

Jorge Dubcovsky

List of Publications by Year in descending order

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252
papers

31,754
citations

4120

87
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4870

168
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272
all docs

272
docs citations

272
times ranked

12594
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutations in the miRNA165/166 binding site of the HB2 gene result in pleiotropic effects on morphological traits in wheat. <i>Crop Journal</i> , 2023, 11, 9-20.	2.3	4
2	Mutant combinations of <i>lycopene É-cyclase</i> and <i>β-carotene hydroxylase 2</i> homoeologs increased β-carotene accumulation in endosperm of tetraploid wheat (<i>Triticum turgidum</i> L.) grains. <i>Plant Biotechnology Journal</i> , 2022, 20, 564-576.	4.1	14
3	Identification and characterization of <i>Sr22b</i> , a new allele of the wheat stem rust resistance gene <i>Sr22</i> effective against the Ug99 race group. <i>Plant Biotechnology Journal</i> , 2022, 20, 554-563.	4.1	17
4	Identification and characterization of a natural polymorphism in FT-A2 associated with increased number of grains per spike in wheat. <i>Theoretical and Applied Genetics</i> , 2022, 135, 679-692.	1.8	13
5	Development of the Wheat Practical Haplotype Graph database as a resource for genotyping data storage and genotype imputation. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
6	WAPO-A1 is the causal gene of the 7AL QTL for spikelet number per spike in wheat. <i>PLoS Genetics</i> , 2022, 18, e1009747.	1.5	50
7	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. <i>Nature Communications</i> , 2022, 13, 826.	5.8	31
8	High-resolution mapping of <i>Yr78</i> , an adult plant resistance gene to wheat stripe rust. <i>Plant Genome</i> , 2022, , e20212.	1.6	2
9	MIR172-APETALA2-like genes integrate vernalization and plant age to control flowering time in wheat. <i>PLoS Genetics</i> , 2022, 18, e1010157.	1.5	16
10	Structural rearrangements in wheat (1BS)–rye (1RS) recombinant chromosomes affect gene dosage and root length. <i>Plant Genome</i> , 2021, 14, e20079.	1.6	14
11	Stripe rust resistance gene Yr34 (synonym Yr48) is located within a distal translocation of <i>Triticum monococcum</i> chromosome 5A _{ML} into common wheat. <i>Theoretical and Applied Genetics</i> , 2021, 134, 2197-2211.	1.8	20
12	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
13	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.	3.1	35
14	Mapping and Characterization of a Wheat Stem Rust Resistance Gene in Durum Wheat “Kronos”. <i>Frontiers in Plant Science</i> , 2021, 12, 751398.	1.7	8
15	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.	1.4	25
16	Wheat gene <i>Sr60</i> encodes a protein with two putative kinase domains that confers resistance to stem rust. <i>New Phytologist</i> , 2020, 225, 948-959.	3.5	102
17	<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.	2.8	56
18	A GRF–GIF chimeric protein improves the regeneration efficiency of transgenic plants. <i>Nature Biotechnology</i> , 2020, 38, 1274-1279.	9.4	272

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19	Epistatic interactions between PHOTOPERIOD1, CONSTANS1 and CONSTANS2 modulate the photoperiodic response in wheat. <i>PLoS Genetics</i> , 2020, 16, e1008812.	1.5	46
20	Contributions of individual and combined Glu-B1x and Glu-B1y high-molecular-weight glutenin subunits to semolina functionality and pasta quality. <i>Journal of Cereal Science</i> , 2020, 93, 102943.	1.8	3
21	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.	1.6	27
22	Three previously characterized resistances to yellow rust are encoded by a single locus <i>Wtk1</i> . <i>Journal of Experimental Botany</i> , 2020, 71, 2561-2572.	2.4	23
23	A haplotype-phased genome of wheat stripe rust pathogen <i>Puccinia striiformis</i> f. sp. <i>tritici</i> , race PST-130 from the Western USA. <i>PLoS ONE</i> , 2020, 15, e0238611.	1.1	10
24	Title is missing!. , 2020, 16, e1008812.		0
25	Title is missing!. , 2020, 16, e1008812.		0
26	Title is missing!. , 2020, 16, e1008812.		0
27	Title is missing!. , 2020, 16, e1008812.		0
28	Title is missing!. , 2020, 15, e0238611.		0
29	Title is missing!. , 2020, 15, e0238611.		0
30	Title is missing!. , 2020, 15, e0238611.		0
31	Title is missing!. , 2020, 15, e0238611.		0
32	Identification of a candidate gene for a QTL for spikelet number per spike on wheat chromosome arm 7AL by high-resolution genetic mapping. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2689-2705.	1.8	118
33	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.	3.9	49
34	A wheat/rye polymorphism affects seminal root length and yield across different irrigation regimes. <i>Journal of Experimental Botany</i> , 2019, 70, 4027-4037.	2.4	27
35	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.	1.6	24
36	Registration of the Triticæaâ€CAP Spring Wheat Nested Association Mapping Population. <i>Journal of Plant Registrations</i> , 2019, 13, 294-297.	0.4	16

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37	Wheat <i>VRN1</i> , <i>FUL2</i> and <i>FUL3</i> play critical and redundant roles in spikelet development and spike determinacy. <i>Development</i> (Cambridge), 2019, 146, .	1.2	96
38	<i>FLOWERING LOCUS T2</i> regulates spike development and fertility in temperate cereals. <i>Journal of Experimental Botany</i> , 2019, 70, 193-204.	2.4	73
39	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.	0.7	50
40	Mapping and characterization of wheat stem rust resistance genes <i>SrTm5</i> and <i>Sr60</i> from <i>Triticum monococcum</i> . <i>Theoretical and Applied Genetics</i> , 2018, 131, 625-635.	1.8	39
41	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.	1.0	69
42	Cloning of the wheat <i>Yr15</i> resistance gene sheds light on the plant tandem kinase-pseudokinase family. <i>Nature Communications</i> , 2018, 9, 3735.	5.8	204
43	Registration of "UC Tahoe", a California Adapted Two-Rowed Spring Barley for Craft Scale Malting. <i>Journal of Plant Registrations</i> , 2018, 12, 163-167.	0.4	3
44	Phenotypic and transcriptomic characterization of a wheat tall mutant carrying an induced mutation in the C-terminal PFYRE motif of <i>RHT-B1b</i> . <i>BMC Plant Biology</i> , 2018, 18, 253.	1.6	15
45	Mapping QTL for Resistance to New Virulent Races of Wheat Stripe Rust from Two Argentinean Wheat Cultivars. <i>Crop Science</i> , 2018, 58, 2470-2483.	0.8	20
46	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.	1.8	90
47	Identification and characterization of <i>Rht25</i> , 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.	1.8	94
48	The genetic architecture of genome-wide recombination rate variation in allopolyploid wheat revealed by nested association mapping. <i>Plant Journal</i> , 2018, 95, 1039-1054.	2.8	97
49	Genome-wide Association Study of Agronomic Traits in a Spring-Planted North American Elite Hard Red Spring Wheat Panel. <i>Crop Science</i> , 2018, 58, 1838-1852.	0.8	29
50	Identification and characterization of wheat stem rust resistance gene <i>Sr21</i> effective against the <i>Ug99</i> race group at high temperature. <i>PLoS Genetics</i> , 2018, 14, e1007287.	1.5	97
51	Single nucleotide polymorphisms in a regulatory site of <i>VRN-A1</i> first intron are associated with differences in vernalization requirement in winter wheat. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1231-1243.	1.0	37
52	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.	3.3	554
53	Night-Break Experiments Shed Light on the Photoperiod1-Mediated Flowering. <i>Plant Physiology</i> , 2017, 174, 1139-1150.	2.3	42
54	<i>microRNA172</i> plays a critical role in wheat spike morphology and grain threshability. <i>Development</i> (Cambridge), 2017, 144, 1966-1975.	1.2	125

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55	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.	1.8	36
56	Identification and characterization of <i>Sr13</i> , a tetraploid wheat gene that confers resistance to the Ug99 stem rust race group. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9483-E9492.	3.3	146
57	Combining Traditional Mutagenesis with New High-Throughput Sequencing and Genome Editing to Reveal Hidden Variation in Polyploid Wheat. <i>Annual Review of Genetics</i> , 2017, 51, 435-454.	3.2	100
58	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.	1.8	65
59	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.	6.0	179
60	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.	1.7	26
61	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.	0.4	26
62	The 2NS Translocation from <i>Aegilops ventricosa</i> Confers Resistance to the <i>Triticum</i> Pathotype of <i>Magnaporthe oryzae</i> . <i>Crop Science</i> , 2016, 56, 990-1000.	0.8	141
63	Endosperm Carotenoid Concentrations in Wheat are Better Correlated with PSY1 Transcript Levels than Enzyme Activities. <i>Crop Science</i> , 2016, 56, 3173-3184.	0.8	5
64	A Conserved <i>Puccinia striiformis</i> Protein Interacts with Wheat NPR1 and Reduces Induction of <i>Pathogenesis-Related</i> Genes in Response to Pathogens. <i>Molecular Plant-Microbe Interactions</i> , 2016, 29, 977-989.	1.4	69
65	Distinct expression and function of carotenoid metabolic genes and homoeologs in developing wheat grains. <i>BMC Plant Biology</i> , 2016, 16, 155.	1.6	29
66	The stay-green phenotype of TaNAM-RNAi wheat plants is associated with maintenance of chloroplast structure and high enzymatic antioxidant activity. <i>Plant Physiology and Biochemistry</i> , 2016, 104, 257-265.	2.8	8
67	Genetic and physical mapping of the earliness per se locus Eps-A m 1 in <i>Triticum monococcum</i> identifies EARLY FLOWERING 3 (ELF3) as a candidate gene. <i>Functional and Integrative Genomics</i> , 2016, 16, 365-382.	1.4	102
68	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.	1.6	67
69	Development and characterization of a spring hexaploid wheat line with no functional VRN2 genes. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1417-1428.	1.8	35
70	Fine mapping of barley locus Rps6 conferring resistance to wheat stripe rust. <i>Theoretical and Applied Genetics</i> , 2016, 129, 845-859.	1.8	21
71	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.	1.8	179
72	Distribution and haplotype diversity of WKS resistance genes in wild emmer wheat natural populations. <i>Theoretical and Applied Genetics</i> , 2016, 129, 921-934.	1.8	24

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73	Mapping of <i>SrTm4</i> , a Recessive Stem Rust Resistance Gene from Diploid Wheat Effective to Ug99. <i>Phytopathology</i> , 2015, 105, 1347-1354.	1.1	27
74	Factorial combinations of protein interactions generate a multiplicity of florigen activation complexes in wheat and barley. <i>Plant Journal</i> , 2015, 84, 70-82.	2.8	95
75	Mutations in Durum Wheat <i>SBEII</i> Genes affect Grain Yield Components, Quality, and Fermentation Responses in Rats. <i>Crop Science</i> , 2015, 55, 2813-2825.	0.8	35
76	A New Map Location of Gene <i>Stb3</i> for Resistance to Septoria Tritici Blotch in Wheat. <i>Crop Science</i> , 2015, 55, 35-43.	0.8	15
77	WheatExp: an RNA-seq expression database for polyploid wheat. <i>BMC Plant Biology</i> , 2015, 15, 299.	1.6	124
78	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.	1.8	56
79	Evaluation of marker-assisted selection for the stripe rust resistance gene Yr15, introgressed from wild emmer wheat. <i>Molecular Breeding</i> , 2015, 35, 1.	1.0	74
80	A Genome-Wide Association Study of Resistance to Stripe Rust (<i>Puccinia striiformis</i> f. sp. <i>tritici</i>) in Wheat. <i>Genetics</i> , 2015, 195, 1049-1060.	0.8	356
81	Wheat Stripe Rust Resistance Protein WKS1 Reduces the Ability of the Thylakoid-Associated Ascorbate Peroxidase to Detoxify Reactive Oxygen Species. <i>Plant Cell</i> , 2015, 27, 1755-1770.	3.1	133
82	A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. <i>Genome Biology</i> , 2015, 16, 48.	3.8	216
83	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.	1.8	37
84	Identification of the <i>VERNALIZATION 4</i> gene reveals the origin of spring growth habit in ancient wheats from South Asia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5401-10.	3.3	131
85	Heterologous expression and transcript analysis of gibberellin biosynthetic genes of grasses reveals novel functionality in the GA3ox family. <i>BMC Plant Biology</i> , 2015, 15, 130.	1.6	115
86	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.	4.1	386
87	Characterization of FLOWERING LOCUS T1 (FT1) Gene in <i>Brachypodium</i> and Wheat. <i>PLoS ONE</i> , 2014, 9, e94171.	1.1	94
88	Mapping of QTL for Tolerance to Cereal Yellow Dwarf Virus in Two-rowed Spring Barley. <i>Crop Science</i> , 2014, 54, 1468-1475.	0.8	18
89	Wheat TaNPSN SNARE homologues are involved in vesicle-mediated resistance to stripe rust (<i>Puccinia</i>) in wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2695-2709.	2.4	29
90	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.	1.8	92

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91	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.	4.1	1,828
92	Efficient Genome-Wide Detection and Cataloging of EMS-Induced Mutations Using Exome Capture and Next-Generation Sequencing. <i>Plant Cell</i> , 2014, 26, 1382-1397.	3.1	277
93	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.	1.2	85
94	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.	3.3	175
95	Fine mapping and epistatic interactions of the vernalization gene <i>VRN-D4</i> in hexaploid wheat. <i>Molecular Genetics and Genomics</i> , 2014, 289, 47-62.	1.0	48
96	Functional characterization of <i>GPC-1</i> genes in hexaploid wheat. <i>Planta</i> , 2014, 239, 313-324.	1.6	85
97	Effect of the <i>Hope FT-B1</i> Allele on Wheat Heading Time and Yield Components. <i>Journal of Heredity</i> , 2014, 105, 666-675.	1.0	22
98	Copy number and haplotype variation at the <i>VRN-A1</i> and central <i>FR-A2</i> loci are associated with frost tolerance in hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1183-1197.	1.8	96
99	Registration of Durum Wheat Germplasm Lines with Combined Mutations in <i>SBEIIa</i> and <i>SBEIIb</i> Genes Conferring Increased Amylose and Resistant Starch. <i>Journal of Plant Registrations</i> , 2014, 8, 334-338.	0.4	22
100	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. <i>BMC Genomics</i> , 2013, 14, 270.	1.2	235
101	Comparative analysis of protein-protein interactions in the defense response of rice and wheat. <i>BMC Genomics</i> , 2013, 14, 166.	1.2	60
102	Increased copy number at the <i>HvFT1</i> locus is associated with accelerated flowering time in barley. <i>Molecular Genetics and Genomics</i> , 2013, 288, 261-275.	1.0	83
103	Large deletions in the <i>CBF</i> gene cluster at the <i>Fr-B2</i> locus are associated with reduced frost tolerance in wheat. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2683-2697.	1.8	47
104	A comparative approach expands the protein-protein interaction node of the immune receptor <i>XA21</i> in wheat and rice. <i>Genome</i> , 2013, 56, 315-326.	0.9	18
105	Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8057-8062.	3.3	1,065
106	Identification of Wheat Gene <i>Sr35</i> That Confers Resistance to Ug99 Stem Rust Race Group. <i>Science</i> , 2013, 341, 783-786.	6.0	283
107	Dissecting the genetic architecture of frost tolerance in Central European winter wheat. <i>Journal of Experimental Botany</i> , 2013, 64, 4453-4460.	2.4	69
108	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.	2.3	89

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109	Separating homeologs by phasing in the tetraploid wheat transcriptome. <i>Genome Biology</i> , 2013, 14, R66.	3.8	126
110	An <i>Aegilops ventricosa</i> Translocation Confers Resistance Against Root-knot Nematodes to Common Wheat. <i>Crop Science</i> , 2013, 53, 1412-1418.	0.8	53
111	Registration of Wheat Lines Carrying the Partial Stripe Rust Resistance Gene <i>Yr36</i> without the <i>Gpc-B1</i> Allele for High Grain Protein Content. <i>Journal of Plant Registrations</i> , 2013, 7, 108-112.	0.4	15
112	Wheat TILLING Mutants Show That the Vernalization Gene <i>VRN1</i> Down-Regulates the Flowering Repressor <i>VRN2</i> in Leaves but Is Not Essential for Flowering. <i>PLoS Genetics</i> , 2012, 8, e1003134.	1.5	213
113	Cloning and comparative analysis of carotenoid β -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.	2.0	47
114	Divergent functions of orthologous NAC transcription factors in wheat and rice. <i>Plant Molecular Biology</i> , 2012, 78, 515-524.	2.0	70
115	Induced Mutations in the <i>Starch Branching Enzyme II</i> (<i>SBEII</i>) Genes Increase Amylose and Resistant Starch Content in Durum Wheat. <i>Crop Science</i> , 2012, 52, 1754-1766.	0.8	97
116	Wheat flowering repressor <i>VRN2</i> and promoter <i>CO2</i> compete for interactions with NUCLEAR FACTOR complexes. <i>Plant Journal</i> , 2011, 67, 763-773.	2.8	115
117	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.	0.6	83
118	Genetic mapping of stem rust resistance gene <i>Sr13</i> in tetraploid wheat (<i>Triticum turgidum</i> ssp. <i>durum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 1.85 65	1.8	65
119	Conflicting mapping results for stem rust resistance gene <i>Sr13</i> . <i>Theoretical and Applied Genetics</i> , 2011, 122, 659-659.	1.8	3
120	Mapping and validation of QTL which confer partial resistance to broadly virulent post-2000 North American races of stripe rust in hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2011, 123, 143-157.	1.8	111
121	Effect of the down-regulation of the high Grain Protein Content (GPC) genes on the wheat transcriptome during monocarpic senescence. <i>BMC Genomics</i> , 2011, 12, 492.	1.2	75
122	Discovery of Rare Mutations in Populations: TILLING by Sequencing $\hat{A} \hat{A} \hat{A}$. <i>Plant Physiology</i> , 2011, 156, 1257-1268.	2.3	266
123	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.	1.1	169
124	Effects of the Chromosome Region Including the <i>Gpc-B1</i> Locus on Wheat Grain and Protein Yield. <i>Crop Science</i> , 2010, 50, 93-104.	0.8	98
125	<i>Vrn-D4</i> is a vernalization gene located on the centromeric region of chromosome 5D in hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2010, 120, 543-552.	1.8	98
126	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.	1.6	90

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127	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.	1.0	54
128	Control of flowering time and spike development in cereals: the earliness per se Eps-1 region in wheat, rice, and Brachypodium. <i>Functional and Integrative Genomics</i> , 2010, 10, 293-306.	1.4	71
129	Haplotype diversity of stem rust resistance loci in uncharacterized wheat lines. <i>Molecular Breeding</i> , 2010, 26, 667-680.	1.0	50
130	Effect of the grain protein content locus Gpc-B1 on bread and pasta quality. <i>Journal of Cereal Science</i> , 2010, 51, 357-365.	1.8	59
131	Small RNAs, DNA methylation and transposable elements in wheat. <i>BMC Genomics</i> , 2010, 11, 408.	1.2	82
132	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	1.2	189
133	Genotyping of U.S. Wheat Germplasm for Presence of Stem Rust Resistance Genes <i>Sr24</i> , <i>Sr36</i> and <i>Sr1RS</i> ^{Amigo} . <i>Crop Science</i> , 2010, 50, 668-675.	0.8	36
134	Genetic Maps of Stem Rust Resistance Gene <i>Sr35</i> in Diploid and Hexaploid Wheat. <i>Crop Science</i> , 2010, 50, 2464-2474.	0.8	51
135	Regulation of Freezing Tolerance and Flowering in Temperate Cereals: The <i>VRN-1</i> Connection. <i>Plant Physiology</i> , 2010, 153, 1846-1858.	2.3	162
136	Population- and genome-specific patterns of linkage disequilibrium and SNP variation in spring and winter wheat (<i>Triticum aestivum</i> L.). <i>BMC Genomics</i> , 2010, 11, 727.	1.2	234
137	Registration of "BIOINTA 2004"™ Wheat. <i>Journal of Plant Registrations</i> , 2009, 3, 165-169.	0.4	20
138	Genetic and Molecular Characterization of the <i>VRN2</i> Loci in Tetraploid Wheat. <i>Plant Physiology</i> , 2009, 149, 245-257.	2.3	129
139	The CARG-Box Located Upstream from the Transcriptional Start of Wheat Vernalization Gene <i>VRN1</i> Is Not Necessary for the Vernalization Response. <i>Journal of Heredity</i> , 2009, 100, 355-364.	1.0	57
140	Regulation of flowering in temperate cereals. <i>Current Opinion in Plant Biology</i> , 2009, 12, 178-184.	3.5	423
141	Physical mapping of durum wheat lipoxigenase genes. <i>Journal of Cereal Science</i> , 2009, 50, 67-73.	1.8	23
142	A modified TILLING approach to detect induced mutations in tetraploid and hexaploid wheat. <i>BMC Plant Biology</i> , 2009, 9, 115.	1.6	323
143	Analysis of gene-derived SNP marker polymorphism in US wheat (<i>Triticum aestivum</i> L.) cultivars. <i>Molecular Breeding</i> , 2009, 23, 23-33.	1.0	153
144	Wheat (<i>Triticum aestivum</i>) NAM proteins regulate the translocation of iron, zinc, and nitrogen compounds from vegetative tissues to grain. <i>Journal of Experimental Botany</i> , 2009, 60, 4263-4274.	2.4	300

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145	Regulatory genes involved in the determination of frost tolerance in temperate cereals. <i>Plant Science</i> , 2009, 176, 12-19.	1.7	158
146	A Kinase-START Gene Confers Temperature-Dependent Resistance to Wheat Stripe Rust. <i>Science</i> , 2009, 323, 1357-1360.	6.0	625
147	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.	3.3	190
148	Identification of candidate CBF genes for the frost tolerance locus Fr-A m 2 in <i>Triticum monococcum</i> . <i>Plant Molecular Biology</i> , 2008, 67, 257-270.	2.0	103
149	Colinearity between the barley grain protein content (GPC) QTL on chromosome arm 6HS and the wheat Gpc-B1 region. <i>Molecular Breeding</i> , 2008, 22, 25-38.	1.0	70
150	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.	1.8	174
151	QTL analysis of pasta quality using a composite microsatellite and SNP map of durum wheat. <i>Theoretical and Applied Genetics</i> , 2008, 117, 1361-1377.	1.8	137
152	Wheat FT protein regulates <i>VRN1</i> transcription through interactions with FDL2. <i>Plant Journal</i> , 2008, 55, 543-554.	2.8	217
153	The chromosome region including the earliness per se locus Eps-Am1 affects the duration of early developmental phases and spikelet number in diploid wheat. <i>Journal of Experimental Botany</i> , 2008, 59, 3595-3607.	2.4	112
154	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.	0.8	28
155	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.	0.8	155
156	Registration of a Hexaploid Wheat Translocation Line Carrying a Short Segment of Chromosome 5A including Softness Genes <i>Pina</i> and <i>Pinb</i> from <i>Triticum monococcum</i> . <i>Journal of Plant Registrations</i> , 2008, 2, 165-166.	0.4	0
157	Genome Plasticity a Key Factor in the Success of Polyploid Wheat Under Domestication. <i>Science</i> , 2007, 316, 1862-1866.	6.0	886
158	Reduction of a <i>Triticum monococcum</i> Chromosome Segment Carrying the Softness Genes <i>Pina</i> and <i>Pinb</i> Translocated to Bread Wheat. <i>Crop Science</i> , 2007, 47, 821-828.	0.8	15
159	Evaluation of Genetic Diversity and Genome-wide Linkage Disequilibrium among U.S. Wheat (<i>Triticum</i>) Tj ETQq1 1 0.784314 rgBT / 0.8 167	0.8	167
160	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.	1.8	88
161	RNA interference for wheat functional gene analysis. <i>Transgenic Research</i> , 2007, 16, 689-701.	1.3	76
162	Wheat VIN3-like PHD finger genes are up-regulated by vernalization. <i>Molecular Genetics and Genomics</i> , 2007, 277, 301-313.	1.0	56

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163	A NAC Gene Regulating Senescence Improves Grain Protein, Zinc, and Iron Content in Wheat. <i>Science</i> , 2006, 314, 1298-1301.	6.0	1,408
164	The wheat and barley vernalization gene VRN3 is an orthologue of FT. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19581-19586.	3.3	937
165	The high grain protein content gene Gpc-B1 accelerates senescence and has pleiotropic effects on protein content in wheat. <i>Journal of Experimental Botany</i> , 2006, 57, 2785-2794.	2.4	252
166	Use of a large-scale Triticeae expressed sequence tag resource to reveal gene expression profiles in hexaploid wheat (<i>Triticum aestivum</i> L.). <i>Genome</i> , 2006, 49, 531-544.	0.9	26
167	Registration of Five Wheat Isogenic Lines for Leaf Rust and Stripe Rust Resistance Genes. <i>Crop Science</i> , 2006, 46, 485-487.	0.8	33
168	Changes in High Molecular Weight Glutenin Subunit Composition Can Be Genetically Engineered without Affecting Wheat Agronomic Performance. <i>Crop Science</i> , 2006, 46, 1553-1563.	0.8	31
169	Physical map of the wheat high-grain protein content gene Gpc-B1 and development of a high-throughput molecular marker. <i>New Phytologist</i> , 2006, 169, 753-763.	3.5	150
170	Effect of Photoperiod on the Regulation of Wheat Vernalization Genes VRN1 and VRN2. <i>Plant Molecular Biology</i> , 2006, 60, 469-480.	2.0	256
171	A cluster of 11 CBF transcription factors is located at the frost tolerance locus Fr-A m 2 in <i>Triticum monococcum</i> . <i>Molecular Genetics and Genomics</i> , 2006, 275, 193-203.	1.0	146
172	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.	1.8	54
173	Identification of microsatellites linked to Lr47. <i>Electronic Journal of Biotechnology</i> , 2006, 9, 0-0.	1.2	3
174	Nitrogen uptake and remobilization in tetraploid 'Langdon' durum wheat and a recombinant substitution line with the high grain protein gene Gpc-B1. <i>Plant Breeding</i> , 2005, 124, 343-349.	1.0	77
175	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.	1.8	208
176	Molecular characterization of durum and common wheat recombinant lines carrying leaf rust resistance (Lr19) and yellow pigment (Y) genes from <i>Lophopyrum ponticum</i> . <i>Theoretical and Applied Genetics</i> , 2005, 111, 573-582.	1.8	80
177	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.	1.0	592
178	The expression of several Cbf genes at the Fr-A2 locus is linked to frost resistance in wheat. <i>Molecular Genetics and Genomics</i> , 2005, 274, 506-514.	1.0	123
179	Molecular characterization of the allelic variation at the VRN-H2 vernalization locus in barley. <i>Molecular Breeding</i> , 2005, 15, 395-407.	1.0	102
180	Molecular and Structural Characterization of Barley Vernalization Genes. <i>Plant Molecular Biology</i> , 2005, 59, 449-467.	2.0	258

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181	Registration of "Clear White"™ Wheat. <i>Crop Science</i> , 2005, 45, 2652-2652.	0.8	5
182	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.	0.8	68
183	Molecular characterization of the duplicated meristem identity genes <i>HvAP1a</i> and <i>HvAP1b</i> in barley. <i>Genome</i> , 2005, 48, 905-912.	0.9	15
184	Regulation of VRN-1 Vernalization Genes in Normal and Transgenic Polyploid Wheat. <i>Plant Physiology</i> , 2005, 138, 2364-2373.	2.3	190
185	Marker-Assisted Selection in Public Breeding Programs. <i>Crop Science</i> , 2004, 44, 1895-1898.	0.8	117
186	Analysis of Expressed Sequence Tag Loci on Wheat Chromosome Group 4. <i>Genetics</i> , 2004, 168, 651-663.	1.2	90
187	Chromosome Bin Map of Expressed Sequence Tags in Homoeologous Group 1 of Hexaploid Wheat and Homoeology With Rice and Arabidopsis. <i>Genetics</i> , 2004, 168, 609-623.	1.2	78
188	A Chromosome Bin Map of 2148 Expressed Sequence Tag Loci of Wheat Homoeologous Group 7. <i>Genetics</i> , 2004, 168, 687-699.	1.2	68
189	Construction and Evaluation of cDNA Libraries for Large-Scale Expressed Sequence Tag Sequencing in Wheat (<i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 595-608.	1.2	57
190	Deletion Mapping of Homoeologous Group 6-Specific Wheat Expressed Sequence Tags. <i>Genetics</i> , 2004, 168, 677-686.	1.2	43
191	A 2500-Locus Bin Map of Wheat Homoeologous Group 5 Provides Insights on Gene Distribution and Colinearity With Rice. <i>Genetics</i> , 2004, 168, 665-676.	1.2	67
192	Group 3 Chromosome Bin Maps of Wheat and Their Relationship to Rice Chromosome 1. <i>Genetics</i> , 2004, 168, 639-650.	1.2	81
193	A Chromosome Bin Map of 16,000 Expressed Sequence Tag Loci and Distribution of Genes Among the Three Genomes of Polyploid Wheat. <i>Genetics</i> , 2004, 168, 701-712.	1.2	369
194	Allelic variation at the VRN-1 promoter region in polyploid wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1677-1686.	1.8	448
195	Development of an Expressed Sequence Tag (EST) Resource for Wheat (<i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 585-593.	1.2	87
196	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.	2.0	65
197	Sequencing of the <i>Triticum monococcum</i> Hardness locus reveals good microcolinearity with rice. <i>Molecular Genetics and Genomics</i> , 2004, 271, 377-386.	1.0	85
198	Microcolinearity between a 2-cM region encompassing the grain protein content locus <i>Gpc-6B1</i> on wheat chromosome 6B and a 350-kb region on rice chromosome 2. <i>Functional and Integrative Genomics</i> , 2004, 4, 59-66.	1.4	109

#	ARTICLE	IF	CITATIONS
199	Genomic organization of the complex $\hat{\pm}$ -gliadin gene loci in wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 648-657.	1.8	62
200	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.	0.9	38
201	A 2600-Locus Chromosome Bin Map of Wheat Homoeologous Group 2 Reveals Interstitial Gene-Rich Islands and Colinearity With Rice. <i>Genetics</i> , 2004, 168, 625-637.	1.2	78
202	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization. <i>Science</i> , 2004, 303, 1640-1644.	6.0	999
203	Molecular Mapping of the Stb4 Gene for Resistance to Septoria tritici Blotch in Wheat. <i>Phytopathology</i> , 2004, 94, 1198-1206.	1.1	79
204	Interaction between resistance to Septoria tritici and phenological stages in wheat. <i>Scientia Agricola</i> , 2004, 61, 422-426.	0.6	6
205	Aggressiveness and physiological specialization of Septoria tritici Rob. isolates. <i>Scientia Agricola</i> , 2004, 61, 414-421.	0.6	4
206	Construction and characterization of a half million clone BAC library of durum wheat (<i>Triticum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Jf 50 46	1.8	124
207	Precise mapping of a locus affecting grain protein content in durum wheat. <i>Theoretical and Applied Genetics</i> , 2003, 107, 1243-1251.	1.8	170
208	The cold-regulated transcriptional activator Cbf3 is linked to the frost-tolerance locus Fr-A2 on wheat chromosome 5A. <i>Molecular Genetics and Genomics</i> , 2003, 269, 60-67.	1.0	212
209	The Organization and Rate of Evolution of Wheat Genomes Are Correlated With Recombination Rates Along Chromosome Arms. <i>Genome Research</i> , 2003, 13, 753-763.	2.4	298
210	Rapid Genome Divergence at Orthologous Low Molecular Weight Glutenin Loci of the A and Am Genomes of Wheat[W]. <i>Plant Cell</i> , 2003, 15, 1186-1197.	3.1	226
211	Positional cloning of the wheat vernalization gene VRN1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6263-6268.	3.3	1,254
212	Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10836-10841.	3.3	159
213	Development of Sequence Tagged Site and Cleaved Amplified Polymorphic Sequence Markers for Wheat Stripe Rust Resistance Gene <i>Yr5</i> . <i>Crop Science</i> , 2003, 43, 2058-2064.	0.8	79
214	PCR Assays for the <i>Lr37</i> - <i>Yr17</i> - <i>Cr38</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.	0.8	334
215	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. <i>Genome Research</i> , 2003, 13, 1818-1827.	2.4	369
216	Substitutions and Deletions of Genes Related to Grain Hardness in Wheat and Their Effect on Grain Texture. <i>Crop Science</i> , 2002, 42, 1812-1817.	0.8	76

#	ARTICLE	IF	CITATIONS
217	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
218	Frequencies of Ty1-copia and Ty3-gypsy retroelements within the Triticeae EST databases. <i>Theoretical and Applied Genetics</i> , 2002, 104, 840-844.	1.8	45
219	Genetic mapping of 66 new microsatellite (SSR) loci in bread wheat. <i>Theoretical and Applied Genetics</i> , 2002, 105, 413-422.	1.8	339
220	Mapping of a thermo-sensitive earliness per se gene on <i>Triticum monococcum</i> chromosome 1Am. <i>Theoretical and Applied Genetics</i> , 2002, 105, 585-593.	1.8	116
221	Cereal genes similar to Snf2 define a new subfamily that includes human and mouse genes. <i>Molecular Genetics and Genomics</i> , 2002, 268, 488-499.	1.0	17
222	Transposable elements, genes and recombination in a 215-kb contig from wheat chromosome 5Am. <i>Functional and Integrative Genomics</i> , 2002, 2, 70-80.	1.4	153
223	Biochemical and molecular characterisation of Glu-1 loci in Argentinean wheat cultivars. <i>Euphytica</i> , 2002, 128, 61-73.	0.6	33
224	Different Types and Rates of Genome Evolution Detected by Comparative Sequence Analysis of Orthologous Segments From Four Cereal Genomes. <i>Genetics</i> , 2002, 162, 1389-1400.	1.2	132
225	Quantitative Evaluation of Genetic Diversity in Wheat Germplasm Using Molecular Markers. <i>Crop Science</i> , 2001, 41, 682-690.	0.8	178
226	Wheat genomics. <i>Plant Physiology and Biochemistry</i> , 2001, 39, 335-344.	2.8	32
227	Comparative Sequence Analysis of Colinear Barley and Rice Bacterial Artificial Chromosomes. <i>Plant Physiology</i> , 2001, 125, 1342-1353.	2.3	204
228	Comparisons of recombination frequencies in hybrids involving telocentric and bibrachial wheat chromosomes. <i>Theoretical and Applied Genetics</i> , 2000, 100, 308-314.	1.8	3
229	Development of PCR markers for the wheat leaf rust resistance gene Lr47. <i>Theoretical and Applied Genetics</i> , 2000, 100, 1137-1143.	1.8	71
230	Development of PCR markers for wheat leaf rust resistance gene Lr47. <i>Theoretical and Applied Genetics</i> , 2000, 101, 625-631.	1.8	43
231	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.	0.8	91
232	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
233	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.	0.8	91
234	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.	0.9	27

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235	Karyotype Variation in South American Elymus (Triticeae). International Journal of Plant Sciences, 1996, 157, 142-150.	0.6	10
236	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. American Journal of Botany, 1996, 83, 1556-1565.	0.8	20
237	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.	1.2	250
238	Recognition of Homeology by the Wheat <i>Ph1</i> Locus. Genetics, 1996, 144, 1195-1203.	1.2	74
239	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. , 1996, 83, 1556.		17
240	Genome identification of the <i>Triticum crassum</i> complex (Poaceae) with the restriction patterns of repeated nucleotide sequences. American Journal of Botany, 1995, 82, 131-140.	0.8	24
241	Differentiation between wheat chromosomes 4B and 4D. Genome, 1995, 38, 1139-1147.	0.9	20
242	Genome identification of the <i>Triticum crassum</i> complex (Poaceae) with the restriction patterns of repeated nucleotide sequences. , 1995, 82, 131.		5
243	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. American Journal of Botany, 1994, 81, 1327-1335.	0.8	23
244	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. , 1994, 81, 1327.		7
245	Infrageneric phenetic relations in new world <i>Panicum</i> (Poaceae: Panicoideae: Paniceae): a numerical analysis. Canadian Journal of Botany, 1993, 71, 1312-1327.	1.2	8
246	Revision of <i>Anthaenantiopsis</i> (Poaceae: Panicoideae: Paniceae). Systematic Botany, 1993, 18, 434.	0.2	10
247	Variation in the restriction fragments of 18S-26S rRNA loci in South American <i>Elymus</i> (Triticeae). Genome, 1992, 35, 881-885.	0.9	18
248	Cytotaxonomy of the <i>Festuca</i> spp. from Patagonia. Canadian Journal of Botany, 1992, 70, 1134-1140.	1.2	15
249	Chromosome complement and nucleoli in the <i>Festuca pallelescens</i> alliance from South America. Canadian Journal of Botany, 1991, 69, 2756-2761.	1.2	11
250	Exomorphological, Anatomical, and Cytological Studies in <i>Panicum validum</i> (Poaceae: Panicoideae: Paniceae). Canadian Journal of Botany, 1991, 69, 2756-2761.	0.2	13
251	Karyotype Analysis of the Patagonian <i>Elymus</i> . Botanical Gazette, 1989, 150, 462-468.	0.6	10
252	Phenetic relationships in the <i>Festuca</i> spp. from Patagonia. Canadian Journal of Botany, 1988, 66, 468-478.	1.2	9