

# Jaroslav Dolezel

## List of Publications by Year in descending order

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392  
papers

32,801  
citations

8159

76  
h-index

5806

161  
g-index

433  
all docs

433  
docs citations

433  
times ranked

18557  
citing authors

#	ARTICLE	IF	CITATIONS
1	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
2	A chromosome-based draft sequence of the hexaploid bread wheat ( <i>Triticum aestivum</i> ) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
3	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
4	Estimation of nuclear DNA content in plants using flow cytometry. <i>Nature Protocols</i> , 2007, 2, 2233-2244.	5.5	1,219
5	The banana ( <i>Musa acuminata</i> ) genome and the evolution of monocotyledonous plants. <i>Nature</i> , 2012, 488, 213-217.	13.7	1,049
6	Draft genome sequence of chickpea ( <i>Cicer arietinum</i> ) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	9.4	1,049
7	Letter to the editor. <i>Cytometry</i> , 2003, 51A, 127-128.	1.8	882
8	Plant DNA Flow Cytometry and Estimation of Nuclear Genome Size. <i>Annals of Botany</i> , 2005, 95, 99-110.	1.4	790
9	The transcriptional landscape of polyploid wheat. <i>Science</i> , 2018, 361, .	6.0	768
10	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
11	The Origin, Evolution and Proposed Stabilization of the Terms 'Genome Size' and 'C-Value' to Describe Nuclear DNA Contents. <i>Annals of Botany</i> , 2005, 95, 255-260.	1.4	622
12	Comparison of three DNA fluorochromes for flow cytometric estimation of nuclear DNA content in plants. <i>Physiologia Plantarum</i> , 1992, 85, 625-631.	2.6	546
13	Structural and functional partitioning of bread wheat chromosome 3B. <i>Science</i> , 2014, 345, 1249721.	6.0	542
14	Two New Nuclear Isolation Buffers for Plant DNA Flow Cytometry: A Test with 37 Species. <i>Annals of Botany</i> , 2007, 100, 875-888.	1.4	472
15	Unlocking the Barley Genome by Chromosomal and Comparative Genomics. <i>Plant Cell</i> , 2011, 23, 1249-1263.	3.1	448
16	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	9.4	363
17	A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B. <i>Science</i> , 2008, 322, 101-104.	6.0	356
18	Genome interplay in the grain transcriptome of hexaploid bread wheat. <i>Science</i> , 2014, 345, 1250091.	6.0	318

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19	The pangenome of hexaploid bread wheat. <i>Plant Journal</i> , 2017, 90, 1007-1013.	2.8	313
20	Plant Genome Size Estimation by Flow Cytometry: Inter-laboratory Comparison*1. <i>Annals of Botany</i> , 1998, 82, 17-26.	1.4	266
21	Rapid gene isolation in barley and wheat by mutant chromosome sequencing. <i>Genome Biology</i> , 2016, 17, 221.	3.8	265
22	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	2.8	264
23	The wheat powdery mildew genome shows the unique evolution of an obligate biotroph. <i>Nature Genetics</i> , 2013, 45, 1092-1096.	9.4	236
24	Sex determination in dioecious plants <i>Melandrium album</i> and <i>M. rubrum</i> using high-resolution flow cytometry. <i>Cytometry</i> , 1995, 19, 103-106.	1.8	226
25	Flow cytometric estimation of nuclear DNA amount in diploid bananas ( <i>Musa acuminata</i> and <i>M. Tj ETQq1 1 0.784314 1.9 rgBT /Overlock 221</i> )	1.9	221
26	Rapid cloning of genes in hexaploid wheat using cultivar-specific long-range chromosome assembly. <i>Nature Biotechnology</i> , 2017, 35, 793-796.	9.4	218
27	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7940-7945.	3.3	214
28	The wheat Sr50 gene reveals rich diversity at a cereal disease resistance locus. <i>Nature Plants</i> , 2015, 1, 15186.	4.7	209
29	Flow Sorting of Mitotic Chromosomes in Common Wheat ( <i>Triticum aestivum</i> L.). <i>Genetics</i> , 2000, 156, 2033-2041.	1.2	200
30	Reticulate Evolution of the Rye Genome. <i>Plant Cell</i> , 2013, 25, 3685-3698.	3.1	194
31	Frequent Gene Movement and Pseudogene Evolution Is Common to the Large and Complex Genomes of Wheat, Barley, and Their Relatives. <i>Plant Cell</i> , 2011, 23, 1706-1718.	3.1	190
32	Plant centromeric retrotransposons: a structural and cytogenetic perspective. <i>Mobile DNA</i> , 2011, 2, 4.	1.3	186
33	Pm21 from <i>Haynaldia villosa</i> Encodes a CC-NBS-LRR Protein Conferring Powdery Mildew Resistance in Wheat. <i>Molecular Plant</i> , 2018, 11, 874-878.	3.9	181
34	Selfish supernumerary chromosome reveals its origin as a mosaic of host genome and organellar sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13343-13346.	3.3	173
35	In Depth Characterization of Repetitive DNA in 23 Plant Genomes Reveals Sources of Genome Size Variation in the Legume Tribe Fabaeae. <i>PLoS ONE</i> , 2015, 10, e0143424.	1.1	172
36	A high-quality genome assembly highlights rye genomic characteristics and agronomically important genes. <i>Nature Genetics</i> , 2021, 53, 574-584.	9.4	164

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37	Flow cytometric analysis of nuclear DNA content in higher plants. <i>Phytochemical Analysis</i> , 1991, 2, 143-154.	1.2	161
38	Estimation of nuclear DNA content in <i>Sesleria</i> (Poaceae). <i>Caryologia</i> , 1998, 51, 123-132.	0.2	159
39	A high-yield procedure for isolation of metaphase chromosomes from root tips of <i>Vicia faba</i> L.. <i>Planta</i> , 1992, 188, 93-98.	1.6	157
40	Comparison of Four Nuclear Isolation Buffers for Plant DNA Flow Cytometry. <i>Annals of Botany</i> , 2006, 98, 679-689.	1.4	152
41	An Improved Consensus Linkage Map of Barley Based on Flow-Sorted Chromosomes and Single Nucleotide Polymorphism Markers. <i>Plant Genome</i> , 2011, 4, 238-249.	1.6	150
42	Dissecting large and complex genomes: flow sorting and BAC cloning of individual chromosomes from bread wheat. <i>Plant Journal</i> , 2004, 39, 960-968.	2.8	146
43	Chromosome-based genomics in the cereals. <i>Chromosome Research</i> , 2007, 15, 51-66.	1.0	146
44	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	9.4	138
45	Next-generation sequencing and syntenic integration of flow-sorted arms of wheat chromosome 4A exposes the chromosome structure and gene content. <i>Plant Journal</i> , 2012, 69, 377-386.	2.8	137
46	Gene Content and Virtual Gene Order of Barley Chromosome 1H. <i>Plant Physiology</i> , 2009, 151, 496-505.	2.3	135
47	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
48	Flow Cytometric and Microscopic Analysis of the Effect of Tannic Acid on Plant Nuclei and Estimation of DNA Content. <i>Annals of Botany</i> , 2006, 98, 515-527.	1.4	129
49	Improvement of the banana <i>Musa acuminata</i> reference sequence using NGS data and semi-automated bioinformatics methods. <i>BMC Genomics</i> , 2016, 17, 243.	1.2	129
50	<i>Rht18</i> Semidwarfism in Wheat Is Due to Increased <i>GA 2-oxidase9</i> Expression and Reduced GA Content. <i>Plant Physiology</i> , 2018, 177, 168-180.	2.3	128
51	Development of Chromosome-Specific BAC Resources for Genomics of Bread Wheat. <i>Cytogenetic and Genome Research</i> , 2010, 129, 211-223.	0.6	127
52	Analysis and sorting of rye ( <i>Secale cereale</i> L.) chromosomes using flow cytometry. <i>Genome</i> , 2003, 46, 893-905.	0.9	122
53	Flow karyotyping and chromosome sorting in bread wheat ( <i>Triticum aestivum</i> L.). <i>Theoretical and Applied Genetics</i> , 2002, 104, 1362-1372.	1.8	120
54	Coupling amplified DNA from flow-sorted chromosomes to high-density SNP mapping in barley. <i>BMC Genomics</i> , 2008, 9, 294.	1.2	120

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55	Toward positional cloning of <i>Fhb1</i> , a major QTL for Fusarium head blight resistance in wheat. <i>Cereal Research Communications</i> , 2008, 36, 195-201.	0.8	118
56	Nuclear genome size: Are we getting closer?. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2010, 77A, 635-642.	1.1	113
57	Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene Structure and Coding Sequence Evolution in Polyploid Wheat. <i>Plant Physiology</i> , 2012, 161, 252-265.	2.3	113
58	Sequencing wheat chromosome arm 7BS delimits the 7BS/4AL translocation and reveals homoeologous gene conservation. <i>Theoretical and Applied Genetics</i> , 2012, 124, 423-432.	1.8	110
59	Molecular and cytological characterization of the global <i>Musa</i> germplasm collection provides insights into the treasure of banana diversity. <i>Biodiversity and Conservation</i> , 2017, 26, 801-824.	1.2	108
60	A first survey of the rye ( <i>Secale cereale</i> ) genome composition through BAC end sequencing of the short arm of chromosome 1R. <i>BMC Plant Biology</i> , 2008, 8, 95.	1.6	106
61	Sequencing and assembly of low copy and genic regions of isolated <i>Triticum aestivum</i> chromosome arm 7DS. <i>Plant Biotechnology Journal</i> , 2011, 9, 768-775.	4.1	105
62	Molecular mapping of stripe rust resistance gene Yr51 in chromosome 4AL of wheat. <i>Theoretical and Applied Genetics</i> , 2014, 127, 317-324.	1.8	105
63	Chromosomes in the flow to simplify genome analysis. <i>Functional and Integrative Genomics</i> , 2012, 12, 397-416.	1.4	104
64	BioNano genome mapping of individual chromosomes supports physical mapping and sequence assembly in complex plant genomes. <i>Plant Biotechnology Journal</i> , 2016, 14, 1523-1531.	4.1	104
65	Wheat syntenome unveils new evidences of contrasted evolutionary plasticity between paleo- and neoduplicated subgenomes. <i>Plant Journal</i> , 2013, 76, 1030-1044.	2.8	99
66	High-resolution FISH on super-stretched flow-sorted plant chromosomes. <i>Plant Journal</i> , 2004, 37, 940-950.	2.8	95
67	Induction and verification of autotetraploids in diploid banana ( <i>Musa acuminata</i> ) by in vitro techniques. <i>Euphytica</i> , 1996, 88, 25-34.	0.6	94
68	Flow cytometric analysis of nuclear DNA content in <i>Musa</i> . <i>Theoretical and Applied Genetics</i> , 1999, 98, 1344-1350.	1.8	92
69	Repetitive part of the banana ( <i>Musa acuminata</i> ) genome investigated by low-depth 454 sequencing. <i>BMC Plant Biology</i> , 2010, 10, 204.	1.6	90
70	Development and Characterization of Microsatellite Markers from Chromosome 1-Specific DNA Libraries of <i>Vicia Faba</i> . <i>Biologia Plantarum</i> , 2002, 45, 337-345.	1.9	87
71	Telomere-to-telomere gapless chromosomes of banana using nanopore sequencing. <i>Communications Biology</i> , 2021, 4, 1047.	2.0	86
72	Wheat Pm4 resistance to powdery mildew is controlled by alternative splice variants encoding chimeric proteins. <i>Nature Plants</i> , 2021, 7, 327-341.	4.7	85

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73	Flow karyotyping and sorting of mitotic chromosomes of barley ( <i>Hordeum vulgare</i> L.). <i>Chromosome Research</i> , 1999, 7, 431-444.	1.0	83
74	SNP Discovery for mapping alien introgressions in wheat. <i>BMC Genomics</i> , 2014, 15, 273.	1.2	82
75	Plant Chromosome Analysis and Sorting by Flow Cytometry. <i>Critical Reviews in Plant Sciences</i> , 1994, 13, 275-309.	2.7	81
76	Duplicative Transfer of a MADS Box Gene to a Plant Y Chromosome. <i>Molecular Biology and Evolution</i> , 2003, 20, 1062-1069.	3.5	80
77	Nuclear genome size and genomic distribution of ribosomal DNA in <i>Musa</i> and <i>Ensete</i> (Musaceae): taxonomic implications. <i>Cytogenetic and Genome Research</i> , 2005, 109, 50-57.	0.6	80
78	Refined examination of plant metaphase chromosome structure at different levels made feasible by new isolation methods. <i>Chromosoma</i> , 1993, 102, 96-101.	1.0	79
79	Assessment of ploidy stability of the somatic embryogenesis process in <i>Quercus suber</i> L. using flow cytometry. <i>Planta</i> , 2005, 221, 815-822.	1.6	79
80	Did backcrossing contribute to the origin of hybrid edible bananas?. <i>Annals of Botany</i> , 2010, 106, 849-857.	1.4	79
81	Dispersion and domestication shaped the genome of bread wheat. <i>Plant Biotechnology Journal</i> , 2013, 11, 564-571.	4.1	79
82	The ITS1-5.8S-ITS2 Sequence Region in the Musaceae: Structure, Diversity and Use in Molecular Phylogeny. <i>PLoS ONE</i> , 2011, 6, e17863.	1.1	79
83	Heterogeneity of rDNA distribution and genome size in <i>Silene</i> spp. <i>Chromosome Research</i> , 2001, 9, 387-393.	1.0	78
84	Rapid detection of aneuploidy in <i>Musa</i> using flow cytometry. <i>Plant Cell Reports</i> , 2003, 21, 483-490.	2.8	78
85	Chromosome Sorting in Tetraploid Wheat and Its Potential for Genome Analysis. <i>Genetics</i> , 2005, 170, 823-829.	1.2	78
86	Genome constitution and evolution in <i>Lolium</i> – <i>Festuca</i> hybrid cultivars ( <i>Festulolium</i> ). <i>Theoretical and Applied Genetics</i> , 2006, 113, 731-742.	1.8	77
87	Dissecting the U, M, S and C genomes of wild relatives of bread wheat ( <i>Aegilops</i> spp.) into chromosomes and exploring their synteny with wheat. <i>Plant Journal</i> , 2016, 88, 452-467.	2.8	77
88	Localization of seed protein genes on flow-sorted field bean chromosomes. <i>Chromosome Research</i> , 1993, 1, 107-115.	1.0	76
89	Advances in plant chromosome genomics. <i>Biotechnology Advances</i> , 2014, 32, 122-136.	6.0	75
90	Cell cycle synchronization in plant root meristems. <i>Cytotechnology</i> , 1999, 21, 95-107.	0.7	71

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91	Advanced resources for plant genomics: a BAC library specific for the short arm of wheat chromosome 1B. <i>Plant Journal</i> , 2006, 47, 977-986.	2.8	71
92	Nuclear DNA content and in vitro induced somatic polyploidization cassava ( <i>Manihot esculenta</i> ) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 70	0.6	70
93	Treatment of <i>Vicia faba</i> root tip cells with specific inhibitors to cyclin-dependent kinases leads to abnormal spindle formation. <i>Plant Journal</i> , 1998, 16, 697-707.	2.8	69
94	Chromosome sorting and PCR-based physical mapping in pea ( <i>Pisum sativum</i> L.). <i>Chromosome Research</i> , 2002, 10, 63-71.	1.0	69
95	Flow karyotyping and sorting of <i>Vicia faba</i> chromosomes. <i>Theoretical and Applied Genetics</i> , 1993, 85-85, 665-672.	1.8	67
96	Preparation of HMW DNA from Plant Nuclei and Chromosomes Isolated from Root Tips. <i>Biologia Plantarum</i> , 2003, 46, 369-373.	1.9	67
97	Comparison of three DNA fluorochromes for flow cytometric estimation of nuclear DNA content in plants. <i>Physiologia Plantarum</i> , 1992, 85, 625-631.	2.6	67
98	Flow cytogenetics and plant genome mapping. <i>Chromosome Research</i> , 2004, 12, 77-91.	1.0	65
99	The <i>Agropyron cristatum</i> karyotype, chromosome structure and cross-genome homoeology as revealed by fluorescence in situ hybridization with tandem repeats and wheat single-gene probes. <i>Theoretical and Applied Genetics</i> , 2018, 131, 2213-2227.	1.8	64
100	Fonio millet genome unlocks African orphan crop diversity for agriculture in a changing climate. <i>Nature Communications</i> , 2020, 11, 4488.	5.8	63
101	A membrane-bound ankyrin repeat protein confers race-specific leaf rust disease resistance in wheat. <i>Nature Communications</i> , 2021, 12, 956.	5.8	63
102	Mapping of repeated DNA sequences in plant chromosomes by PRINS and C-PRINS. <i>Theoretical and Applied Genetics</i> , 1997, 94, 758-763.	1.8	62
103	Nuclear $\beta$ -Tubulin during Acentriolar Plant Mitosis. <i>Plant Cell</i> , 2000, 12, 433-442.	3.1	62
104	A multi gene sequence-based phylogeny of the Musaceae (banana) family. <i>BMC Evolutionary Biology</i> , 2011, 11, 103.	3.2	62
105	Sequence-Based Analysis of Translocations and Inversions in Bread Wheat ( <i>Triticum aestivum</i> L.). <i>PLoS ONE</i> , 2013, 8, e79329.	1.1	62
106	Association of gamma-tubulin with kinetochore/centromeric region of plant chromosomes. <i>Plant Journal</i> , 1998, 14, 751-757.	2.8	61
107	Construction of a subgenomic BAC library specific for chromosomes 1D, 4D and 6D of hexaploid wheat. <i>Theoretical and Applied Genetics</i> , 2004, 109, 1337-1345.	1.8	60
108	Chromosome Painting Facilitates Anchoring Reference Genome Sequence to Chromosomes In Situ and Integrated Karyotyping in Banana ( <i>Musa</i> Spp.). <i>Frontiers in Plant Science</i> , 2019, 10, 1503.	1.7	59

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109	Development of a composite map in <i>Vicia faba</i> , breeding applications and future prospects. <i>Theoretical and Applied Genetics</i> , 2004, 108, 1079-1088.	1.8	58
110	Limited Genome Size Variation in <i>Sesleria albicans</i> . <i>Annals of Botany</i> , 2000, 86, 399-403.	1.4	57
111	First Survey of the Wheat Chromosome 5A Composition through a Next Generation Sequencing Approach. <i>PLoS ONE</i> , 2011, 6, e26421.	1.1	57
112	Localization of Male-Specifically Expressed <i>MROS</i> Genes of <i>Silene latifolia</i> by PCR on Flow-Sorted Sex Chromosomes and Autosomes. <i>Genetics</i> , 2001, 158, 1269-1277.	1.2	56
113	Nuclear genome stability of <i>Mammillaria san-angelensis</i> (Cactaceae) regenerants induced by auxins in long-term in vitro culture. <i>Plant Science</i> , 1999, 141, 191-200.	1.7	54
114	A chromosomal genomics approach to assess and validate the <i>desi</i> and <i>kabuli</i> draft chickpea genome assemblies. <i>Plant Biotechnology Journal</i> , 2014, 12, 778-786.	4.1	54
115	Genome-Wide Analysis of Repeat Diversity across the Family Musaceae. <i>PLoS ONE</i> , 2014, 9, e98918.	1.1	54
116	A platform for efficient genotyping in <i>Musa</i> using microsatellite markers. <i>AoB PLANTS</i> , 2011, 2011, plr024.	1.2	53
117	The Coiled-Coil NLR <i>Rph1</i> , Confers Leaf Rust Resistance in Barley Cultivar Sudan. <i>Plant Physiology</i> , 2019, 179, 1362-1372.	2.3	53
118	Construction of chromosome-specific DNA libraries covering the whole genome of field bean ( <i>Vicia</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.0	52
119	Dissection of the nuclear genome of barley by chromosome flow sorting. <i>Theoretical and Applied Genetics</i> , 2006, 113, 651-659.	1.8	52
120	Stem rust resistance in wheat is suppressed by a subunit of the mediator complex. <i>Nature Communications</i> , 2020, 11, 1123.	5.8	52
121	High-resolution flow karyotyping and chromosome sorting in <i>Vicia faba</i> lines with standard and reconstructed karyotypes. <i>Theoretical and Applied Genetics</i> , 1995, 90, 797-802.	1.8	51
122	Challenges of flow-cytometric estimation of nuclear genome size in orchids, a plant group with both whole-genome and progressively partial endoreplication. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2015, 87, 958-966.	1.1	51
123	Rye B chromosomes encode a functional Argonaute-like protein with <i>in vitro</i> slicer activities similar to its A chromosome paralog. <i>New Phytologist</i> , 2017, 213, 916-928.	3.5	51
124	Subtelomeric assembly of a multi-gene pathway for antimicrobial defense compounds in cereals. <i>Nature Communications</i> , 2021, 12, 2563.	5.8	51
125	Subtraction with 3' Modified Oligonucleotides Eliminates Amplification Artifacts in DNA Libraries Enriched for Microsatellites. <i>BioTechniques</i> , 1998, 25, 32-38.	0.8	50
126	Creation of a BAC resource to study the structure and evolution of the banana ( <i>Musa balbisiana</i> ) genome. <i>Genome</i> , 2004, 47, 1182-1191.	0.9	50



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127	A major invasion of transposable elements accounts for the large size of the <i>Blumeria graminis</i> f.sp. <i>tritici</i> genome. <i>Functional and Integrative Genomics</i> , 2011, 11, 671-677.	1.4	50
128	Genomic Prediction in a Multiploid Crop: Genotype by Environment Interaction and Allele Dosage Effects on Predictive Ability in Banana. <i>Plant Genome</i> , 2018, 11, 170090.	1.6	50
129	Molecular and Cytogenetic Study of East African Highland Banana. <i>Frontiers in Plant Science</i> , 2018, 9, 1371.	1.7	50
130	The bacterial artificial chromosome (BAC) library of the narrow-leafed lupin ( <i>Lupinus angustifolius</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	2.7	49
131	Development and mapping of DArT markers within the <i>Festuca - Lolium</i> complex. <i>BMC Genomics</i> , 2009, 10, 473.	1.2	49
132	A 3,000-Loci Transcription Map of Chromosome 3B Unravels the Structural and Functional Features of Gene Islands in Hexaploid Wheat. <i>Plant Physiology</i> , 2011, 157, 1596-1608.	2.3	49
133	Molecular Analysis and Genomic Organization of Major DNA Satellites in Banana ( <i>Musa</i> spp.). <i>PLoS ONE</i> , 2013, 8, e54808.	1.1	49
134	Flow cytometric chromosome sorting from diploid progenitors of bread wheat, <i>T. urartu</i> , <i>Ae. speltoides</i> and <i>Ae. tauschii</i> . <i>Theoretical and Applied Genetics</i> , 2014, 127, 1091-1104.	1.8	49
135	Development of microsatellite markers specific for the short arm of rye ( <i>Secale cereale</i> L.) chromosome 1. <i>Theoretical and Applied Genetics</i> , 2008, 117, 915-926.	1.8	48
136	Flow cytometric chromosome sorting in plants: The next generation. <i>Methods</i> , 2012, 57, 331-337.	1.9	48
137	Exploring the tertiary gene pool of bread wheat: sequence assembly and analysis of chromosome 5M <sup>g</sup> of <i>Aegilops geniculata</i> . <i>Plant Journal</i> , 2015, 84, 733-746.	2.8	48
138	<i>Aegilops sharonensis</i> genome-assisted identification of stem rust resistance gene Sr62. <i>Nature Communications</i> , 2022, 13, 1607.	5.8	48
139	Analysis of Nuclear DNA Content and Ploidy in Higher Plants. <i>Current Protocols in Cytometry</i> , 1997, 2, Unit 7.6.	3.7	46
140	A novel resource for genomics of Triticeae: BAC library specific for the short arm of rye ( <i>Secale</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	1.2	45
141	A high density physical map of chromosome 1BL supports evolutionary studies, map-based cloning and sequencing in wheat. <i>Genome Biology</i> , 2013, 14, R64.	3.8	45
142	Whole-genome profiling and shotgun sequencing delivers an anchored, gene-decorated, physical map assembly of bread wheat chromosome 6A. <i>Plant Journal</i> , 2014, 79, 334-347.	2.8	45
143	Next-Generation Survey Sequencing and the Molecular Organization of Wheat Chromosome 6B. <i>DNA Research</i> , 2014, 21, 103-114.	1.5	45
144	Primed in situ labelling facilitates flow sorting of similar sized chromosomes. <i>Plant Journal</i> , 1995, 7, 1039-1044.	2.8	44

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145	Isolation, characterization and chromosome localization of repetitive DNA sequences in bananas ( <i>Musa</i> spp.). <i>Chromosome Research</i> , 2002, 10, 89-100.	1.0	44
146	DART whole genome profiling provides insights on the evolution and taxonomy of edible Banana ( <i>Musa</i> spp.). <i>Annals of Botany</i> , 2016, 118, 1269-1278.	1.4	44
147	Ploidy instability of embryogenic cucumber ( <i>Cucumis sativus</i> L.) callus culture. <i>Biologia Plantarum</i> , 1996, 38, 475.	1.9	43
148	Subgenomic analysis of microRNAs in polyploid wheat. <i>Functional and Integrative Genomics</i> , 2012, 12, 465-479.	1.4	43
149	Development of COS-SNP and HRM markers for high-throughput and reliable haplotype-based detection of Lr14a in durum wheat ( <i>Triticum durum</i> Desf.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 1077-1101.	1.8	43
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