-Dependent Resistance to Wheat Stripe Rust. <i>Science</i> , 2009, 323, 1357-1360.	12.6	625
9	Large deletions within the first intron in VRN-1 are associated with spring growth habit in barley and wheat. <i>Molecular Genetics and Genomics</i> , 2005, 273, 54-65.	2.1	592
10	Uncovering hidden variation in polyploid wheat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E913-E921.	7.1	554
11	Allelic variation at the VRN-1 promoter region in polyploid wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1677-1686.	3.6	448
12	Regulation of flowering in temperate cereals. <i>Current Opinion in Plant Biology</i> , 2009, 12, 178-184.	7.1	423
13	A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. <i>Plant Biotechnology Journal</i> , 2015, 13, 648-663.	8.3	386
14	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.	2.9	369
15	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. <i>Genome Research</i> , 2003, 13, 1818-1827.	5.5	369
16	A Genome-Wide Association Study of Resistance to Stripe Rust ( <i>Puccinia striiformis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 147 G3: Genes, Genomes, Genetics, 2015, 5, 449-465.	1.8	356
17	Genetic mapping of 66 new microsatellite (SSR) loci in bread wheat. <i>Theoretical and Applied Genetics</i> , 2002, 105, 413-422.	3.6	339
18	PCR Assays for the <i>Lr37</i> - <i>Yr17</i> - <i>Sr38</i> Cluster of Rust Resistance Genes and Their Use to Develop Isogenic Hard Red Spring Wheat Lines. <i>Crop Science</i> , 2003, 43, 1839-1847.	1.8	334

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19	A modified TILLING approach to detect induced mutations in tetraploid and hexaploid wheat. BMC Plant Biology, 2009, 9, 115.	3.6	323
20	Wheat ( <i>Triticum aestivum</i> ) NAM proteins regulate the translocation of iron, zinc, and nitrogen compounds from vegetative tissues to grain. Journal of Experimental Botany, 2009, 60, 4263-4274.	4.8	300
21	The Organization and Rate of Evolution of Wheat Genomes Are Correlated With Recombination Rates Along Chromosome Arms. Genome Research, 2003, 13, 753-763.	5.5	298
22	Identification of Wheat Gene <i>Sr35</i> That Confers Resistance to Ug99 Stem Rust Race Group. Science, 2013, 341, 783-786.	12.6	283
23	Efficient Genome-Wide Detection and Cataloging of EMS-Induced Mutations Using Exome Capture and Next-Generation Sequencing. Plant Cell, 2014, 26, 1382-1397.	6.6	277
24	A GRF-GIF chimeric protein improves the regeneration efficiency of transgenic plants. Nature Biotechnology, 2020, 38, 1274-1279.	17.5	272
25	Discovery of Rare Mutations in Populations: TILLING by Sequencing. Plant Physiology, 2011, 156, 1257-1268.	4.8	266
26	Molecular and Structural Characterization of Barley Vernalization Genes. Plant Molecular Biology, 2005, 59, 449-467.	3.9	258
27	Effect of Photoperiod on the Regulation of Wheat Vernalization Genes VRN1 and VRN2. Plant Molecular Biology, 2006, 60, 469-480.	3.9	256
28	The high grain protein content gene Gpc-B1 accelerates senescence and has pleiotropic effects on protein content in wheat. Journal of Experimental Botany, 2006, 57, 2785-2794.	4.8	252
29	Genetic Map of Diploid Wheat, <i>Triticum monococcum</i> L., and Its Comparison With Maps of <i>Hordeum vulgare</i> L.. Genetics, 1996, 143, 983-999.	2.9	250
30	Genome analyses of the wheat yellow (stripe) rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> reveal polymorphic and haustorial expressed secreted proteins as candidate effectors. BMC Genomics, 2013, 14, 270.	2.8	235
31	Population- and genome-specific patterns of linkage disequilibrium and SNP variation in spring and winter wheat ( <i>Triticum aestivum</i> L.). BMC Genomics, 2010, 11, 727.	2.8	234
32	Rapid Genome Divergence at Orthologous Low Molecular Weight Glutenin Loci of the A and Am Genomes of Wheat[W]. Plant Cell, 2003, 15, 1186-1197.	6.6	226
33	Wheat FT protein regulates <i>VRN1</i> transcription through interactions with FDL2. Plant Journal, 2008, 55, 543-554.	5.7	217
34	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. Genome Biology, 2015, 16, 48.	8.8	216
35	Wheat TILLING Mutants Show That the Vernalization Gene VRN1 Down-Regulates the Flowering Repressor VRN2 in Leaves but Is Not Essential for Flowering. PLoS Genetics, 2012, 8, e1003134.	3.5	213
36	The cold-regulated transcriptional activator Cbf3 is linked to the frost-tolerance locus Fr-A2 on wheat chromosome 5A. Molecular Genetics and Genomics, 2003, 269, 60-67.	2.1	212

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37	High-temperature adult-plant (HTAP) stripe rust resistance gene Yr36 from <i>Triticum turgidum</i> ssp. <i>dicoccoides</i> is closely linked to the grain protein content locus Gpc-B1. <i>Theoretical and Applied Genetics</i> , 2005, 112, 97-105.	3.6	208
38	Comparative Sequence Analysis of Colinear Barley and Rice Bacterial Artificial Chromosomes. <i>Plant Physiology</i> , 2001, 125, 1342-1353.	4.8	204
39	Cloning of the wheat Yr15 resistance gene sheds light on the plant tandem kinase-pseudokinase family. <i>Nature Communications</i> , 2018, 9, 3735.	12.8	204
40	Regulation of VRN-1 Vernalization Genes in Normal and Transgenic Polyploid Wheat. <i>Plant Physiology</i> , 2005, 138, 2364-2373.	4.8	190
41	Genome comparisons reveal a dominant mechanism of chromosome number reduction in grasses and accelerated genome evolution in Triticeae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15780-15785.	7.1	190
42	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	2.8	189
43	A splice acceptor site mutation in TaGW2-A1 increases thousand grain weight in tetraploid and hexaploid wheat through wider and longer grains. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1099-1112.	3.6	179
44	Variation in the <i>AvrSr35</i> gene determines <i>Sr35</i> resistance against wheat stem rust race Ug99. <i>Science</i> , 2017, 358, 1604-1606.	12.6	179
45	Quantitative Evaluation of Genetic Diversity in Wheat Germplasm Using Molecular Markers. <i>Crop Science</i> , 2001, 41, 682-690.	1.8	178
46	PHYTOCHROME C plays a major role in the acceleration of wheat flowering under long-day photoperiod. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10037-10044.	7.1	175
47	Association between allelic variation at the Phytoene synthase 1 gene and yellow pigment content in the wheat grain. <i>Theoretical and Applied Genetics</i> , 2008, 116, 635-645.	3.6	174
48	Precise mapping of a locus affecting grain protein content in durum wheat. <i>Theoretical and Applied Genetics</i> , 2003, 107, 1243-1251.	3.6	170
49	Next Generation Sequencing Provides Rapid Access to the Genome of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , the Causal Agent of Wheat Stripe Rust. <i>PLoS ONE</i> , 2011, 6, e24230.	2.5	169
50	Evaluation of Genetic Diversity and Genome-wide Linkage Disequilibrium among U.S. Wheat ( <i>Triticum</i> ) Tj ETQq0 0.0 rgBT /Overlock 1	1.8	167
51	Regulation of Freezing Tolerance and Flowering in Temperate Cereals: The <i>VRN-1</i> Connection Â Â. <i>Plant Physiology</i> , 2010, 153, 1846-1858.	4.8	162
52	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.	7.1	159
53	Regulatory genes involved in the determination of frost tolerance in temperate cereals. <i>Plant Science</i> , 2009, 176, 12-19.	3.6	158
54	Allelic Variation at the Vernalization Genes <i>VrnA1</i> , <i>VrnB1</i> , <i>VrnD1</i> , and <i>VrnB3</i> in Chinese Wheat Cultivars and Their Association with Growth Habit. <i>Crop Science</i> , 2008, 48, 458-470.	1.8	155

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55	Transposable elements, genes and recombination in a 215-kb contig from wheat chromosome 5Am. Functional and Integrative Genomics, 2002, 2, 70-80.	3.5	153
56	Analysis of gene-derived SNP marker polymorphism in US wheat ( <i>Triticum aestivum</i> L.) cultivars. Molecular Breeding, 2009, 23, 23-33.	2.1	153
57	Physical map of the wheat high-grain protein content gene Gpc-B1 and development of a high-throughput molecular marker. New Phytologist, 2006, 169, 753-763.	7.3	150
58	A cluster of 11 CBF transcription factors is located at the frost tolerance locus Fr-A m 2 in <i>Triticum monococcum</i> . Molecular Genetics and Genomics, 2006, 275, 193-203.	2.1	146
59	Identification and characterization of <i>Sr13</i> , a tetraploid wheat gene that confers resistance to the Ug99 stem rust race group. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9483-E9492.	7.1	146
60	The 2NS Translocation from <i>Aegilops ventricosa</i> Confers Resistance to the <i>Triticum</i> Pathotype of <i>Magnaporthe oryzae</i> . Crop Science, 2016, 56, 990-1000.	1.8	141
61	QTL analysis of pasta quality using a composite microsatellite and SNP map of durum wheat. Theoretical and Applied Genetics, 2008, 117, 1361-1377.	3.6	137
62	Wheat Stripe Rust Resistance Protein WKS1 Reduces the Ability of the Thylakoid-Associated Ascorbate Peroxidase to Detoxify Reactive Oxygen Species. Plant Cell, 2015, 27, 1755-1770.	6.6	133
63	Different Types and Rates of Genome Evolution Detected by Comparative Sequence Analysis of Orthologous Segments From Four Cereal Genomes. Genetics, 2002, 162, 1389-1400.	2.9	132
64	Identification of the <i>VERNALIZATION 4</i> gene reveals the origin of spring growth habit in ancient wheats from South Asia. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5401-10.	7.1	131
65	Genetic and Molecular Characterization of the <i>VRN2</i> Loci in Tetraploid Wheat. Plant Physiology, 2009, 149, 245-257.	4.8	129
66	Separating homeologs by phasing in the tetraploid wheat transcriptome. Genome Biology, 2013, 14, R66.	8.8	126
67	microRNA172 plays a critical role in wheat spike morphology and grain threshability. Development (Cambridge), 2017, 144, 1966-1975.	2.5	125
68	Construction and characterization of a half million clone BAC library of durum wheat ( <i>Triticum</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	3.6	124
69	WheatExp: an RNA-seq expression database for polyploid wheat. BMC Plant Biology, 2015, 15, 299.	3.6	124
70	The expression of several Cbf genes at the Fr-A2 locus is linked to frost resistance in wheat. Molecular Genetics and Genomics, 2005, 274, 506-514.	2.1	123
71	Identification of a candidate gene for a QTL for spikelet number per spike on wheat chromosome arm 7AL by high-resolution genetic mapping. Theoretical and Applied Genetics, 2019, 132, 2689-2705.	3.6	118
72	Marker-Assisted Selection in Public Breeding Programs. Crop Science, 2004, 44, 1895-1898.	1.8	117

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73	Mapping of a thermo-sensitive earliness per se gene on Triticum monococcum chromosome 1Am. Theoretical and Applied Genetics, 2002, 105, 585-593.	3.6	116
74	Wheat flowering repressor VRN2 and promoter CO2 compete for interactions with NUCLEAR FACTOR-1 complexes. Plant Journal, 2011, 67, 763-773.	5.7	115
75	Heterologous expression and transcript analysis of gibberellin biosynthetic genes of grasses reveals novel functionality in the GA3ox family. BMC Plant Biology, 2015, 15, 130.	3.6	115
76	The chromosome region including the earliness per se locus Eps-Am1 affects the duration of early developmental phases and spikelet number in diploid wheat. Journal of Experimental Botany, 2008, 59, 3595-3607.	4.8	112
77	Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat. Theoretical and Applied Genetics, 2011, 123, 143-157.	3.6	111
78	Microcolinearity between a 2-cM region encompassing the grain protein content locus Gpc-6B1 on wheat chromosome 6B and a 350-kb region on rice chromosome 2. Functional and Integrative Genomics, 2004, 4, 59-66.	3.5	109
79	Identification of candidate CBF genes for the frost tolerance locus Fr-A m 2 in Triticum monococcum. Plant Molecular Biology, 2008, 67, 257-270.	3.9	103
80	Molecular characterization of the allelic variation at the VRN-H2 vernalization locus in barley. Molecular Breeding, 2005, 15, 395-407.	2.1	102
81	Genetic and physical mapping of the earliness per se locus Eps-A m 1 in Triticum monococcum identifies EARLY FLOWERING 3 (ELF3) as a candidate gene. Functional and Integrative Genomics, 2016, 16, 365-382.	3.5	102
82	Wheat gene <i>Sr60</i> encodes a protein with two putative kinase domains that confers resistance to stem rust. New Phytologist, 2020, 225, 948-959.	7.3	102
83	Combining Traditional Mutagenesis with New High-Throughput Sequencing and Genome Editing to Reveal Hidden Variation in Polyploid Wheat. Annual Review of Genetics, 2017, 51, 435-454.	7.6	100
84	Effects of the Chromosome Region Including the <i>Gpc-B1</i> Locus on Wheat Grain and Protein Yield. Crop Science, 2010, 50, 93-104.	1.8	98
85	Vrn-D4 is a vernalization gene located on the centromeric region of chromosome 5D in hexaploid wheat. Theoretical and Applied Genetics, 2010, 120, 543-552.	3.6	98
86	The genetic architecture of genome-wide recombination rate variation in allopolyploid wheat revealed by nested association mapping. Plant Journal, 2018, 95, 1039-1054.	5.7	97
87	Identification and characterization of wheat stem rust resistance gene Sr21 effective against the Ug99 race group at high temperature. PLoS Genetics, 2018, 14, e1007287.	3.5	97
88	Induced Mutations in the <i>Starch Branching Enzyme II</i> ( <i>SBEII</i> ) Genes Increase Amylose and Resistant Starch Content in Durum Wheat. Crop Science, 2012, 52, 1754-1766.	1.8	97
89	Copy number and haplotype variation at the VRN-A1 and central FR-A2 loci are associated with frost tolerance in hexaploid wheat. Theoretical and Applied Genetics, 2014, 127, 1183-1197.	3.6	96
90	Wheat <i>VRN1</i> , <i>FUL2</i> and <i>FUL3</i> play critical and redundant roles in spikelet development and spike determinacy. Development (Cambridge), 2019, 146, .	2.5	96

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91	Factorial combinations of protein interactions generate a multiplicity of florigen activation complexes in wheat and barley. <i>Plant Journal</i> , 2015, 84, 70-82.	5.7	95
92	Characterization of FLOWERING LOCUS T1 (FT1) Gene in <i>Brachypodium</i> and Wheat. <i>PLoS ONE</i> , 2014, 9, e94171.	2.5	94
93	Identification and characterization of Rht25, a locus on chromosome arm 6AS affecting wheat plant height, heading time, and spike development. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2021-2035.	3.6	94
94	Mapping a region within the 1RS.1BL translocation in common wheat affecting grain yield and canopy water status. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2695-2709.	3.6	92
95	Molecular Characterization of Two <i>Triticum speltoides</i> Interstitial Translocations Carrying Leaf Rust and Greenbug Resistance Genes. <i>Crop Science</i> , 1998, 38, 1655-1660.	1.8	91
96	Development of PCR-Based Markers for a High Grain Protein Content Gene from <i>Triticum turgidum</i> ssp. <i>dicoccoides</i> Transferred to Bread Wheat. <i>Crop Science</i> , 2000, 40, 518-524.	1.8	91
97	Analysis of Expressed Sequence Tag Loci on Wheat Chromosome Group 4. <i>Genetics</i> , 2004, 168, 651-663.	2.9	90
98	Down-regulation of four putative arabinoxylan feruloyl transferase genes from family PF02458 reduces ester-linked ferulate content in rice cell walls. <i>Planta</i> , 2010, 231, 677-691.	3.2	90
99	Identification and validation of QTL for grain yield and plant water status under contrasting water treatments in fall-sown spring wheats. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1741-1759.	3.6	90
100	Exogenous Gibberellins Induce Wheat Spike Development under Short Days Only in the Presence of <i>VERNALIZATION1</i> . <i>Plant Physiology</i> , 2013, 163, 1433-1445.	4.8	89
101	Genetic and physical characterization of grain texture-related loci in diploid wheat. <i>Molecular Genetics and Genomics</i> , 1999, 262, 846-850.	2.4	88
102	A deletion at the Lpx-B1 locus is associated with low lipoxygenase activity and improved pasta color in durum wheat ( <i>Triticum turgidum</i> ssp. <i>durum</i> ). <i>Journal of Cereal Science</i> , 2007, 45, 67-77.	3.7	88
103	Development of an Expressed Sequence Tag (EST) Resource for Wheat ( <i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 585-593.	2.9	87
104	Sequencing of the <i>Triticum monococcum</i> Hardness locus reveals good microcolinearity with rice. <i>Molecular Genetics and Genomics</i> , 2004, 271, 377-386.	2.1	85
105	A consensus framework map of durum wheat ( <i>Triticum durum</i> Desf.) suitable for linkage disequilibrium analysis and genome-wide association mapping. <i>BMC Genomics</i> , 2014, 15, 873.	2.8	85
106	Functional characterization of GPC-1 genes in hexaploid wheat. <i>Planta</i> , 2014, 239, 313-324.	3.2	85
107	Durable resistance to the wheat rusts: integrating systems biology and traditional phenotype-based research methods to guide the deployment of resistance genes. <i>Euphytica</i> , 2011, 179, 69-79.	1.2	83
108	Increased copy number at the HvFT1 locus is associated with accelerated flowering time in barley. <i>Molecular Genetics and Genomics</i> , 2013, 288, 261-275.	2.1	83

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109	Small RNAs, DNA methylation and transposable elements in wheat. BMC Genomics, 2010, 11, 408.	2.8	82
110	Group 3 Chromosome Bin Maps of Wheat and Their Relationship to Rice Chromosome 1. Genetics, 2004, 168, 639-650.	2.9	81
111	Molecular characterization of durum and common wheat recombinant lines carrying leaf rust resistance (Lr19) and yellow pigment (Y) genes from <i>Lophopyrum ponticum</i> . Theoretical and Applied Genetics, 2005, 111, 573-582.	3.6	80
112	Development of Sequence Tagged Site and Cleaved Amplified Polymorphic Sequence Markers for Wheat Stripe Rust Resistance Gene <i>Yr5</i> . Crop Science, 2003, 43, 2058-2064.	1.8	79
113	Molecular Mapping of the Stb4 Gene for Resistance to Septoria tritici Blotch in Wheat. Phytopathology, 2004, 94, 1198-1206.	2.2	79
114	Chromosome Bin Map of Expressed Sequence Tags in Homoeologous Group 1 of Hexaploid Wheat and Homoeology With Rice and Arabidopsis. Genetics, 2004, 168, 609-623.	2.9	78
115	A 2600-Locus Chromosome Bin Map of Wheat Homoeologous Group 2 Reveals Interstitial Gene-Rich Islands and Colinearity With Rice. Genetics, 2004, 168, 625-637.	2.9	78
116	Nitrogen uptake and remobilization in tetraploid 'Langdon' durum wheat and a recombinant substitution line with the high grain protein gene Gpc-B1. Plant Breeding, 2005, 124, 343-349.	1.9	77
117	Substitutions and Deletions of Genes Related to Grain Hardness in Wheat and Their Effect on Grain Texture. Crop Science, 2002, 42, 1812-1817.	1.8	76
118	RNA interference for wheat functional gene analysis. Transgenic Research, 2007, 16, 689-701.	2.4	76
119	Effect of the down-regulation of the high Grain Protein Content (GPC) genes on the wheat transcriptome during monocarpic senescence. BMC Genomics, 2011, 12, 492.	2.8	75
120	Evaluation of marker-assisted selection for the stripe rust resistance gene Yr15, introgressed from wild emmer wheat. Molecular Breeding, 2015, 35, 1.	2.1	74
121	Recognition of Homeology by the Wheat <i>Ph1</i> Locus. Genetics, 1996, 144, 1195-1203.	2.9	74
122	<i>FLOWERING LOCUS T2</i> regulates spike development and fertility in temperate cereals. Journal of Experimental Botany, 2019, 70, 193-204.	4.8	73
123	Development of PCR markers for the wheat leaf rust resistance gene Lr47. Theoretical and Applied Genetics, 2000, 100, 1137-1143.	3.6	71
124	Control of flowering time and spike development in cereals: the earliness per se Eps-1 region in wheat, rice, and Brachypodium. Functional and Integrative Genomics, 2010, 10, 293-306.	3.5	71
125	Colinearity between the barley grain protein content (GPC) QTL on chromosome arm 6HS and the wheat Gpc-B1 region. Molecular Breeding, 2008, 22, 25-38.	2.1	70
126	Divergent functions of orthologous NAC transcription factors in wheat and rice. Plant Molecular Biology, 2012, 78, 515-524.	3.9	70

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127	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. <i>Journal of Experimental Botany</i> , 2013, 64, 4453-4460.	4.8	69
128	A Conserved <i>Puccinia striiformis</i> Protein Interacts with Wheat NPR1 and Reduces Induction of Pathogenesis-Related Genes in Response to Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 977-989.	2.6	69
129	Mapping causal mutations by exome sequencing in a wheat TILLING population: a tall mutant case study. <i>Molecular Genetics and Genomics</i> , 2018, 293, 463-477.	2.1	69
130	A Chromosome Bin Map of 2148 Expressed Sequence Tag Loci of Wheat Homoeologous Group 7. <i>Genetics</i> , 2004, 168, 687-699.	2.9	68
131	PCR Markers for <i>Triticum speltoides</i> Leaf Rust Resistance Gene <i>Lr51</i> and Their Use to Develop Isogenic Hard Red Spring Wheat Lines. <i>Crop Science</i> , 2005, 45, 728-734.	1.8	68
132	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.	2.9	67
133	RNA-seq studies using wheat PHYTOCHROME B and PHYTOCHROME C mutants reveal shared and specific functions in the regulation of flowering and shade-avoidance pathways. <i>BMC Plant Biology</i> , 2016, 16, 141.	3.6	67
134	Dynamics of the evolution of orthologous and paralogous portions of a complex locus region in two genomes of allopolyploid wheat. <i>Plant Molecular Biology</i> , 2004, 54, 55-69.	3.9	65
135	Genetic mapping of stem rust resistance gene Sr13 in tetraploid wheat ( <i>Triticum turgidum</i> ssp. <i>durum</i> ) Tj ETQq1 1 0.784314 rgBT /Ow	3.6	65
136	Validation and characterization of a QTL for adult plant resistance to stripe rust on wheat chromosome arm 6BS (Yr78). <i>Theoretical and Applied Genetics</i> , 2017, 130, 2127-2137.	3.6	65
137	Genomic organization of the complex $\alpha$ -gliadin gene loci in wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 648-657.	3.6	62
138	Comparative analysis of protein-protein interactions in the defense response of rice and wheat. <i>BMC Genomics</i> , 2013, 14, 166.	2.8	60
139	Effect of the grain protein content locus Gpc-B1 on bread and pasta quality. <i>Journal of Cereal Science</i> , 2010, 51, 357-365.	3.7	59
140	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.	2.9	57
141	The CARG-Box Located Upstream from the Transcriptional Start of Wheat Vernalization Gene VRN1 Is Not Necessary for the Vernalization Response. <i>Journal of Heredity</i> , 2009, 100, 355-364.	2.4	57
142	Wheat VIN3-like PHD finger genes are up-regulated by vernalization. <i>Molecular Genetics and Genomics</i> , 2007, 277, 301-313.	2.1	56
143	Fine mapping and characterization of Sr21, a temperature-sensitive diploid wheat resistance gene effective against the <i>Puccinia graminis</i> f. sp. <i>tritici</i> Ug99 race group. <i>Theoretical and Applied Genetics</i> , 2015, 128, 645-656.	3.6	56
144	<i>APETALA2</i> -like genes <i>AP2L2</i> and <i>Q</i> specify lemma identity and axillary floral meristem development in wheat. <i>Plant Journal</i> , 2020, 101, 171-187.	5.7	56

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145	A microcolinearity study at the earliness per se gene Eps-A m 1 region reveals an ancient duplication that preceded the wheat-rice divergence. <i>Theoretical and Applied Genetics</i> , 2006, 112, 945-957.	3.6	54
146	Characterization of the maintained vegetative phase deletions from diploid wheat and their effect on VRN2 and FT transcript levels. <i>Molecular Genetics and Genomics</i> , 2010, 283, 223-232.	2.1	54
147	An <i>Aegilops ventricosa</i> Translocation Confers Resistance Against Root-knot Nematodes to Common Wheat. <i>Crop Science</i> , 2013, 53, 1412-1418.	1.8	53
148	Genetic Maps of Stem Rust Resistance Gene <i>Sr35</i> in Diploid and Hexaploid Wheat. <i>Crop Science</i> , 2010, 50, 2464-2474.	1.8	51
149	Haplotype diversity of stem rust resistance loci in uncharacterized wheat lines. <i>Molecular Breeding</i> , 2010, 26, 667-680.	2.1	50
150	Genetic Relationship of Stripe Rust Resistance Genes <i>Yr34</i> and <i>Yr48</i> in Wheat and Identification of Linked KASP Markers. <i>Plant Disease</i> , 2018, 102, 413-420.	1.4	50
151	WAOA-A1 is the causal gene of the 7AL QTL for spikelet number per spike in wheat. <i>PLoS Genetics</i> , 2022, 18, e1009747.	3.5	50
152	YR36/WKS1-Mediated Phosphorylation of PsbO, an Extrinsic Member of Photosystem II, Inhibits Photosynthesis and Confers Stripe Rust Resistance in Wheat. <i>Molecular Plant</i> , 2019, 12, 1639-1650.	8.3	49
153	Fine mapping and epistatic interactions of the vernalization gene VRN-D4 in hexaploid wheat. <i>Molecular Genetics and Genomics</i> , 2014, 289, 47-62.	2.1	48
154	Cloning and comparative analysis of carotenoid $\beta$ -hydroxylase genes provides new insights into carotenoid metabolism in tetraploid ( <i>Triticum turgidum</i> ssp. <i>durum</i> ) and hexaploid ( <i>Triticum aestivum</i> ) wheat grains. <i>Plant Molecular Biology</i> , 2012, 80, 631-646.	3.9	47
155	Large deletions in the CBF gene cluster at the Fr-B2 locus are associated with reduced frost tolerance in wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2683-2697.	3.6	47
156	Epistatic interactions between PHOTOPERIOD1, CONSTANS1 and CONSTANS2 modulate the photoperiodic response in wheat. <i>PLoS Genetics</i> , 2020, 16, e1008812.	3.5	46
157	Frequencies of Ty1-copia and Ty3-gypsy retroelements within the Triticeae EST databases. <i>Theoretical and Applied Genetics</i> , 2002, 104, 840-844.	3.6	45
158	Development of PCR markers for wheat leaf rust resistance gene Lr47. <i>Theoretical and Applied Genetics</i> , 2000, 101, 625-631.	3.6	43
159	Deletion Mapping of Homoeologous Group 6-Specific Wheat Expressed Sequence Tags. <i>Genetics</i> , 2004, 168, 677-686.	2.9	43
160	Night-Break Experiments Shed Light on the Photoperiod1-Mediated Flowering. <i>Plant Physiology</i> , 2017, 174, 1139-1150.	4.8	42
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162	PCR identification of durum wheat BAC clones containing genes coding for carotenoid biosynthesis enzymes and their chromosome localization. <i>Genome</i> , 2004, 47, 911-917.	2.0	38

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163	Effect of allelic variation at the Glu-3/Gli-1 loci on breadmaking quality parameters in hexaploid wheat ( <i>Triticum aestivum</i> L.). <i>Journal of Cereal Science</i> , 2015, 62, 143-150.	3.7	37
164	Single nucleotide polymorphisms in a regulatory site of VRN-A1 first intron are associated with differences in vernalization requirement in winter wheat. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1231-1243.	2.1	37
165	Genotyping of U.S. Wheat Germplasm for Presence of Stem Rust Resistance Genes <i>Sr24</i> , <i>Sr36</i> and <i>Sr1RS</i> <sup>Amigo</sup> . <i>Crop Science</i> , 2010, 50, 668-675.	1.8	36
166	Combined mutations in five wheat STARCH BRANCHING ENZYME II genes improve resistant starch but affect grain yield and bread-making quality. <i>Journal of Cereal Science</i> , 2017, 75, 165-174.	3.7	36
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169	Interactions between SQUAMOSA and SHORT VEGETATIVE PHASE MADS-box proteins regulate meristem transitions during wheat spike development. <i>Plant Cell</i> , 2021, 33, 3621-3644.	6.6	35
170	Biochemical and molecular characterisation of Glu-1 loci in Argentinean wheat cultivars. <i>Euphytica</i> , 2002, 128, 61-73.	1.2	33
171	Registration of Five Wheat Isogenic Lines for Leaf Rust and Stripe Rust Resistance Genes. <i>Crop Science</i> , 2006, 46, 485-487.	1.8	33
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174	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. <i>Nature Communications</i> , 2022, 13, 826.	12.8	31
175	Wheat TaNPSN SNARE homologues are involved in vesicle-mediated resistance to stripe rust ( <i>Puccinia</i> ) Tj ETQq1 1 0.784314rgBT /Ov 4.8 29	4.8	29
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178	Agronomic and Quality Evaluation of Common Wheat Near-isogenic Lines Carrying the Leaf Rust Resistance Gene <i>Lr47</i> . <i>Crop Science</i> , 2008, 48, 1441-1451.	1.8	28
179	Genome analysis of South American <i>Elymus</i> ( <i>Triticeae</i> ) and <i>Leymus</i> ( <i>Triticeae</i> ) species based on variation in repeated nucleotide sequences. <i>Genome</i> , 1997, 40, 505-520.	2.0	27
180	Mapping of <i>SrTm4</i> , a Recessive Stem Rust Resistance Gene from Diploid Wheat Effective to Ug99. <i>Phytopathology</i> , 2015, 105, 1347-1354.	2.2	27

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182	Effect of phyB and phyC loss-of-function mutations on the wheat transcriptome under short and long day photoperiods. <i>BMC Plant Biology</i> , 2020, 20, 297.	3.6	27
183	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.	2.0	26
184	Registration of Common Wheat Germplasm with Mutations in <i>SBEII</i> Genes Conferring Increased Grain Amylose and Resistant Starch Content. <i>Journal of Plant Registrations</i> , 2016, 10, 200-205.	0.5	26
185	Characterization and Mapping of Leaf Rust and Stripe Rust Resistance Loci in Hexaploid Wheat Lines UC1110 and PI610750 under Mexican Environments. <i>Frontiers in Plant Science</i> , 2017, 8, 1450.	3.6	26
186	Dissection of Cell Death Induction by Wheat Stem Rust Resistance Protein Sr35 and Its Matching Effector AvrSr35. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 308-319.	2.6	25
187	Genome identification of the <i>Triticum crassum</i> complex (Poaceae) with the restriction patterns of repeated nucleotide sequences. <i>American Journal of Botany</i> , 1995, 82, 131-140.	1.7	24
188	Distribution and haplotype diversity of WKS resistance genes in wild emmer wheat natural populations. <i>Theoretical and Applied Genetics</i> , 2016, 129, 921-934.	3.6	24
189	A High-Resolution Map of Wheat <i>QYr.ucw-1BL</i> , an Adult Plant Stripe Rust Resistance Locus in the Same Chromosomal Region as <i>Yr29</i> . <i>Plant Genome</i> , 2019, 12, 180055.	2.8	24
190	Genome origins of <i>Triticum cylindricum</i> , <i>Triticum triunciale</i> , and <i>Triticum ventricosum</i> (Poaceae) inferred from variation in restriction patterns of repeated nucleotide sequences: a methodological study. <i>American Journal of Botany</i> , 1994, 81, 1327-1335.	1.7	23
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195	Fine mapping of barley locus <i>Rps6</i> conferring resistance to wheat stripe rust. <i>Theoretical and Applied Genetics</i> , 2016, 129, 845-859.	3.6	21
196	Differentiation between wheat chromosomes 4B and 4D. <i>Genome</i> , 1995, 38, 1139-1147.	2.0	20
197	The origins of the genomes of <i>Triticum biunciale</i> , <i>t. ovatum</i> , <i>t. neglectum</i> , <i>t. columnare</i> , and <i>t. rectum</i> (poaceae) based on variation in repeated nucleotide sequences. <i>American Journal of Botany</i> , 1996, 83, 1556-1565.	1.7	20
198	Registration of "BIOINTA 2004"™ Wheat. <i>Journal of Plant Registrations</i> , 2009, 3, 165-169.	0.5	20

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200	Stripe rust resistance gene Yr34 (synonym Yr48) is located within a distal translocation of Triticum monococcum chromosome 5A <sub>ML</sub> into common wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2197-2211.	3.6	20
201	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	19
202	Variation in the restriction fragments of 18Sâ€“26S rRNA loci in South American <i>Elymus</i> (Triticeae). <i>Genome</i> , 1992, 35, 881-885.	2.0	18
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204	Mapping of QTL for Tolerance to <i>Cereal Yellow Dwarf Virus</i> in Twoâ€“rowed Spring Barley. <i>Crop Science</i> , 2014, 54, 1468-1475.	1.8	18
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206	The Origins of the Genomes of <i>Triticum biunciale</i> , <i>T. ovatum</i> , <i>T. neglectum</i> , <i>T. columnare</i> , and <i>T. rectum</i> (Poaceae) Based on Variation in Repeated Nucleotide Sequences. <i>American Journal of Botany</i> , 1996, 83, 1556.	1.7	17
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210	Cytotaxonomy of the <i>Festuca</i> spp. from Patagonia. <i>Canadian Journal of Botany</i> , 1992, 70, 1134-1140.	1.1	15
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212	Reduction of a Triticum monococcum Chromosome Segment Carrying the Softness Genes Pina and Pinb Translocated to Bread Wheat. <i>Crop Science</i> , 2007, 47, 821-828.	1.8	15
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215	Phenotypic and transcriptomic characterization of a wheat tall mutant carrying an induced mutation in the C-terminal PFYRE motif of RHT-B1b. <i>BMC Plant Biology</i> , 2018, 18, 253.	3.6	15
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217	Mutant combinations of <i>lycopene cyclase</i> and <i>carotene hydroxylase 2</i> homoeologs increased <i>carotene</i> accumulation in endosperm of tetraploid wheat ( <i>Triticum turgidum</i> L.) grains. <i>Plant Biotechnology Journal</i> , 2022, 20, 564-576.	8.3	14
218	Exomorphological, Anatomical, and Cytological Studies in <i>Panicum validum</i> (Poaceae: Panicoideae: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	13
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223	Karyotype Analysis of the Patagonian <i>Elymus</i> . <i>Botanical Gazette</i> , 1989, 150, 462-468.	0.6	10
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228	Mapping and Characterization of a Wheat Stem Rust Resistance Gene in Durum Wheat "Kronos". <i>Frontiers in Plant Science</i> , 2021, 12, 751398.	3.6	8
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231	Interaction between resistance to <i>Septoria tritici</i> and phenological stages in wheat. <i>Scientia Agricola</i> , 2004, 61, 422-426.	1.2	6
232	Frequent Genic Rearrangements in Two Regions of Grass Genomes Identified by Comparative Sequence Analysis. <i>Comparative and Functional Genomics</i> , 2002, 3, 165-166.	2.0	5
233	Registration of "Clear White" Wheat. <i>Crop Science</i> , 2005, 45, 2652-2652.	1.8	5
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236	Aggressiveness and physiological specialization of Septoria tritici Rob. isolates. Scientia Agricola, 2004, 61, 414-421.	1.2	4
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244	Registration of a Hexaploid Wheat Translocation Line Carrying a Short Segment of Chromosome 5A including Softness Genes Pina and Pinb from Triticum monococcum. Journal of Plant Registrations, 2008, 2, 165-166.	0.5	0
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