

Richard R-C Wang

List of Publications by Year in descending order

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117
papers

2,977
citations

147801

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120
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times ranked

1708
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Characterization of DGATs and Their Expression Diversity Analysis in Response to Abiotic Stresses in <i>Brassica napus</i> . <i>Plants</i> , 2022, 11, 1156.	3.5	3
2	Genome evolution during bread wheat formation unveiled by the distribution dynamics of SSR sequences on chromosomes using FISH. <i>BMC Genomics</i> , 2021, 22, 55.	2.8	7
3	Overexpression of the Transcription Factor AtLEC1 Significantly Improved the Lipid Content of <i>Chlorella ellipsoidea</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 626162.	4.1	8
4	Characterization of chromosome constitution in three wheat - <i>Thinopyrum intermedium</i> amphiploids revealed frequent rearrangement of alien and wheat chromosomes. <i>BMC Plant Biology</i> , 2021, 21, 129.	3.6	10
5	Precise Characterization and Tracking of Stably Inherited Artificial Minichromosomes Made by Telomere-Mediated Chromosome Truncation in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 743792.	3.6	6
6	Chromosomal Distribution of Genes Conferring Tolerance to Abiotic Stresses Versus That of Genes Controlling Resistance to Biotic Stresses in Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1820.	4.1	7
7	Histone Deacetylase (HDAC) Gene Family in Allotetraploid Cotton and Its Diploid Progenitors: In Silico Identification, Molecular Characterization, and Gene Expression Analysis under Multiple Abiotic Stresses, DNA Damage and Phytohormone Treatments. <i>International Journal of Molecular Sciences</i> , 2020, 21, 321.	4.1	26
8	DNA sequence-based mapping and comparative genomics of the St genome of <i>Pseudoroegneria spicata</i> (Pursh) A. Love versus wheat (<i>Triticum aestivum</i> L.) and barley (<i>Hordeum</i>) <i>Tj ETQq0 0 0 rgBT Overlock 40 Tf 50 45</i>	4.1	10
9	Breeding strategies for structuring salinity tolerance in wheat. <i>Advances in Agronomy</i> , 2019, 155, 121-187.	5.2	53
10	Comparative Genome-wide Analysis and Expression Profiling of Histone Acetyltransferase (HAT) Gene Family in Response to Hormonal Applications, Metal and Abiotic Stresses in Cotton. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5311.	4.1	26
11	Identification of chromosomes in <i>Thinopyrum intermedium</i> and wheat <i>Th. intermedium</i> amphiploids based on multiplex oligonucleotide probes. <i>Genome</i> , 2018, 61, 515-521.	2.0	19
12	Differential transferability of EST-SSR primers developed from the diploid species <i>Pseudoroegneria spicata</i> , <i>Thinopyrum bessarabicum</i> , and <i>Thinopyrum elongatum</i> . <i>Genome</i> , 2017, 60, 530-536.	2.0	13
13	<i>Roegneria alashanica</i> Keng: a species with the StStSt^YSt^Y genome constitution. <i>Genome</i> , 2017, 60, 546-551.	2.0	4
14	Characterization of genome in tetraploid StY species of <i>Elymus</i> (Triticeae: Poaceae) using sequential FISH and GISH. <i>Genome</i> , 2017, 60, 679-685.	2.0	6
15	Identification and characterization of an efficient acyl-CoA: diacylglycerol acyltransferase 1 (DGAT1) gene from the microalga <i>Chlorella ellipsoidea</i> . <i>BMC Plant Biology</i> , 2017, 17, 48.	3.6	36
16	The Diversity of Sequence and Chromosomal Distribution of New Transposable Element-Related Segments in the Rye Genome Revealed by FISH and Lineage Annotation. <i>Frontiers in Plant Science</i> , 2017, 8, 1706.	3.6	10
17	Agronomic and genetic diversity in intermediate wheatgrass (<i>Thinopyrum intermedium</i>). <i>Plant Breeding</i> , 2016, 135, 751-758.	1.9	11
18	Genome evolution of intermediate wheatgrass as revealed by EST-SSR markers developed from its three progenitor diploid species. <i>Genome</i> , 2015, 58, 63-70.	2.0	35

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19	Biosystematics and evolutionary relationships of perennial Triticeae species revealed by genomic analyses. <i>Journal of Systematics and Evolution</i> , 2014, 52, 697-705.	3.1	49
20	DOPâ€“PCR based painting of rye chromosomes in a wheat background. <i>Genome</i> , 2014, 57, 473-479.	2.0	7
21	Identification of the substrate recognition region in the δ^6 -fatty acid and δ^8 -sphingolipid desaturase by fusion mutagenesis. <i>Planta</i> , 2014, 239, 753-763.	3.2	12
22	Overexpression of the soybean transcription factor GmDof4 significantly enhances the lipid content of <i>Chlorella ellipsoidea</i> . <i>Biotechnology for Biofuels</i> , 2014, 7, 128.	6.2	47
23	Genetic Diversity for Wheat Improvement as a Conduit to Food Security. <i>Advances in Agronomy</i> , 2013, , 179-257.	5.2	124
24	Genome analysis of seven species of Kengyilia (Triticeae: Poaceae) with FISH and GISH. <i>Genome</i> , 2013, 56, 641-649.	2.0	15
25	The role of C-terminal amino acid residues of a δ^6 -fatty acid desaturase from blackcurrant. <i>Biochemical and Biophysical Research Communications</i> , 2013, 431, 675-679.	2.1	8
26	Microdissection and Chromosome Painting of the Alien Chromosome in an Addition Line of Wheat - <i>Thinopyrum intermedium</i> . <i>PLoS ONE</i> , 2013, 8, e72564.	2.5	24
27	A New Strategy to Produce a Defensin: Stable Production of Mutated NP-1 in Nitrate Reductase-Deficient <i>Chlorella ellipsoidea</i> . <i>PLoS ONE</i> , 2013, 8, e54966.	2.5	38
28	Homoeology of <i>Thinopyrum junceum</i> and <i>Elymus rectisetus</i> chromosomes to wheat and disease resistance conferred by the <i>Thinopyrum</i> and <i>Elymus</i> chromosomes in wheat. <i>Chromosome Research</i> , 2012, 20, 699-715.	2.2	25
29	Characterization of alien chromosomes in backcross derivatives of <i>Triticum aestivum</i> — <i>Elymus rectisetus</i> hybrids by using molecular markers and sequential multicolor FISH/GISH. <i>Genome</i> , 2012, 55, 337-347.	2.0	11
30	Isolation and Functional Characterisation of the Genes Encoding δ^8 -Sphingolipid Desaturase from <i>Brassica rapa</i> . <i>Journal of Genetics and Genomics</i> , 2012, 39, 47-59.	3.9	10
31	Enhanced tolerance to NaCl and LiCl stresses by over-expressing <i>Caragana korshinskii</i> sodium/proton exchanger 1 (CkNHX1) and the hydrophilic C terminus is required for the activity of CkNHX1 in <i>Atsos3-1</i> mutant and yeast. <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 732-737.	2.1	11
32	Genetic variation among laboratory accessions of Chinese Spring wheat (<i>Triticum aestivum</i> L.). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2012, 10, 97-100.	0.8	3
33	<i>Leymus</i> EST linkage maps identify 4NsLâ€“5NsL reciprocal translocation, wheat- <i>Leymus</i> chromosome introgressions, and functionally important gene loci. <i>Theoretical and Applied Genetics</i> , 2012, 124, 189-206.	3.6	42
34	<i>Agropyron</i> and <i>Psathyrostachys</i> . , 2011, , 77-108.		56
35	Newly identified essential amino acid residues affecting δ^8 -sphingolipid desaturase activity revealed by site-directed mutagenesis. <i>Biochemical and Biophysical Research Communications</i> , 2011, 416, 165-171.	2.1	7
36	Characterization of HMW Glutenin Subunits in <i>Thinopyrum intermedium</i> , <i>Thinopyrum bessarabicum</i> , <i>Lophopyrum elongatum</i> , <i>Aegilops markgrafii</i> , and Their Addition Lines in Wheat. <i>Crop Science</i> , 2011, 51, 667-677.	1.8	24

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37	Genes encoding the biotin carboxylase subunit of acetyl-CoA carboxylase from <i>Brassica napus</i> and parental species: cloning, expression patterns, and evolution. <i>Genome</i> , 2011, 54, 202-211.	2.0	11
38	Analyses of <i>Thinopyrum bessarabicum</i> , <i>T. elongatum</i> , and <i>T. junceum</i> chromosomes using EST-SSR markers. <i>Genome</i> , 2010, 53, 1083-1089.	2.0	32
39	Identification and functional analysis of the genes encoding Δ^6 -desaturase from <i>Ribes nigrum</i> . <i>Journal of Experimental Botany</i> , 2010, 61, 1827-1838.	4.8	25
40	Genes encoding the Δ^3 -carboxyltransferase subunit of acetyl-CoA carboxylase from <i>Brassica napus</i> and parental species: cloning, expression patterns, and evolution. <i>Genome</i> , 2010, 53, 360-370.	2.0	11
41	Evaluation and Characterization of Seedling Resistances to Stem Rust Ug99 Races in Wheat "Alien Species Derivatives. <i>Crop Science</i> , 2009, 49, 2167-2175.	1.8	62
42	A Y genome specific STS marker in <i>Pseudoroegneria</i> and <i>Elymus</i> species (Triticeae: Gramineae) Parts of this paper were derived from the thesis research that partially fulfilled the requirements of an M.S. degree earned by Mr. Pungu Okito at the Graduate School, Utah State University. This research was supported in part by the Utah Agricultural Experiment Station, Utah State University, Logan, UT 84322-4810, USA. Approved as Utah Agricultural Experiment Station journal paper No. 7973.. <i>Genome</i> , 2009, 52, 391-400.	2.0	32
43	Isolation of expressed sequences from a specific chromosome of <i>Thinopyrum intermedium</i> infected by BYDV. <i>Genome</i> , 2009, 52, 68-76.	2.0	11
44	BAC library development for allotetraploid <i>Leymus</i> (Triticeae) wildryes enable comparative genetic analysis of <i>lax-barrenstalk1</i> orthogene sequences and growth habit QTLs. <i>Plant Science</i> , 2009, 177, 427-438.	3.6	9
45	Wheatgrass and Wildrye Grasses (Triticeae). <i>Genetic Resources, Chromosome Engineering, and Crop Improvement Series</i> , 2009, , 41-79.	0.3	6
46	Genes controlling plant growth habit in <i>Leymus</i> (Triticeae): maize barren stalk1 (<i>ba1</i>), rice lax panicle, and wheat tiller inhibition (<i>tin3</i>) genes as possible candidates. <i>Functional and Integrative Genomics</i> , 2008, 8, 375-386.	3.5	21
47	Structure and dynamics of retrotransposons at wheat centromeres and pericentromeres. <i>Chromosoma</i> , 2008, 117, 445-456.	2.2	107
48	Rapid EST isolation from chromosome 1R of rye. <i>BMC Plant Biology</i> , 2008, 8, 28.	3.6	14
49	Development and annotation of perennial Triticeae ESTs and SSR markers. <i>Genome</i> , 2008, 51, 779-788.	2.0	36
50	Comparative transcriptome analysis of salt-tolerant wheat germplasm lines using wheat genome arrays. <i>Plant Science</i> , 2007, 173, 327-339.	3.6	45
51	CAPS markers specific to Eb, Ee, and R genomes in the tribe Triticeae. <i>Genome</i> , 2007, 50, 400-411.	2.0	31
52	Variations in abundance of 2 repetitive sequences in <i>Leymus</i> and <i>Psathyrostachys</i> species. <i>Genome</i> , 2006, 49, 511-519.	2.0	19
53	Cytological evidence for assortment mitosis leading to loss of heterozygosity in rice. <i>Genome</i> , 2006, 49, 556-557.	2.0	5
54	Cloning of resistance gene analogs located on the alien chromosome in an addition line of wheat- <i>Thinopyrum intermedium</i> . <i>Theoretical and Applied Genetics</i> , 2005, 111, 923-931.	3.6	19

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55	Detection of linkage disequilibrium QTLs controlling low-temperature growth and metabolite accumulations in an admixed breeding population of <i>Leymus wildryes</i> . <i>Euphytica</i> , 2005, 141, 263-280.	1.2	8
56	Relationships among 3 <i>Kochia</i> species based on PCR-generated molecular sequences and molecular cytogenetics. <i>Genome</i> , 2005, 48, 1104-1115.	2.0	9
57	Screening and analysis of differentially expressed genes from an alien addition line of wheat <i>Thinopyrum intermedium</i> induced by barley yellow dwarf virus infection. <i>Genome</i> , 2004, 47, 1114-1121.	2.0	11
58	Characteristics and behaviour of the chromosomes of <i>Leymus mollis</i> and <i>L. racemosus</i> (Triticeae). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50</i>	2.2	27
59	Molecular genetic linkage maps for allotetraploid <i>Leymus wildryes</i> (Gramineae: Triticeae). <i>Genome</i> , 2003, 46, 627-646.	2.0	55
60	Development of Salinity-tolerant Wheat Recombinant Lines from a Wheat Disomic Addition Line Carrying a <i>Thinopyrum junceum</i> Chromosome. <i>International Journal of Plant Sciences</i> , 2003, 164, 25-33.	1.3	55
61	Molecular Cytogenetic Characterization of E ^b Genome Chromosomes in <i>Thinopyrum bessarabicum</i> Disomic Addition Lines of Bread Wheat. <i>International Journal of Plant Sciences</i> , 2002, 163, 167-174.	1.3	31
62	Development of STS and CAPS markers for identification of three tall larkspurs (<i>Delphinium</i> spp.). <i>Genome</i> , 2002, 45, 229-235.	2.0	8
63	Characterization of mRNAs that accumulate during illumination of excised leaves of big bluegrass (<i>Poa secunda</i>). <i>Journal of Plant Physiology</i> , 2002, 159, 661-670.	3.5	2
64	Characterization of fructan biosynthesis in big bluegrass (<i>Poa secunda</i>). <i>Journal of Plant Physiology</i> , 2002, 159, 705-715.	3.5	32
65	Genetic variation within and among 22 accessions of three tall larkspur species (<i>Delphinium</i> spp.) based on RAPD markers. <i>Biochemical Systematics and Ecology</i> , 2002, 30, 91-102.	1.3	20
66	Selection response for molecular markers associated with anthocyanin coloration and low-temperature growth traits in crested wheatgrasses. <i>Canadian Journal of Plant Science</i> , 2001, 81, 665-671.	0.9	12
67	A proposed mechanism for loss of heterozygosity in rice hybrids. <i>Euphytica</i> , 2001, 118, 119-126.	1.2	7
68	Linkage mapping and nucleotide polymorphisms of the 6-SFT gene of cool-season grasses. <i>Genome</i> , 2000, 43, 931-938.	2.0	23
69	Genome Characterization of MT ² Perennial and OK ⁹⁰⁶ Annual Wheat - Intermediate Wheatgrass Hybrids. <i>Crop Science</i> , 1999, 39, 1041-1043.	1.8	22
70	Molecular Marker Analysis of <i>Leymus flavescens</i> and Chromosome Pairing in <i>Leymus flavescens</i> Hybrids (Poaceae: Triticeae). <i>International Journal of Plant Sciences</i> , 1999, 160, 371-376.	1.3	9
71	Genome-specific repetitive DNA and RAPD markers for genome identification in <i>Elymus</i> and <i>Hordelymus</i> . <i>Genome</i> , 1998, 41, 120-128.	2.0	59
72	Cytological and Molecular Evidence for Transferring <i>Elymus coreanus</i> from the Genus <i>Elymus</i> to <i>Leymus</i> and Molecular Evidence for <i>Elymus californicus</i> (Poaceae: Triticeae). <i>International Journal of Plant Sciences</i> , 1997, 158, 872-877.	1.3	37

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73	Meiotic Anomalies in Hybrids between Wheat and Apomictic <i>Elymus rectisetus</i> (Nees in Lehm.) A. Lve & Connor. <i>Crop Science</i> , 1997, 37, 717-723.	1.8	17
74	Genetic variability in Russian wildrye (<i>Psathyrostachys juncea</i>) assessed by RAPD. <i>Genetic Resources and Crop Evolution</i> , 1997, 44, 117-125.	1.6	9
75	Characterization of genomes and chromosomes in partial amphiploids of the hybrid <i>Triticum aestivum</i> – <i>Thinopyrum ponticum</i> by in situ hybridization, isozyme analysis, and RAPD. <i>Genome</i> , 1996, 39, 1062-1071.	2.0	110
76	Allozyme Variation in Accessions of Russian Wildrye. <i>Crop Science</i> , 1996, 36, 785-790.	1.8	4
77	Characterization of the translocated chromosome using fluorescence in situ hybridization and random amplified polymorphic DNA on two <i>Triticum aestivum</i> – <i>Thinopyrum intermedium</i> translocation lines resistant to wheat streak mosaic or barley yellow dwarf virus. <i>Chromosome Research</i> , 1996, 4, 583-587.	2.2	63
78	Molecular verification and characterization of BYDV-resistant germ plasms derived from hybrids of wheat with <i>Thinopyrum ponticum</i> and <i>Th. intermedium</i> . <i>Theoretical and Applied Genetics</i> , 1996, 93, 1033-1039.	3.6	60
79	Variations of two repetitive DNA sequences in several <i>Triticeae</i> genomes revealed by polymerase chain reaction and sequencing. <i>Genome</i> , 1995, 38, 1221-1229.	2.0	22
80	Genome- and species-specific markers and genome relationships of diploid perennial species in <i>Triticeae</i> based on RAPD analyses. <i>Genome</i> , 1995, 38, 1230-1236.	2.0	52
81	Cytological identification of some trisomics of Russian wildrye (<i>Psathyrostachys juncea</i>). <i>Genome</i> , 1995, 38, 1271-1278.	2.0	7
82	Standard Giemsa C-banded karyotype of Russian wildrye (<i>Psathyrostachys juncea</i>) and its use in identification of a deletion – translocation heterozygote. <i>Genome</i> , 1995, 38, 1262-1270.	2.0	6
83	Production and Identification of Chromosome Specific RAPD Markers for Langdon Durum Wheat Disomic Substitution Lines. <i>Crop Science</i> , 1995, 35, 886-888.	1.8	12
84	Meiotic Stability of Intersubspecific Hybrids of Snake River – Thickspike Wheatgrasses. <i>Crop Science</i> , 1995, 35, 962-964.	1.8	2
85	Hybrids and backcross progenies between wheat (<i>Triticum aestivum</i> L.) and apomictic Australian wheatgrass [<i>Elymus rectisetus</i> (Nees in Lehm.) A. Lve & Connor]: karyotypic and genomic analyses. <i>Theoretical and Applied Genetics</i> , 1994, 89, 599-605.	3.6	22
86	Absence of the J genome in <i>Leymus</i> species (Poaceae: <i>Triticeae</i>): evidence from DNA hybridization and meiotic pairing. <i>Genome</i> , 1994, 37, 231-235.	2.0	83
87	Resistance to powdery mildew and barley yellow dwarf in perennial <i>Triticeae</i> species. <i>Genetic Resources and Crop Evolution</i> , 1993, 40, 171-176.	1.6	3
88	Varying chromosome composition of 56-chromosome wheat – <i>Thinopyrum intermedium</i> partial amphiploids. <i>Genome</i> , 1993, 36, 207-215.	2.0	52
89	Genome analysis of <i>Elytrigia caespitosa</i> , <i>Lophopyrum nodosum</i> , <i>Pseudoroegneria geniculata</i> ssp. <i>scythica</i> , and <i>Thinopyrum intermedium</i> (<i>Triticeae</i> : <i>Gramineae</i>). <i>Genome</i> , 1993, 36, 102-111.	2.0	94
90	Genome constitutions of <i>Thinopyrum curvifolium</i> , <i>T. scirpeum</i> , <i>T. distichum</i> , and <i>T. junceum</i> (<i>Triticeae</i> : <i>Gramineae</i>). <i>Genome</i> , 1993, 36, 641-651.	2.0	25

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91	Amphidiploids of perennial Triticeae. I. Synthetic <i>Thinopyrum</i> species and their hybrids. <i>Genome</i> , 1992, 35, 951-956.	2.0	4
92	Genome analysis of <i>Thinopyrum junceiforme</i> and <i>T. sartorii</i> . <i>Genome</i> , 1992, 35, 758-764.	2.0	19
93	New intergeneric diploid hybrids among <i>Agropyron</i> , <i>Thinopyrum</i> , <i>Pseudoroegneria</i> , <i>Psathyrostachys</i> , <i>Hordeum</i> , and <i>Secale</i> . <i>Genome</i> , 1992, 35, 545-550.	2.0	6
94	Nucleotide sequence of the internal transcribed spacer region of rDNA in mountain rye, <i>Secale montanum</i> Guss. (Gramineae). <i>Plant Molecular Biology</i> , 1992, 20, 161-162.	3.9	6
95	Nucleotide sequence of the internal transcribed spacer region of rDNA in diploid wheat, <i>Triticum speltoides</i> L. (Tausch) Gren. ex Richter (Gramineae). <i>Plant Molecular Biology</i> , 1992, 20, 157-158.	3.9	3
96	Nucleotide sequence of the internal transcribed spacer region of rDNA in wheat, <i>Triticum aestivum</i> L. (Gramineae). <i>Plant Molecular Biology</i> , 1992, 20, 159-160.	3.9	1
97	Nucleotide sequence of the internal transcribed spacer region of rDNA in the primitive oat species, <i>Avena longiglumis</i> Durieu (Gramineae). <i>Plant Molecular Biology</i> , 1992, 20, 163-164.	3.9	8
98	Nucleotide sequence of the internal transcribed spacer region of rDNA in barley, <i>Hordeum vulgare</i> L. (Gramineae). <i>Plant Molecular Biology</i> , 1992, 20, 165-166.	3.9	6
99	Genome relationships in the perennial Triticeae based on diploid hybrids and beyond. <i>Hereditas</i> , 1992, 116, 133-136.	1.4	26
100	Tissue-culture-facilitated production of aneupolyhaploid <i>Thinopyrum ponticum</i> and amphidiploid <i>Hordeum violaceum</i> x <i>H. bogdanii</i> and their uses in phylogenetic studies. <i>Theoretical and Applied Genetics</i> , 1991, 81, 151-156.	3.6	36
101	Cytogenetics of <i>Elymus caucasicus</i> and <i>Elymus longearistatus</i> (Poaceae: Triticeae). <i>Genome</i> , 1991, 34, 860-867.	2.0	19
102	Meiotic associations at metaphase I in diploid, triploid, and tetraploid Russian wildrye		

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109	Coenocytism, ameiosis, and chromosome diminution in intergeneric hybrids in the perennial Triticeae. <i>Genome</i> , 1988, 30, 766-775.	2.0	10
110	Diploid perennial intergeneric hybrids in the tribe Triticeae. IV. Hybrids among <i>Thinopyrum bessarabicum</i> , <i>Pseudoroegneria spicata</i> , and <i>Secale montanum</i> . <i>Genome</i> , 1988, 30, 356-360.	2.0	12
111	Diploid perennial intergeneric hybrids in the tribe Triticeae. III. Hybrids among <i>Secale montanum</i> , <i>Pseudoroegneria spicata</i> , and <i>Agropyron mongolicum</i> . <i>Genome</i> , 1987, 29, 80-84.	2.0	17
112	Progenies of <i>Thinopyrum elongatum</i> × <i>Agropyron mongolicum</i> . <i>Genome</i> , 1987, 29, 738-743.	2.0	12
113	Karyotype analysis and genome relationships of 22 diploid species in the tribe Triticeae. <i>Genome</i> , 1986, 28, 109-120.	0.7	111
114	Genome Analysis of the Tetraploid <i>Pseudoroegneria tauri</i> 1. <i>Crop Science</i> , 1986, 26, 723-727.	1.8	41
115	Diploid Perennial Intergeneric Hybrids in the Tribe Triticeae . I. <i>Agropyron cristatum</i> × <i>Pseudoroegneria libanotica</i> and <i>Critesion violaceum</i> × <i>Psathyrostachys juncea</i> 1. <i>Crop Science</i> , 1986, 26, 75-78.	1.8	19
116	Morphology and cytology of interspecific hybrids of <i>Leymus mollis</i> . <i>Journal of Heredity</i> , 1984, 75, 488-492.	2.4	38
117	Genome relationships in the perennial Triticeae based on diploid hybrids and beyond. <i>Hereditas</i> , 0, 116, 133-136.	1.4	37