

Jacqueline Batley

List of Publications by Year in descending order

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Version: 2024-02-01

249
papers

23,052
citations

19608

61
h-index

10127

140
g-index

266
all docs

266
docs citations

266
times ranked

15819
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	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
3	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
4	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
5	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
6	Speed breeding is a powerful tool to accelerate crop research and breeding. <i>Nature Plants</i> , 2018, 4, 23-29.	4.7	770
7	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
8	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid <i>Brassica oleracea</i> . <i>Genome Biology</i> , 2014, 15, R77.	13.9	456
9	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	5.8	375
10	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , 2019, 51, 1411-1422.	9.4	363
11	The pangenome of hexaploid bread wheat. <i>Plant Journal</i> , 2017, 90, 1007-1013.	2.8	313
12	Plant pan-genomes are the new reference. <i>Nature Plants</i> , 2020, 6, 914-920.	4.7	302
13	Plant genome sequencing: applications for crop improvement. <i>Plant Biotechnology Journal</i> , 2010, 8, 2-9.	4.1	267
14	Mining for Single Nucleotide Polymorphisms and Insertions/Deletions in Maize Expressed Sequence Tag Data. <i>Plant Physiology</i> , 2003, 132, 84-91.	2.3	263
15	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	1.7	243
16	Accessing complex crop genomes with next-generation sequencing. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1-11.	1.8	241
17	Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. <i>Plant Biotechnology Journal</i> , 2017, 15, 149-161.	4.1	240
18	Towards CRISPR/Cas crops “bringing together genomics and genome editing. <i>New Phytologist</i> , 2017, 216, 682-698.	3.5	235

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19	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1095-1098.	4.1	221
20	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1265-1274.	4.1	217
21	A high-density SNP genotyping array for <i>Brassica napus</i> and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1887-1899.	1.8	205
22	Towards plant pangenomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1099-1105.	4.1	203
23	Genome-Wide Delineation of Natural Variation for Pod Shatter Resistance in <i>Brassica napus</i> . <i>PLoS ONE</i> , 2014, 9, e101673.	1.1	182
24	The reference genetic linkage map for the multinational <i>Brassica rapa</i> genome sequencing project. <i>Theoretical and Applied Genetics</i> , 2007, 115, 777-792.	1.8	160
25	Redundancy based detection of sequence polymorphisms in expressed sequence tag data using autoSNP. <i>Bioinformatics</i> , 2003, 19, 421-422.	1.8	156
26	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , 2017, 15, 1602-1610.	4.1	150
27	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. <i>Trends in Genetics</i> , 2020, 36, 132-145.	2.9	137
28	Prioritization of candidate genes in a QTL-hotspot region for drought tolerance in chickpea (<i>Cicer</i>) Tj ETQq0 0,0rgBT /Overlock 10	1.6	131
29	INTRASPECIFIC GENETIC DIVERSITY IN THE MARINE COCCOLITHOPHORE EMILIANA HUXLEYI (PRYMNESIOPHYCEAE): THE USE OF MICROSATELLITE ANALYSIS IN MARINE PHYTOPLANKTON POPULATION STUDIES1. <i>Journal of Phycology</i> , 2006, 42, 526-536.	1.0	121
30	Molecular Genetic Markers: Discovery, Applications, Data Storage and Visualisation. <i>Current Bioinformatics</i> , 2009, 4, 16-27.	0.7	121
31	Discovering genetic polymorphisms in next-generation sequencing data. <i>Plant Biotechnology Journal</i> , 2009, 7, 312-317.	4.1	118
32	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	2.8	113
33	Investigating Drought Tolerance in Chickpea Using Genome-Wide Association Mapping and Genomic Selection Based on Whole-Genome Resequencing Data. <i>Frontiers in Plant Science</i> , 2018, 9, 190.	1.7	111
34	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
35	Molecular mapping of qualitative and quantitative loci for resistance to <i>Leptosphaeria maculans</i> causing blackleg disease in canola (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 405-418.	1.8	108
36	New Technologies for Ultra-High Throughput Genotyping in Plants. <i>Methods in Molecular Biology</i> , 2009, 513, 19-39.	0.4	107

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37	Plant bioinformatics: from genome to phenome. <i>Trends in Biotechnology</i> , 2004, 22, 232-237.	4.9	106
38	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
39	Genetic and physical mapping of flowering time loci in canola (<i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , 2013, 126, 119-132.	1.8	105
40	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
41	Investigation of the diversity of effector genes in the banana pathogen, <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> , reveals evidence of horizontal gene transfer. <i>Molecular Plant Pathology</i> , 2018, 19, 1155-1171.	2.0	102
42	Simple sequence repeat marker loci discovery using SSR primer. <i>Bioinformatics</i> , 2004, 20, 1475-1476.	1.8	101
43	Variation in abundance of predicted resistance genes in the <i>Brassica oleracea</i> pangenome. <i>Plant Biotechnology Journal</i> , 2019, 17, 789-800.	4.1	92
44	Single nucleotide polymorphism discovery from wheat next-generation sequence data. <i>Plant Biotechnology Journal</i> , 2012, 10, 743-749.	4.1	91
45	The development of multiplex simple sequence repeat (SSR) markers to complement distinctness, uniformity and stability testing of rape (<i>Brassica napus</i> L.) varieties. <i>Theoretical and Applied Genetics</i> , 2003, 106, 1091-1101.	1.8	90
46	A user guide to the Brassica 60K Illumina Infinium SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2017, 130, 621-633.	1.8	90
47	The Genome of a Southern Hemisphere Seagrass Species (<i>Zostera muelleri</i>). <i>Plant Physiology</i> , 2016, 172, 272-283.	2.3	88
48	Genetic map construction and QTL mapping of resistance to blackleg (<i>Leptosphaeria maculans</i>) disease in Australian canola (<i>Brassica napus</i> L.) cultivars. <i>Theoretical and Applied Genetics</i> , 2009, 120, 71-83.	1.8	85
49	Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 2062.	1.7	84
50	AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants. <i>Nucleic Acids Research</i> , 2009, 37, D951-D953.	6.5	83
51	Characterization of disease resistance genes in the <i>Brassica napus</i> pangenome reveals significant structural variation. <i>Plant Biotechnology Journal</i> , 2020, 18, 969-982.	4.1	83
52	Current Status and Challenges in Identifying Disease Resistance Genes in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 1788.	1.7	81
53	Genome sequence data: management, storage, and visualization. <i>BioTechniques</i> , 2009, 46, 333-336.	0.8	79
54	Dispersion and domestication shaped the genome of bread wheat. <i>Plant Biotechnology Journal</i> , 2013, 11, 564-571.	4.1	79

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55	Trait associations in the pangenome of pigeon pea (<i>Cajanus cajan</i>). <i>Plant Biotechnology Journal</i> , 2020, 18, 1946-1954.	4.1	79
56	High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in <i>Cicer arietinum</i> and <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , 2015, 128, 1039-1047.	1.8	76
57	DNA Methylation: Toward Crop Disease Resistance Improvement. <i>Trends in Plant Science</i> , 2019, 24, 1137-1150.	4.3	76
58	Identification of Putative Candidate Genes for Water Stress Tolerance in Canola (<i>Brassica napus</i>). <i>Frontiers in Plant Science</i> , 2015, 6, 1058.	1.7	73
59	Genome-wide Association Study Identifies New Loci for Resistance to <i>Leptosphaeria maculans</i> in Canola. <i>Frontiers in Plant Science</i> , 2016, 7, 1513.	1.7	73
60	Capturing the Biofuel Wellhead and Powerhouse: The Chloroplast and Mitochondrial Genomes of the Leguminous Feedstock Tree <i>Pongamia pinnata</i> . <i>PLoS ONE</i> , 2012, 7, e51687.	1.1	73
61	Improvements in Genomic Technologies: Application to Crop Genomics. <i>Trends in Biotechnology</i> , 2017, 35, 547-558.	4.9	72
62	The loss of vernalization requirement in narrow-leaved lupin is associated with a deletion in the promoter and de-repressed expression of a <i>Flowering Locus T</i> (<i>FT</i>) homologue. <i>New Phytologist</i> , 2017, 213, 220-232.	3.5	70
63	Genome-wide identification and comparative analysis of NBS-LRR resistance genes in <i>Brassica napus</i> . <i>Crop and Pasture Science</i> , 2018, 69, 72.	0.7	70
64	Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , 2010, 11, R94.	13.9	66
65	Current status of structural variation studies in plants. <i>Plant Biotechnology Journal</i> , 2021, 19, 2153-2163.	4.1	65
66	Discovery of Single Nucleotide Polymorphisms in Complex Genomes Using SGSautoSNP. <i>Biology</i> , 2012, 1, 370-382.	1.3	64
67	High-throughput genotyping for species identification and diversity assessment in germplasm collections. <i>Molecular Ecology Resources</i> , 2015, 15, 1091-1101.	2.2	64
68	Creating new interspecific hybrid and polyploid crops. <i>Trends in Biotechnology</i> , 2015, 33, 436-441.	4.9	64
69	SSRPrimer and SSR Taxonomy Tree: Biome SSR discovery. <i>Nucleic Acids Research</i> , 2006, 34, W656-W659.	6.5	62
70	A consensus map of rapeseed (<i>Brassica napus</i> L.) based on diversity array technology markers: applications in genetic dissection of qualitative and quantitative traits. <i>BMC Genomics</i> , 2013, 14, 277.	1.2	62
71	Genomic advances will herald new insights into the <i>Brassica: Leptosphaeria maculans</i> pathosystem. <i>Plant Biology</i> , 2012, 14, 1-10.	1.8	59
72	SNP markers-based map construction and genome-wide linkage analysis in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2014, 12, 851-860.	4.1	59

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73	Bias in resistance gene prediction due to repeat masking. <i>Nature Plants</i> , 2018, 4, 762-765.	4.7	58
74	SNPServer: a real-time SNP discovery tool. <i>Nucleic Acids Research</i> , 2005, 33, W493-W495.	6.5	56
75	SNP Applications in Plants. , 2007, , 95-102.		56
76	Single nucleotide polymorphism discovery in barley using autoSNPdb. <i>Plant Biotechnology Journal</i> , 2009, 7, 326-333.	4.1	56
77	The application of genomics and bioinformatics to accelerate crop improvement in a changing climate. <i>Current Opinion in Plant Biology</i> , 2016, 30, 78-81.	3.5	56
78	Genomic selection and genetic architecture of agronomic traits during modern rapeseed breeding. <i>Nature Genetics</i> , 2022, 54, 694-704.	9.4	55
79	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
80	Genomic distribution of simple sequence repeats in <i>Brassica rapa</i> . <i>Molecules and Cells</i> , 2007, 23, 349-56.	1.0	54
81	Copy number variation and disease resistance in plants. <i>Theoretical and Applied Genetics</i> , 2017, 130, 2479-2490.	1.8	53
82	Genome Analysis Identified Novel Candidate Genes for Ascochyta Blight Resistance in Chickpea Using Whole Genome Re-sequencing Data. <i>Frontiers in Plant Science</i> , 2017, 8, 359.	1.7	53
83	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , 2022, 15, e20109.	1.6	53
84	Degradation of the benzoxazolinone class of phytoalexins is important for virulence of <i>Fusarium pseudograminearum</i> towards wheat. <i>Molecular Plant Pathology</i> , 2015, 16, 946-962.	2.0	51
85	Gene loss in the fungal canola pathogen <i>Leptosphaeria maculans</i> . <i>Functional and Integrative Genomics</i> , 2015, 15, 189-196.	1.4	50
86	Characterization of the flanking regions of <i>Zea mays</i> microsatellites reveals a large number of useful sequence polymorphisms. <i>Theoretical and Applied Genetics</i> , 2002, 105, 532-543.	1.8	47
87	Title is missing!. <i>Molecular Breeding</i> , 2003, 11, 111-120.	1.0	47
88	Centromere Locations in <i>Brassica</i> A and C Genomes Revealed Through Half-Tetrad Analysis. <i>Genetics</i> , 2016, 202, 513-523.	1.2	47
89	Wild Origins of Macadamia Domestication Identified Through Intraspecific Chloroplast Genome Sequencing. <i>Frontiers in Plant Science</i> , 2019, 10, 334.	1.7	47
90	Future tools for association mapping in crop plants This article is one of a selection of papers from the conference "Exploiting Genome-wide Association in Oilseed Brassicas: a model for genetic improvement of major OECD crops for sustainable farming". <i>Genome</i> , 2010, 53, 1017-1023.	0.9	46

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91	Rapid divergence of repetitive DNAs in Brassica relatives. <i>Genomics</i> , 2011, 97, 173-185.	1.3	46
92	Genome-wide survey of the seagrass <i>Zostera muelleri</i> suggests modification of the ethylene signalling network. <i>Journal of Experimental Botany</i> , 2015, 66, 1489-1498.	2.4	46
93	Identification and characterization of candidate <i>Rlm4</i> blackleg resistance genes in <i>Brassica napus</i> using next-generation sequencing. <i>Plant Biotechnology Journal</i> , 2012, 10, 709-715.	4.1	44
94	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	4.1	44
95	Molecular Marker Applications in Plants. <i>Methods in Molecular Biology</i> , 2015, 1245, 13-27.	0.4	44
96	A high-throughput SNP array in the amphidiploid species <i>Brassica napus</i> shows diversity in resistance genes. <i>Functional and Integrative Genomics</i> , 2014, 14, 643-655.	1.4	43
97	Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. <i>Plant Biotechnology Journal</i> , 2015, 13, 97-104.	4.1	43
98	Targeted Knockout of <i>BnTT2</i> Homologues for Yellow-Seeded <i>Brassica napus</i> with Reduced Flavonoids and Improved Fatty Acid Composition. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 5676-5690.	2.4	43
99	Genetic Maps and the Use of Synteny. <i>Methods in Molecular Biology</i> , 2009, 513, 41-55.	0.4	42
100	Inherited allelic variants and novel karyotype changes influence fertility and genome stability in <i>Brassica</i> allohexaploids. <i>New Phytologist</i> , 2019, 223, 965-978.	3.5	42
101	What Are SNPs?. , 2007, , 41-52.		41
102	A Complex Recombination Pattern in the Genome of Allotetraploid <i>Brassica napus</i> as Revealed by a High-Density Genetic Map. <i>PLoS ONE</i> , 2014, 9, e109910.	1.1	41
103	Transcriptomic comparison between developing seeds of yellow- and black-seeded <i>Brassica napus</i> reveals that genes influence seed quality. <i>BMC Plant Biology</i> , 2019, 19, 203.	1.6	40
104	Exploring the application of wild species for crop improvement in a changing climate. <i>Current Opinion in Plant Biology</i> , 2020, 56, 218-222.	3.5	40
105	Genotype-Environment mismatch of kelp forests under climate change. <i>Molecular Ecology</i> , 2021, 30, 3730-3746.	2.0	39
106	Comparison of transcription of multiple genes at three developmental stages of the plant pathogen <i>Sclerotinia sclerotiorum</i> . <i>FEMS Microbiology Letters</i> , 2006, 258, 150-160.	0.7	38
107	Type B Heterotrimeric G Protein β^3 -Subunit Regulates Auxin and ABA Signaling in Tomato. <i>Plant Physiology</i> , 2016, 170, 1117-1134.	2.3	38
108	An advanced reference genome of <i>Trifolium subterraneum</i> L. reveals genes related to agronomic performance. <i>Plant Biotechnology Journal</i> , 2017, 15, 1034-1046.	4.1	38

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109	Genetic and Molecular Regulation of Seed Storage Proteins (SSPs) to Improve Protein Nutritional Value of Oilseed Rape (<i>Brassica napus</i> L.) Seeds. <i>Frontiers in Plant Science</i> , 2018, 9, 890.	1.7	38
110	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1677-1690.	1.8	38
111	Polymorphic microsatellite loci in global populations of the marine coccolithophorid <i>Emiliana huxleyi</i> . <i>Molecular Ecology Notes</i> , 2002, 2, 495-497.	1.7	37
112	Single Nucleotide Polymorphism Genotyping in Plants. , 2007, , 77-94.		37
113	The pangenome of banana highlights differences between genera and genomes. <i>Plant Genome</i> , 2022, 15, e20100.	1.6	37
114	Genome Wide Analysis of Flowering Time Trait in Multiple Environments via High-Throughput Genotyping Technique in <i>Brassica napus</i> L.. <i>PLoS ONE</i> , 2015, 10, e0119425.	1.1	37
115	Sixteen new simple sequence repeat markers from <i>Brassica juncea</i> expressed sequences and their cross-species amplification. <i>Molecular Ecology Notes</i> , 2007, 7, 697-700.	1.7	36
116	Epigenetics: Potentials and Challenges in Crop Breeding. <i>Molecular Plant</i> , 2019, 12, 1309-1311.	3.9	36
117	Molecular breeding for resistance to black rot [<i>Xanthomonas campestris</i> pv. <i>campestris</i> (Pammel) Dowson] in Brassicas: recent advances. <i>Euphytica</i> , 2018, 214, 1.	0.6	35
118	SNP discovery and applications in <i>Brassica napus</i> . <i>Journal of Plant Biotechnology</i> , 2012, 39, 49-61.	0.1	35
119	Identification and characterization of simple sequence repeat (SSR) markers derived in silico from <i>Brassica oleracea</i> genome shotgun sequences. <i>Molecular Ecology Notes</i> , 2006, 6, 1191-1194.	1.7	34
120	Targeted identification of genomic regions using TAGdb. <i>Plant Methods</i> , 2010, 6, 19.	1.9	34
121	The Fate of Chromosomes and Alleles in an Allohexaploid <i>Brassica</i> Population. <i>Genetics</i> , 2014, 197, 273-283.	1.2	34
122	Identification and characterization of simple sequence repeat (SSR) markers from <i>Fragaria x ananassa</i> expressed sequences. <i>Molecular Ecology Notes</i> , 2006, 6, 319-322.	1.7	33
123	Scanning the Effects of Ethyl Methanesulfonate on the Whole Genome of <i>Lotus japonicus</i> Using Second-Generation Sequencing Analysis. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 559-567.	0.8	33
124	RNA-Seq and metabolic flux analysis of <i>Tetraselmis</i> sp. M8 during nitrogen starvation reveals a two-stage lipid accumulation mechanism. <i>Bioresource Technology</i> , 2017, 244, 1281-1293.	4.8	33
125	Resistance Gene Analogs in the Brassicaceae: Identification, Characterization, Distribution, and Evolution. <i>Plant Physiology</i> , 2020, 184, 909-922.	2.3	33
126	Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	1.6	33

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127	Single Nucleotide Polymorphism Discovery. , 2007, , 53-76.		31
128	High-resolution molecular karyotyping uncovers pairing between ancestrally related Brassica chromosomes. <i>New Phytologist</i> , 2014, 202, 964-974.	3.5	31
129	Assessing Variations in Host Resistance to <i>Fusarium oxysporum</i> f sp. <i>cubense</i> Race 4 in <i>Musa</i> Species, With a Focus on the Subtropical Race 4. <i>Frontiers in Microbiology</i> , 2019, 10, 1062.	1.5	30
130	Brassica ASTRA: an integrated database for Brassica genomic research. <i>Nucleic Acids Research</i> , 2004, 33, D656-D659.	6.5	29
131	Identification and characterization of simple sequence repeat markers from <i>Brassica napus</i> expressed sequences. <i>Molecular Ecology Notes</i> , 2007, 7, 886-889.	1.7	29
132	Understanding Host-Pathogen Interactions in <i>Brassica napus</i> in the Omics Era. <i>Plants</i> , 2020, 9, 1336.	1.6	29
133	The application of pangenomics and machine learning in genomic selection in plants. <i>Plant Genome</i> , 2021, 14, e20112.	1.6	29
134	Characterization of simple sequence repeat markers derived in silico from <i>Brassica rapa</i> bacterial artificial chromosome sequences and their application in <i>Brassica napus</i> . <i>Molecular Ecology Notes</i> , 2007, 7, 273-277.	1.7	27
135	A bi-filtering method for processing single nucleotide polymorphism array data improves the quality of genetic map and accuracy of quantitative trait locus mapping in doubled haploid populations of polyploid <i>Brassica napus</i> . <i>BMC Genomics</i> , 2015, 16, 409.	1.2	27
136	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. <i>Journal of Experimental Botany</i> , 2018, 69, 3689-3702.	2.4	27
137	Extensive polyploid clonality was a successful strategy for seagrass to expand into a newly submerged environment. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	27
138	Genetic diversity within populations of cyanobacteria assessed by analysis of single filaments. <i>Antonie Van Leeuwenhoek</i> , 2002, 81, 197-202.	0.7	26
139	Molecular Marker-Based Genetic Analysis of Pasture and Turf Grasses. , 2004, , 197-238.		25
140	New Computational Tools for Brassica Genome Research. <i>Comparative and Functional Genomics</i> , 2004, 5, 276-280.	2.0	25
141	Neodiversification of homeologous CLAVATA1-like receptor kinase genes in soybean leads to distinct developmental outcomes. <i>Scientific Reports</i> , 2017, 7, 8878.	1.6	25
142	Whole Genome Diversity, Population Structure, and Linkage Disequilibrium Analysis of Chickpea (<i>Cicer</i>) Tj ETQq0 0,0 rgt /Overlock 10	1.0	25
143	Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives. <i>Agronomy</i> , 2020, 10, 1484.	1.3	25
144	A comparative map viewer integrating genetic maps for <i>Brassica</i> and <i>Arabidopsis</i> . <i>BMC Plant Biology</i> , 2007, 7, 40.	1.6	24

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145	Genome Sequencing Approaches and Successes. <i>Methods in Molecular Biology</i> , 2009, 513, 345-358.	0.4	24
146	Microspore culture reveals complex meiotic behaviour in a trigenomic Brassica hybrid. <i>BMC Plant Biology</i> , 2015, 15, 173.	1.6	24
147	Segregation for fertility and meiotic stability in novel Brassica allohexaploids. <i>Theoretical and Applied Genetics</i> , 2017, 130, 767-776.	1.8	24
148	<i>Brassica napus</i> genes <i>Rlm4</i> and <i>Rlm7</i> , conferring resistance to <i>Leptosphaeria maculans</i> , are alleles of the <i>Rlm9</i> wall-associated kinase-like resistance locus. <i>Plant Biotechnology Journal</i> , 2022, 20, 1229-1231.	4.1	24
149	A β -lactamase from cereal infecting <i>Fusarium</i> spp. catalyses the first step in the degradation of the benzoxazinone class of phytoalexins. <i>Fungal Genetics and Biology</i> , 2015, 83, 1-9.	0.9	23
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