

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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46
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120
docs citations

120
times ranked

1708
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Diversity for Wheat Improvement as a Conduit to Food Security. <i>Advances in Agronomy</i> , 2013, , 179-257.	5.2	124
2	Karyotype analysis and genome relationships of 22 diploid species in the tribe Triticeae. <i>Genome</i> , 1986, 28, 109-120.	0.7	111
3	Characterization of genomes and chromosomes in partial amphiploids of the hybrid <i>Triticum aestivum</i> Å— <i>Thinopyrum ponticum</i> by in situ hybridization, isozyme analysis, and RAPD. <i>Genome</i> , 1996, 39, 1062-1071.	2.0	110
4	Structure and dynamics of retrotransposons at wheat centromeres and pericentromeres. <i>Chromosoma</i> , 2008, 117, 445-456.	2.2	107
5	Genome analysis of <i>Elytrigia caespitosa</i> , <i>Lophopyrum nodosum</i> , <i>Pseudoroegneria geniculata</i> ssp. <i>scythica</i> , and <i>Thinopyrum intermedium</i> (Triticeae: Gramineae). <i>Genome</i> , 1993, 36, 102-111.	2.0	94
6	Absence of the J genome in <i>Leymus</i> species (Poaceae: Triticeae): evidence from DNA hybridization and meiotic pairing. <i>Genome</i> , 1994, 37, 231-235.	2.0	83
7	An assessment of genome analysis based on chromosome pairing in hybrids of perennial Triticeae. <i>Genome</i> , 1989, 32, 179-189.	2.0	70
8	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
9	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
10	Molecular verification and characterization of BYDV-resistant germ plasms derived from hybrids of wheat with <i>Thinopyrum ponticum</i> and Th. <i>intermedium</i> . <i>Theoretical and Applied Genetics</i> , 1996, 93, 1033-1039.	3.6	60
11	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
12	<i>Agropyron</i> and <i>Psathyrostachys</i> . , 2011, , 77-108.		56
13	Molecular genetic linkage maps for allotetraploid <i>Leymus wildryes</i> (Gramineae: Triticeae). <i>Genome</i> , 2003, 46, 627-646.	2.0	55
14	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
15	Breeding strategies for structuring salinity tolerance in wheat. <i>Advances in Agronomy</i> , 2019, 155, 121-187.	5.2	53
16	Varying chromosome composition of 56-chromosome wheat Å— <i>Thinopyrum intermedium</i> partial amphiploids. <i>Genome</i> , 1993, 36, 207-215.	2.0	52
17	Genome- and species-specific markers and genome relationships of diploid perennial species in Triticeae based on RAPD analyses. <i>Genome</i> , 1995, 38, 1230-1236.	2.0	52
18	Genome relationship between <i>Thinopyrum bessarabicum</i> and <i>T. elongatum</i> : revisited. <i>Genome</i> , 1989, 32, 802-809.	2.0	51

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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	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
21	Comparative transcriptome analysis of salt-tolerant wheat germplasm lines using wheat genome arrays. <i>Plant Science</i> , 2007, 173, 327-339.	3.6	45
22	Leymus EST linkage maps identify 4NsL-5NsL reciprocal translocation, wheat-Leymus chromosome introgressions, and functionally important gene loci. <i>Theoretical and Applied Genetics</i> , 2012, 124, 189-206.	3.6	42
23	Genome Analysis of the Tetraploid <i>Pseudoroegneria tauri</i> 1. <i>Crop Science</i> , 1986, 26, 723-727.	1.8	41
24	Morphology and cytology of interspecific hybrids of <i>Leymus mollis</i> . <i>Journal of Heredity</i> , 1984, 75, 488-492.	2.4	38
25	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
26	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
27	Genome relationships in the perennial Triticeae based on diploid hybrids and beyond. <i>Hereditas</i> , 0, 116, 133-136.	1.4	37
28	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
29	Development and annotation of perennial Triticeae ESTs and SSR markers. <i>Genome</i> , 2008, 51, 779-788.	2.0	36
30	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
31	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
32	Characterization of fructan biosynthesis in big bluegrass (<i>Poa secunda</i>). <i>Journal of Plant Physiology</i> , 2002, 159, 705-715.	3.5	32
33	A <i>trv</i> 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
34	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
35	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
36	CAPS markers specific to Eb, Ee, and R genomes in the tribe Triticeae. <i>Genome</i> , 2007, 50, 400-411.	2.0	31

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37	Characteristics and behaviour of the chromosomes of <i>Leymus mollis</i> and <i>L. racemosus</i> (Triticeae.) <i>Tj ETQq1</i> 1 0.784314 rgBT JOverloc	2.2	27
38	Genome relationships in the perennial Triticeae based on diploid hybrids and beyond. <i>Hereditas</i> , 1992, 116, 133-136.	1.4	26
39	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
40	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
41	Genome constitutions of <i>Thinopyrum curvifolium</i> , <i>T. distichum</i> , and <i>T. junceum</i> (Triticeae: Gramineae). <i>Genome</i> , 1993, 36, 641-651.	2.0	25
42	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
43	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
44	Characterization of HMW Glutenin Subunits in <i>Thinopyrum intermedium</i> , <i>Th. 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
45	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
46	Linkage mapping and nucleotide polymorphisms of the 6-SFT gene of cool-season grasses. <i>Genome</i> , 2000, 43, 931-938.	2.0	23
47	Hybrids and backcross progenies between wheat (<i>Triticum aestivum</i> L.) and apomictic Australian wheatgrass [<i>Elymus rectisetus</i> (Nees in Lehm.) A. L. & Connor]: karyotypic and genomic analyses. <i>Theoretical and Applied Genetics</i> , 1994, 89, 599-605.	3.6	22
48	Variations of two repetitive DNA sequences in several Triticeae genomes revealed by polymerase chain reaction and sequencing. <i>Genome</i> , 1995, 38, 1221-1229.	2.0	22
49	Genome Characterization of MT Perennial and OK906 Annual Wheat - Intermediate Wheatgrass Hybrids. <i>Crop Science</i> , 1999, 39, 1041-1043.	1.8	22
50	Genes controlling plant growth habit in <i>Leymus</i> (Triticeae): maize barren stalk1 (ba1), rice lax panicle, and wheat tiller inhibition (tin3) genes as possible candidates. <i>Functional and Integrative Genomics</i> , 2008, 8, 375-386.	3.5	21
51	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
52	Cytogenetics of <i>Elymus caucasicus</i> and <i>Elymus longearistatus</i> (Poaceae: Triticeae). <i>Genome</i> , 1991, 34, 860-867.	2.0	19
53	Genome analysis of <i>Thinopyrum junceiforme</i> and <i>T. sartorii</i> . <i>Genome</i> , 1992, 35, 758-764.	2.0	19
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	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
56	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
57	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> L. <i>Crop Science</i> , 1986, 26, 75-78.	1.8	19
58	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
59	Meiotic Anomalies in Hybrids between Wheat and Apomictic <i>Elymus rectisetus</i> (Nees in Lehm.) A. Löve & Connor. <i>Crop Science</i> , 1997, 37, 717-723.	1.8	17
60	Anther culture of some perennial triticeae. <i>Plant Cell Reports</i> , 1988, 7, 313-317.	5.6	16
61	Genome analysis of seven species of <i>Kengyilia</i> (Triticeae: Poaceae) with FISH and GISH. <i>Genome</i> , 2013, 56, 641-649.	2.0	15
62	Rapid EST isolation from chromosome 1R of rye. <i>BMC Plant Biology</i> , 2008, 8, 28.	3.6	14
63	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
64	Progenies of <i>Thinopyrum elongatum</i> × <i>Agropyron mongolicum</i> . <i>Genome</i> , 1987, 29, 738-743.	2.0	12
65	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
66	Meiotic associations at metaphase I in diploid, triploid, and tetraploid Russian wildrye		

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73	Genes encoding the β -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
74	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
75	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
76	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
77	Agronomic and genetic diversity in intermediate wheatgrass (<i>Thinopyrum intermedium</i>). <i>Plant Breeding</i> , 2016, 135, 751-758.	1.9	11
78	Coenocytism, ameiosis, and chromosome diminution in intergeneric hybrids in the perennial Triticeae. <i>Genome</i> , 1988, 30, 766-775.	2.0	10
79	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
80	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
81	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
82	Comparative chromosome pairing in triploids and diploids of perennial Triticeae. <i>Genome</i> , 1990, 33, 89-94.	2.0	9
83	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
84	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
85	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
86	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
87	DNA sequence-based mapping and comparative genomics of the <i>St</i> genome of <i>Pseudoroegneria spicata</i> (Pursh) Δ^8 versus wheat (<i>Triticum aestivum</i> L.) and barley (<i>Hordeum</i>) Tj ETQq1 1 0.784314.orgBT /Overlock 10		
88	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
89	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
90	Detection of linkage disequilibrium QTLs controlling low-temperature growth and metabolite accumulations in an admixed breeding population of <i>Leymus</i> wildryes. <i>Euphytica</i> , 2005, 141, 263-280.	1.2	8

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91	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
92	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
93	Cytological identification of some trisomics of Russian wildrye (<i>Psathyrostachys juncea</i>). <i>Genome</i> , 1995, 38, 1271-1278.	2.0	7
94	A proposed mechanism for loss of heterozygosity in rice hybrids. <i>Euphytica</i> , 2001, 118, 119-126.	1.2	7
95	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
96	DOP-PCR based painting of rye chromosomes in a wheat background. <i>Genome</i> , 2014, 57, 473-479.	2.0	7
97	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
98	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
99	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
100	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
101	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
102	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
103	Characterization of genome in tetraploid <i>StY</i> species of <i>Elymus</i> (Triticeae: Poaceae) using sequential FISH and GISH. <i>Genome</i> , 2017, 60, 679-685.	2.0	6
104	Wheatgrass and Wildrye Grasses (Triticeae). <i>Genetic Resources, Chromosome Engineering, and Crop Improvement Series</i> , 2009, , 41-79.	0.3	6
105	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
106	Cytological evidence for assortment mitosis leading to loss of heterozygosity in rice. <i>Genome</i> , 2006, 49, 556-557.	2.0	5
107	Cytological studies on a polyhaploid of <i>Critesion iranicum</i> obtained after hybridization with <i>C. bulbosum</i> . <i>Genetica</i> , 1988, 76, 225-228.	1.1	4
108	Amphidiploids of perennial Triticeae. I. Synthetic <i>Thinopyrum</i> species and their hybrids. <i>Genome</i> , 1992, 35, 951-956.	2.0	4

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109	Allozyme Variation in Accessions of Russian Wildrye. <i>Crop Science</i> , 1996, 36, 785-790.	1.8	4
110	<i>Roegneria alashanica</i> Keng: a species with the StStSt^YSt^Y genome constitution. <i>Genome</i> , 2017, 60, 546-551.	2.0	4
111	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
112	Resistance to powdery mildew and barley yellow dwarf in perennial Triticeae species. <i>Genetic Resources and Crop Evolution</i> , 1993, 40, 171-176.	1.6	3
113	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
114	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
115	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
116	Meiotic Stability of Intersubspecific Hybrids of Snake River Å— Thickspike Wheatgrasses. <i>Crop Science</i> , 1995, 35, 962-964.	1.8	2
117	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