

# Jacqueline Batley

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

244  
papers

15,143  
citations

53  
h-index

119  
g-index

266  
ext. papers

20,084  
ext. citations

7.2  
avg, IF

6.38  
L-index

#	Paper	IF	Citations
244	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003.. <i>Theoretical and Applied Genetics</i> , <b>2022</b> , 135, 1443	6	1
243	Genome Analysis of the Broad Host Range Necrotroph Highlights Genes Associated With Virulence.. <i>Frontiers in Plant Science</i> , <b>2022</b> , 13, 811152	6.2	
242	Expanding Gene-Editing Potential in Crop Improvement with Pangenomes.. <i>International Journal of Molecular Sciences</i> , <b>2022</b> , 23,	6.3	1
241	Brassica napus genes Rlm4 and Rlm7, conferring resistance to <i>Leptosphaeria maculans</i> , are alleles of the Rlm9 wall-associated kinase-like resistance locus.. <i>Plant Biotechnology Journal</i> , <b>2022</b> ,	11.6	2
240	Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction.. <i>BMC Plant Biology</i> , <b>2022</b> , 22, 180	5.3	0
239	Systematic trait dissection in oilseed rape provides a comprehensive view, further insight, and exact roadmap for yield determination. <b>2022</b> , 15, 38		0
238	Molecular Markers for Identifying Resistance Genes in Brassica napus. <i>Agronomy</i> , <b>2022</b> , 12, 985	3.6	1
237	Allele segregation analysis of F hybrids between independent Brassica allohexaploid lineages.. <i>Chromosoma</i> , <b>2022</b> , 1	2.8	1
236	Advancing designer crops for climate resilience through an integrated genomics approach.. <i>Current Opinion in Plant Biology</i> , <b>2022</b> , 67, 102220	9.9	0
235	Mining of Cloned Disease Resistance Gene Homologs (CDRHs) in Brassica Species and <i>Arabidopsis thaliana</i> . <i>Biology</i> , <b>2022</b> , 11, 821	4.9	0
234	Development of monoclonal antibodies against <i>Perkinsus olseni</i> using whole cells. <i>Aquaculture Reports</i> , <b>2022</b> , 24, 101179	2.3	
233	Quantitative Trait Locus Mapping of Resistance to Turnip Yellow Virus in and and Introgression of These Resistances by Resynthesis Into Allotetraploid Plants for Deployment in .. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 781385	6.2	2
232	Formulation and efficacy testing of bio-organic fertilizer produced through solid-state fermentation of agro-waste by <i>Burkholderia cenocepacia</i> . <i>Chemosphere</i> , <b>2021</b> , 132762	8.4	0
231	Stable, fertile lines produced by hybridization between allotetraploids Brassica juncea (AABB) and Brassica carinata (BBCC) have merged the A and C genomes. <i>New Phytologist</i> , <b>2021</b> , 230, 1242-1257	9.8	3
230	Candidate Rlm6 resistance genes against <i>Leptosphaeria. maculans</i> identified through a genome-wide association study in Brassica juncea (L.) Czern. <i>Theoretical and Applied Genetics</i> , <b>2021</b> , 134, 2035-2050	6	4
229	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. <i>Theoretical and Applied Genetics</i> , <b>2021</b> , 134, 1677-1690	6	10
228	The Gene, a New Player of - Interaction Maps on Chromosome C03 in Canola. <i>Frontiers in Plant Science</i> , <b>2021</b> , 12, 654604	6.2	3

227	Studying the Genetic Diversity of Yam Bean Using a New Draft Genome Assembly. <i>Agronomy</i> , <b>2021</b> , 11, 953	3.6	1
226	Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. <i>Plant Genome</i> , <b>2021</b> , e20109	4.4	11
225	Genotype-Environment mismatch of kelp forests under climate change. <i>Molecular Ecology</i> , <b>2021</b> , 30, 3730-3746	5.7	7
224	Status and advances in mining for blackleg ( <i>Leptosphaeria maculans</i> ) quantitative resistance (QR) in oilseed rape ( <i>Brassica napus</i> ). <i>Theoretical and Applied Genetics</i> , <b>2021</b> , 134, 3123-3145	6	1
223	De Novo SNP Discovery and Genotyping of Iranian Pimpinella Species Using ddRAD Sequencing. <i>Agronomy</i> , <b>2021</b> , 11, 1342	3.6	1
222	The pangenome of banana highlights differences between genera and genomes. <i>Plant Genome</i> , <b>2021</b> , e20100	4.4	10
221	The application of pangenomics and machine learning in genomic selection in plants. <i>Plant Genome</i> , <b>2021</b> , 14, e20112	4.4	4
220	Comparison and evolutionary analysis of Brassica nucleotide binding site leucine rich repeat (NLR) genes and importance for disease resistance breeding. <i>Plant Genome</i> , <b>2021</b> , 14, e20060	4.4	2
219	Molecular characterization of disease resistance in Brassica juncea □The current status and the way forward. <i>Plant Pathology</i> , <b>2021</b> , 70, 13-34	2.8	10
218	Immunoassays and diagnostic antibodies for Perkinsus spp. pathogens of marine molluscs. <i>Diseases of Aquatic Organisms</i> , <b>2021</b> , 147, 13-23	1.7	1
217	Genomics Armed With Diversity Leads the Way in Improvement in a Changing Global Environment. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 600789	4.5	8
216	Modeling first order additive □additive epistasis improves accuracy of genomic prediction for sclerotinia stem rot resistance in canola. <i>Plant Genome</i> , <b>2021</b> , 14, e20088	4.4	5
215	Current status of structural variation studies in plants. <i>Plant Biotechnology Journal</i> , <b>2021</b> , 19, 2153-2163	11.6	7
214	Draft Genome Assembly and Transcriptome Dataset for European Turnip ( <i>L. ssp.</i> ), ECD4 Carrying Clubroot Resistance. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 651298	4.5	2
213	Amborella gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. <i>New Phytologist</i> , <b>2021</b> ,	9.8	3
212	QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape ( <i>L.</i> ). <i>Genes</i> , <b>2021</b> , 12,	4.2	4
211	Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , <b>2021</b> , 19, 2488-2500	11.6	7
210	Detection of Epistasis for Seed and Some Phytochemical Traits in Coriander under Different Irrigation Regimes. <i>Agronomy</i> , <b>2021</b> , 11, 1891	3.6	0

209	Pangenomics in crop improvement-from coding structural variations to finding regulatory variants with pangenome graphs.. <i>Plant Genome</i> , <b>2021</b> , e20177	4.4	2
208	Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. <i>Agronomy</i> , <b>2021</b> , 11, 2587	3.6	
207	Targeted Knockout of Homologues for Yellow-Seeded with Reduced Flavonoids and Improved Fatty Acid Composition. <i>Journal of Agricultural and Food Chemistry</i> , <b>2020</b> , 68, 5676-5690	5.7	10
206	Virulence/avirulence patterns among <i>Leptosphaeria maculans</i> isolates determines expression of resistance, senescence and yellowing in cotyledons of <i>Brassica napus</i> . <i>European Journal of Plant Pathology</i> , <b>2020</b> , 156, 1077-1089	2.1	0
205	Genome-Wide Analysis of the Lateral Organ Boundaries Domain Gene Family in <i>Brassica Napus</i> . <i>Genes</i> , <b>2020</b> , 11,	4.2	7
204	Trait associations in the pangenome of pigeon pea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 1946-1954	11.6	36
203	Exploring the application of wild species for crop improvement in a changing climate. <i>Current Opinion in Plant Biology</i> , <b>2020</b> , 56, 218-222	9.9	17
202	Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in. <i>Biology</i> , <b>2020</b> , 10,	4.9	9
201	Recent Findings Unravel Genes and Genetic Factors Underlying Resistance in and Its Relatives. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 22,	6.3	2
200	The importance of plant pan-genomes in breeding. <b>2020</b> , 27-32		4
199	Identification and QTL mapping of resistance to Turnip yellows virus (TuYV) in oilseed rape, <i>Brassica napus</i> . <i>Theoretical and Applied Genetics</i> , <b>2020</b> , 133, 383-393	6	11
198	Fertile allohexaploid <i>Brassica</i> hybrids obtained from crosses between <i>B. oleracea</i> and <i>B. juncea</i> via ovule rescue and colchicine treatment of cuttings. <i>Plant Cell, Tissue and Organ Culture</i> , <b>2020</b> , 140, 301-313	2.7	5
197	Characterization of disease resistance genes in the <i>Brassica napus</i> pangenome reveals significant structural variation. <i>Plant Biotechnology Journal</i> , <b>2020</b> , 18, 969-982	11.6	41
196	Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. <i>Trends in Genetics</i> , <b>2020</b> , 36, 132-145	8.5	57
195	Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives. <i>Agronomy</i> , <b>2020</b> , 10, 1484	3.6	11
194	The Use of Genetic and Gene Technologies in Shaping Modern Rapeseed Cultivars ( <i>L.</i> ). <i>Genes</i> , <b>2020</b> , 11,	4.2	3
193	Plant pan-genomes are the new reference. <i>Nature Plants</i> , <b>2020</b> , 6, 914-920	11.5	129
192	Frontiers in Dissecting and Managing Diseases: From Reference-Based RGA Candidate Identification to Building Pan-RGAomes. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	6

191	Genome-wide identification and comparative analysis of resistance genes in Brassica juncea. <i>Molecular Breeding</i> , <b>2020</b> , 40, 1	3.4	10
190	Resistance Gene Analogs in the Brassicaceae: Identification, Characterization, Distribution, and Evolution. <i>Plant Physiology</i> , <b>2020</b> , 184, 909-922	6.6	15
189	Understanding Host-Pathogen Interactions in the Omics Era. <i>Plants</i> , <b>2020</b> , 9,	4.5	12
188	Effect of Leptosphaeria maculans Infection on Promoter DNA Methylation of Defence Genes in Brassica napus. <i>Agronomy</i> , <b>2020</b> , 10, 1072	3.6	4
187	Linkage mapping and QTL analysis of flowering time using ddRAD sequencing with genotype error correction in Brassica napus. <i>BMC Plant Biology</i> , <b>2020</b> , 20, 546	5.3	3
186	Genome-Wide Mining of Disease Resistance Gene Analogs Using Conserved Domains. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2107, 365-375	1.4	1
185	Genotyping for Species Identification and Diversity Assessment Using Double-Digest Restriction Site-Associated DNA Sequencing (ddRAD-Seq). <i>Methods in Molecular Biology</i> , <b>2020</b> , 2107, 159-187	1.4	2
184	Whole Genome Diversity, Population Structure, and Linkage Disequilibrium Analysis of Chickpea (L.) Genotypes Using Genome-Wide DArTseq-Based SNP Markers. <i>Genes</i> , <b>2019</b> , 10,	4.2	11
183	A reference genome for pea provides insight into legume genome evolution. <i>Nature Genetics</i> , <b>2019</b> , 51, 1411-1422	36.3	157
182	Epigenetics: Potentials and Challenges in Crop Breeding. <i>Molecular Plant</i> , <b>2019</b> , 12, 1309-1311	14.4	23
181	Using Genomics to Adapt Crops to Climate Change <b>2019</b> , 91-109		2
180	First report of genome size and ploidy of the underutilized leguminous tuber crop Yam Bean (Pachyrhizus erosus and P. tuberosus) by flow cytometry. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , <b>2019</b> , 17, 456-459	1	8
179	Transcriptomic comparison between developing seeds of yellow- and black-seeded Brassica napus reveals that genes influence seed quality. <i>BMC Plant Biology</i> , <b>2019</b> , 19, 203	5.3	17
178	Assessing Variations in Host Resistance to f sp. Race 4 in Species, With a Focus on the Subtropical Race 4. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1062	5.7	11
177	Inherited allelic variants and novel karyotype changes influence fertility and genome stability in Brassica allohexaploids. <i>New Phytologist</i> , <b>2019</b> , 223, 965-978	9.8	20
176	Wild Origins of Macadamia Domestication Identified Through Intraspecific Chloroplast Genome Sequencing. <i>Frontiers in Plant Science</i> , <b>2019</b> , 10, 334	6.2	31
175	"Doubled-haploid" allohexaploid Brassica lines lose fertility and viability and accumulate genetic variation due to genomic instability. <i>Chromosoma</i> , <b>2019</b> , 128, 521-532	2.8	5
174	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , <b>2019</b> , 100, 1066-1082	6.9	32

173	DNA Methylation: Toward Crop Disease Resistance Improvement. <i>Trends in Plant Science</i> , <b>2019</b> , 24, 1137-1150	11.50	34
172	Integration of metabolome and transcriptome reveals flavonoid accumulation in the intergeneric hybrid between <i>Brassica rapa</i> and <i>Raphanus sativus</i> . <i>Scientific Reports</i> , <b>2019</b> , 9, 18368	4.9	13
171	Variation in abundance of predicted resistance genes in the <i>Brassica oleracea</i> pangenome. <i>Plant Biotechnology Journal</i> , <b>2019</b> , 17, 789-800	11.6	60
170	Regulation of a novel <i>Fusarium</i> cytokinin in <i>Fusarium pseudograminearum</i> . <i>Fungal Biology</i> , <b>2019</b> , 123, 255-266	2.8	5
169	CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. <i>Plant Journal</i> , <b>2019</b> , 98, 142-152	6.9	16
168	A differential k-mer analysis pipeline for comparing RNA-Seq transcriptome and meta-transcriptome datasets without a reference. <i>Functional and Integrative Genomics</i> , <b>2019</b> , 19, 363-374	3.8	1
167	Integrated physical map of bread wheat chromosome arm 7DS to facilitate gene cloning and comparative studies. <i>New Biotechnology</i> , <b>2019</b> , 48, 12-19	6.4	6
166	Genome-wide identification and comparative analysis of NBS-LRR resistance genes in <i>Brassica napus</i> . <i>Crop and Pasture Science</i> , <b>2018</b> , 69, 72	2.2	37
165	Revolution in Genotyping Platforms for Crop Improvement. <i>Advances in Biochemical Engineering/Biotechnology</i> , <b>2018</b> , 164, 37-52	1.7	8
164	Speed breeding is a powerful tool to accelerate crop research and breeding. <i>Nature Plants</i> , <b>2018</b> , 4, 23-29	11.5	448
163	Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. <i>Journal of Experimental Botany</i> , <b>2018</b> , 69, 3689-3702	7	9
162	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> , <b>2018</b> , 9, 190	6.2	69
161	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , <b>2018</b> , 361,	33.3	1296
160	Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , <b>2018</b> , 16, 1265-1274	11.6	130
159	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> , <b>2018</b> , 19, 1155-1171	5.7	50
158	Bias in resistance gene prediction due to repeat masking. <i>Nature Plants</i> , <b>2018</b> , 4, 762-765	11.5	30
157	Molecular breeding for resistance to black rot [ <i>Xanthomonas campestris</i> pv. <i>campestris</i> (Pammel) Dowson] in Brassicas: recent advances. <i>Euphytica</i> , <b>2018</b> , 214, 1	2.1	20
156	Case Study for Trait-Related Gene Evolution: Disease Resistance Genes in <i>Brassica napus</i> . <i>Compendium of Plant Genomes</i> , <b>2018</b> , 223-232	0.8	

155	Genetic and Molecular Regulation of Seed Storage Proteins (SSPs) to Improve Protein Nutritional Value of Oilseed Rape () Seeds. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 890	6.2	23
154	Agricultural selection and presence-absence variation in spring-type canola germplasm. <i>Crop and Pasture Science</i> , <b>2018</b> , 69, 55	2.2	6
153	Segregation for fertility and meiotic stability in novel Brassica allohexaploids. <i>Theoretical and Applied Genetics</i> , <b>2017</b> , 130, 767-776	6	15
152	A user guide to the Brassica 60K Illumina Infinium SNP genotyping array. <i>Theoretical and Applied Genetics</i> , <b>2017</b> , 130, 621-633	6	56
151	The pangenome of hexaploid bread wheat. <i>Plant Journal</i> , <b>2017</b> , 90, 1007-1013	6.9	206
150	An advanced reference genome of <i>Trifolium subterraneum</i> L. reveals genes related to agronomic performance. <i>Plant Biotechnology Journal</i> , <b>2017</b> , 15, 1034-1046	11.6	17
149	Improvements in Genomic Technologies: Application to Crop Genomics. <i>Trends in Biotechnology</i> , <b>2017</b> , 35, 547-558	15.1	50
148	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , <b>2017</b> , 15, 1602-1610	11.6	103
147	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> , <b>2017</b> , 244, 1281-1293	11	22
146	Genoproteomics-assisted improvement of <i>Andrographis paniculata</i> : toward a promising molecular and conventional breeding platform for autogamous plants affecting the pharmaceutical industry. <i>Critical Reviews in Biotechnology</i> , <b>2017</b> , 37, 803-816	9.4	9
145	Copy number variation and disease resistance in plants. <i>Theoretical and Applied Genetics</i> , <b>2017</b> , 130, 2479-2490	9.33	2490
144	Neodiversification of homeologous CLAVATA1-like receptor kinase genes in soybean leads to distinct developmental outcomes. <i>Scientific Reports</i> , <b>2017</b> , 7, 8878	4.9	10
143	Towards CRISPR/Cas crops - bringing together genomics and genome editing. <i>New Phytologist</i> , <b>2017</b> , 216, 682-698	9.8	165
142	Cytogenetic and Molecular Characterization of B-Genome Introgression Lines of <i>Brassica napus</i> L. G3: <i>Genes, Genomes, Genetics</i> , <b>2017</b> , 7, 77-86	3.2	9
141	Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. <i>Plant Biotechnology Journal</i> , <b>2017</b> , 15, 149-161	11.6	159
140	The loss of vernalization requirement in narrow-leaved lupin is associated with a deletion in the promoter and de-repressed expression of a Flowering Locus T (FT) homologue. <i>New Phytologist</i> , <b>2017</b> , 213, 220-232	9.8	51
139	Genome Analysis Identified Novel Candidate Genes for Ascochyta Blight Resistance in Chickpea Using Whole Genome Re-sequencing Data. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 359	6.2	29
138	Current Status and Challenges in Identifying Disease Resistance Genes in. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 1788	6.2	53

137	Germin-like protein 2 gene promoter from rice is responsive to fungal pathogens in transgenic potato plants. <i>Functional and Integrative Genomics</i> , <b>2016</b> , 16, 19-27	3.8	9
136	The Genome of a Southern Hemisphere Seagrass Species ( <i>Zostera muelleri</i> ). <i>Plant Physiology</i> , <b>2016</b> , 172, 272-83	6.6	41
135	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , <b>2016</b> , 7, 13390	17.4	240
134	An efficient approach to BAC based assembly of complex genomes. <i>Plant Methods</i> , <b>2016</b> , 12, 2	5.8	10
133	Towards plant pangenomics. <i>Plant Biotechnology Journal</i> , <b>2016</b> , 14, 1099-105	11.6	130
132	The Fdb3 transcription factor of the Fusarium Detoxification of Benzoxazolinone gene cluster is required for MBOA but not BOA degradation in <i>Fusarium pseudograminearum</i> . <i>Fungal Genetics and Biology</i> , <b>2016</b> , 88, 44-53	3.9	6
131	Type B Heterotrimeric G Protein $\beta$ Subunit Regulates Auxin and ABA Signaling in Tomato. <i>Plant Physiology</i> , <b>2016</b> , 170, 1117-34	6.6	27
130	Centromere Locations in Brassica A and C Genomes Revealed Through Half-Tetrad Analysis. <i>Genetics</i> , <b>2016</b> , 202, 513-23	4	23
129	Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 2062	6.2	38
128	Genome-wide Association Study Identifies New Loci for Resistance to in Canola. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 1513	6.2	41
127	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> , <b>2016</b> , 129, 1887-99	6	138
126	SNP analysis of <i>Macadamia integrifolia</i> chloroplast genomes to determine the genetic structure of wild populations. <i>Acta Horticulturae</i> , <b>2016</b> , 175-180	0.3	1
125	Can genomics assist the phenological adaptation of canola to new and changing environments?. <i>Crop and Pasture Science</i> , <b>2016</b> , 67, 284	2.2	14
124	High-throughput FACS-based mutant screen identifies a gain-of-function allele of the <i>Fusarium graminearum</i> adenylyl cyclase causing deoxynivalenol over-production. <i>Fungal Genetics and Biology</i> , <b>2016</b> , 90, 1-11	3.9	18
123	BioNano genome mapping of individual chromosomes supports physical mapping and sequence assembly in complex plant genomes. <i>Plant Biotechnology Journal</i> , <b>2016</b> , 14, 1523-31	11.6	82
122	Plant Genomics and Climate Change <b>2016</b> ,		2
121	Molecular-cytogenetic characterization of C-genome chromosome substitution lines in <i>Brassica juncea</i> (L.) Czern and Coss. <i>Theoretical and Applied Genetics</i> , <b>2016</b> , 129, 1153-66	6	10
120	The application of genomics and bioinformatics to accelerate crop improvement in a changing climate. <i>Current Opinion in Plant Biology</i> , <b>2016</b> , 30, 78-81	9.9	40



119	Global agricultural intensification during climate change: a role for genomics. <i>Plant Biotechnology Journal</i> , <b>2016</b> , 14, 1095-8	11.6	138
118	Gene loss in the fungal canola pathogen <i>Leptosphaeria maculans</i> . <i>Functional and Integrative Genomics</i> , <b>2015</b> , 15, 189-96	3.8	30
117	Creating new interspecific hybrid and polyploid crops. <i>Trends in Biotechnology</i> , <b>2015</b> , 33, 436-41	15.1	41
116	Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. <i>Theoretical and Applied Genetics</i> , <b>2015</b> , 128, 1373-83	6	4
115	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> , <b>2015</b> , 128, 1039-47	6	52
114	Mapping QTLs of resistance to head splitting in cabbage ( <i>Brassica oleracea</i> L.var. <i>capitata</i> L.). <i>Molecular Breeding</i> , <b>2015</b> , 35, 1	3.4	9
113	Microspore culture reveals complex meiotic behaviour in a trigonomic <i>Brassica</i> hybrid. <i>BMC Plant Biology</i> , <b>2015</b> , 15, 173	5.3	18
112	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> , <b>2015</b> , 16, 409	4.5	14
111	A $\beta$ -lactamase from cereal infecting <i>Fusarium</i> spp. catalyses the first step in the degradation of the benzoxazolinone class of phytoalexins. <i>Fungal Genetics and Biology</i> , <b>2015</b> , 83, 1-9	3.9	19
110	Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. <i>Plant Biotechnology Journal</i> , <b>2015</b> , 13, 97-104	11.6	32
109	Prioritization of candidate genes in "QTL-hotspot" region for drought tolerance in chickpea ( <i>Cicer arietinum</i> L.). <i>Scientific Reports</i> , <b>2015</b> , 5, 15296	4.9	96
108	Degradation of the benzoxazolinone class of phytoalexins is important for virulence of <i>Fusarium pseudograminearum</i> towards wheat. <i>Molecular Plant Pathology</i> , <b>2015</b> , 16, 946-62	5.7	36
107	Population Diversity of <i>Leptosphaeria maculans</i> in Australia. <i>International Journal of Biology</i> , <b>2015</b> , 7,	1.1	3
106	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 563	6.2	161
105	Identification of Putative Candidate Genes for Water Stress Tolerance in Canola ( <i>Brassica napus</i> ). <i>Frontiers in Plant Science</i> , <b>2015</b> , 6, 1058	6.2	48
104	Advances in plant genotyping: where the future will take us. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1245, 1-11	1.4	8
103	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> , <b>2015</b> , 5, 559-67	3.2	10
102	Genome-wide survey of the seagrass <i>Zostera muelleri</i> suggests modification of the ethylene signalling network. <i>Journal of Experimental Botany</i> , <b>2015</b> , 66, 1489-98	7	31

101	High-throughput genotyping for species identification and diversity assessment in germplasm collections. <i>Molecular Ecology Resources</i> , <b>2015</b> , 15, 1091-101	8.4	36
100	Genome wide analysis of flowering time trait in multiple environments via high-throughput genotyping technique in Brassica napus L. <i>PLoS ONE</i> , <b>2015</b> , 10, e0119425	3.7	22
99	Molecular marker applications in plants. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1245, 13-27	1.4	29
98	Computational Identification and Comparative Analysis of miRNAs in Wheat Group 7 Chromosomes. <i>Plant Molecular Biology Reporter</i> , <b>2014</b> , 32, 487-500	1.7	8
97	High-resolution molecular karyotyping uncovers pairing between ancestrally related Brassica chromosomes. <i>New Phytologist</i> , <b>2014</b> , 202, 964-974	9.8	25
96	New technologies for ultrahigh-throughput genotyping in plant taxonomy. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1115, 151-75	1.4	2
95	A high-throughput SNP array in the amphidiploid species Brassica napus shows diversity in resistance genes. <i>Functional and Integrative Genomics</i> , <b>2014</b> , 14, 643-55	3.8	36
94	SNP markers-based map construction and genome-wide linkage analysis in Brassica napus. <i>Plant Biotechnology Journal</i> , <b>2014</b> , 12, 851-60	11.6	55
93	A chromosome-based draft sequence of the hexaploid bread wheat ( <i>Triticum aestivum</i> ) genome. <i>Science</i> , <b>2014</b> , 345, 1251788	33.3	1129
92	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , <b>2014</b> , 345, 1250092	33.3	419
91	A chromosomal genomics approach to assess and validate the desi and kabuli draft chickpea genome assemblies. <i>Plant Biotechnology Journal</i> , <b>2014</b> , 12, 778-86	11.6	48
90	The fate of chromosomes and alleles in an allohexaploid Brassica population. <i>Genetics</i> , <b>2014</b> , 197, 273-834		27
89	Plant genetics. Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. <i>Science</i> , <b>2014</b> , 345, 950-3	33.3	1348
88	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , <b>2014</b> , 5, 3930	17.4	676
87	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid Brassica oleracea. <i>Genome Biology</i> , <b>2014</b> , 15, R77	18.3	306
86	A complex recombination pattern in the genome of allotetraploid Brassica napus as revealed by a high-density genetic map. <i>PLoS ONE</i> , <b>2014</b> , 9, e109910	3.7	36
85	Next-generation genome sequencing can be used to rapidly characterise sequences flanking T-DNA insertions in random insertional mutants of. <i>Fungal Biology and Biotechnology</i> , <b>2014</b> , 1, 10	7.5	9
84	Next Generation Sequencing and Germplasm Resources <b>2014</b> , 369-390		

83	Genome-wide delineation of natural variation for pod shatter resistance in <i>Brassica napus</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e101673	3.7	133
82	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> , <b>2013</b> , 14, 277	4.5	49
81	Dispersion and domestication shaped the genome of bread wheat. <i>Plant Biotechnology Journal</i> , <b>2013</b> , 11, 564-71	11.6	55
80	Accessing complex crop genomes with next-generation sequencing. <i>Theoretical and Applied Genetics</i> , <b>2013</b> , 126, 1-11	6	210
79	Genetic and physical mapping of flowering time loci in canola ( <i>Brassica napus</i> L.). <i>Theoretical and Applied Genetics</i> , <b>2013</b> , 126, 119-32	6	80
78	Predicting polymorphic EST-SSRs in silico. <i>Molecular Ecology Resources</i> , <b>2013</b> , 13, 538-45	8.4	17
77	Identifying genetic diversity of avirulence genes in <i>Leptosphaeria maculans</i> using whole genome sequencing. <i>Functional and Integrative Genomics</i> , <b>2013</b> , 13, 295-308	3.8	14
76	Next generation characterisation of cereal genomes for marker discovery. <i>Biology</i> , <b>2013</b> , 2, 1357-77	4.9	11
75	Identification and characterization of candidate Rlm4 blackleg resistance genes in <i>Brassica napus</i> using next-generation sequencing. <i>Plant Biotechnology Journal</i> , <b>2012</b> , 10, 709-15	11.6	32
74	Single nucleotide polymorphism discovery from wheat next-generation sequence data. <i>Plant Biotechnology Journal</i> , <b>2012</b> , 10, 743-9	11.6	80
73	Second-generation sequencing for gene discovery in the Brassicaceae. <i>Plant Biotechnology Journal</i> , <b>2012</b> , 10, 750-9	11.6	13
72	Genomic advances will herald new insights into the Brassica: <i>Leptosphaeria maculans</i> pathosystem. <i>Plant Biology</i> , <b>2012</b> , 14 Suppl 1, 1-10	3.7	25
71	Sequencing wheat chromosome arm 7BS delimits the 7BS/4AL translocation and reveals homoeologous gene conservation. <i>Theoretical and Applied Genetics</i> , <b>2012</b> , 124, 423-32	6	79
70	Discovery of Single Nucleotide Polymorphisms in Complex Genomes Using SGSautoSNP. <i>Biology</i> , <b>2012</b> , 1, 370-82	4.9	53
69	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> , <b>2012</b> , 125, 405-18 <sup>6</sup>		75
68	Capturing the biofuel wellhead and powerhouse: the chloroplast and mitochondrial genomes of the leguminous feedstock tree <i>Pongamia pinnata</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e51687	3.7	52
67	SNP discovery and applications in <i>Brassica napus</i> . <i>Journal of Plant Biotechnology</i> , <b>2012</b> , 39, 49-61	0.6	31
66	Rapid divergence of repetitive DNAs in Brassica relatives. <i>Genomics</i> , <b>2011</b> , 97, 173-85	4.3	38

65	Sequencing and assembly of low copy and genic regions of isolated <i>Triticum aestivum</i> chromosome arm 7DS. <i>Plant Biotechnology Journal</i> , <b>2011</b> , 9, 768-75	11.6	91
64	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , <b>2011</b> , 43, 1035-9	36.3	1490
63	Plant genome sequencing: applications for crop improvement. <i>Plant Biotechnology Journal</i> , <b>2010</b> , 8, 2-9	11.6	218
62	CMap3D: a 3D visualization tool for comparative genetic maps. <i>Bioinformatics</i> , <b>2010</b> , 26, 273-4	7.2	17
61	Targeted identification of genomic regions using TAGdb. <i>Plant Methods</i> , <b>2010</b> , 6, 19	5.8	29
60	Sequence and structure of <i>Brassica rapa</i> chromosome A3. <i>Genome Biology</i> , <b>2010</b> , 11, R94	18.3	53
59	Future tools for association mapping in crop plants. <i>Genome</i> , <b>2010</b> , 53, 1017-23	2.4	42
58	Molecular Genetic Markers: Discovery, Applications, Data Storage and Visualisation. <i>Current Bioinformatics</i> , <b>2009</b> , 4, 16-27	4.7	95
57	AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D951-3	20.1	73
56	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> , <b>2009</b> , 120, 71-83	6	60
55	Discovering genetic polymorphisms in next-generation sequencing data. <i>Plant Biotechnology Journal</i> , <b>2009</b> , 7, 312-7	11.6	107
54	Single nucleotide polymorphism discovery in barley using autoSNPdb. <i>Plant Biotechnology Journal</i> , <b>2009</b> , 7, 326-33	11.6	48
53	New technologies for ultra-high throughput genotyping in plants. <i>Methods in Molecular Biology</i> , <b>2009</b> , 513, 19-39	1.4	89
52	Genetic maps and the use of synteny. <i>Methods in Molecular Biology</i> , <b>2009</b> , 513, 41-55	1.4	29
51	Mining for SNPs and SSRs using SNPServer, dbSNP and SSR taxonomy tree. <i>Methods in Molecular Biology</i> , <b>2009</b> , 537, 303-21	1.4	19
50	Genome sequencing approaches and successes. <i>Methods in Molecular Biology</i> , <b>2009</b> , 513, 345-58	1.4	22
49	Genome sequence data: management, storage, and visualization. <i>BioTechniques</i> , <b>2009</b> , 46, 333-4, 336	2.5	65
48	Molecular Marker Discovery and Genetic Map Visualisation <b>2009</b> , 165-189		6

47	Characterization of simple sequence repeat markers derived in silico from Brassica rapa bacterial artificial chromosome sequences and their application in Brassica napus. <i>Molecular Ecology Notes</i> , <b>2007</b> , 7, 273-277		20
46	Sixteen new simple sequence repeat markers from Brassica juncea expressed sequences and their cross-species amplification. <i>Molecular Ecology Notes</i> , <b>2007</b> , 7, 697-700		27
45	Identification and characterization of simple sequence repeat markers from Brassica napus expressed sequences. <i>Molecular Ecology Notes</i> , <b>2007</b> , 7, 886-889		26
44	A comparative map viewer integrating genetic maps for Brassica and Arabidopsis. <i>BMC Plant Biology</i> , <b>2007</b> , 7, 40	5.3	20
43	Automated discovery of single nucleotide polymorphism and simple sequence repeat molecular genetic markers. <i>Methods in Molecular Biology</i> , <b>2007</b> , 406, 473-94	1.4	9
42	The reference genetic linkage map for the multinational Brassica rapa genome sequencing project. <i>Theoretical and Applied Genetics</i> , <b>2007</b> , 115, 777-92	6	144
41	BASC: an integrated bioinformatics system for Brassica research. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D870-30.1	30.1	17
40	What Are SNPs? <b>2007</b> , 41-52		27
39	Single Nucleotide Polymorphism Discovery <b>2007</b> , 53-76		27
38	Single Nucleotide Polymorphism Genotyping in Plants <b>2007</b> , 77-94		27
37	SNP Applications in Plants <b>2007</b> , 95-102		39
36	Genomic distribution of simple sequence repeats in Brassica rapa. <i>Molecules and Cells</i> , <b>2007</b> , 23, 349-56	3.5	50
35	Microsatellite cross-amplification in coccolithophores: application in population diversity studies. <i>Hereditas</i> , <b>2006</b> , 143, 99-102	2.4	4
34	SSRPrimer and SSR Taxonomy Tree: Biome SSR discovery. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W656-9	20.1	53
33	Identification and characterization of simple sequence repeat (SSR) markers from Fragaria ananassa expressed sequences. <i>Molecular Ecology Notes</i> , <b>2006</b> , 6, 319-322		29
32	Identification and characterization of simple sequence repeat (SSR) markers derived in silico from Brassica oleracea genome shotgun sequences. <i>Molecular Ecology Notes</i> , <b>2006</b> , 6, 1191-1194		27
31	INTRASPECIFIC GENETIC DIVERSITY IN THE MARINE COCCOLITHOPHORE EMILIANIA HUXLEYI (PRYMNESIOPHYCEAE): THE USE OF MICROSATELLITE ANALYSIS IN MARINE PHYTOPLANKTON POPULATION STUDIES1. <i>Journal of Phycology</i> , <b>2006</b> , 42, 526-536	3	112
30	Comparison of transcription of multiple genes at three developmental stages of the plant pathogen Sclerotinia sclerotiorum. <i>FEMS Microbiology Letters</i> , <b>2006</b> , 258, 150-60	2.9	37

29	SNPServer: a real-time SNP discovery tool. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W493-5	20.1	46
28	Brassica ASTRA: an integrated database for Brassica genomic research. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D656-9	20.1	21
27	Simple sequence repeat marker loci discovery using SSR primer. <i>Bioinformatics</i> , <b>2004</b> , 20, 1475-6	7.2	86
26	Molecular Marker-Based Genetic Analysis of Pasture and Turf Grasses <b>2004</b> , 197-238		23
25	Genetic Diversity in the Perennial Ryegrass Fungal Endophyte <i>Neotyphodium lolii</i> . <i>Developments in Plant Breeding</i> , <b>2004</b> , 155-164		2
24	Population structure of the beetle pests <i>Phyllodecta vulgatissima</i> and <i>P. vitellinae</i> on UK willow plantations. <i>Insect Molecular Biology</i> , <b>2004</b> , 13, 413-21	3.4	5
23	Plant bioinformatics: from genome to phenome. <i>Trends in Biotechnology</i> , <b>2004</b> , 22, 232-7	15.1	85
22	A comparative study of interspecies mating of <i>Phratora vulgatissima</i> and <i>P. vitellinae</i> using behavioural tests and molecular markers. <i>Entomologia Experimentalis Et Applicata</i> , <b>2004</b> , 110, 231-241	2.1	6
21	New computational tools for brassica genome research. <i>Comparative and Functional Genomics</i> , <b>2004</b> , 5, 276-80		20
20	Redundancy based detection of sequence polymorphisms in expressed sequence tag data using autoSNP. <i>Bioinformatics</i> , <b>2003</b> , 19, 421-2	7.2	142
19	Mining for single nucleotide polymorphisms and insertions/deletions in maize expressed sequence tag data. <i>Plant Physiology</i> , <b>2003</b> , 132, 84-91	6.6	230
18	A high-throughput SNUPE assay for genotyping SNPs in the flanking regions of <i>Zea mays</i> sequence tagged simple sequence repeats. <i>Molecular Breeding</i> , <b>2003</b> , 11, 111-120	3.4	34
17	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> , <b>2003</b> , 106, 1091-101	6	69
16	DEVELOPMENT OF HIGH THROUGHPUT SINGLE NUCLEOTIDE POLYMORPHISM GENOTYPING FOR THE ANALYSIS OF NODULARIA (CYANOBACTERIA) POPULATION GENETICS1. <i>Journal of Phycology</i> , <b>2003</b> , 39, 248-252	3	15
15	Amplification and detection of transposon insertion flanking sequences using fluorescent muAFLP. <i>BioTechniques</i> , <b>2002</b> , 32, 1090-2, 1094, 1096-7	2.5	17
14	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> , <b>2002</b> , 105, 532-543	6	46
13	Polymorphic microsatellite loci in global populations of the marine coccolithophorid <i>Emiliania huxleyi</i> . <i>Molecular Ecology Notes</i> , <b>2002</b> , 2, 495-497		31
12	Genetic diversity within populations of cyanobacteria assessed by analysis of single filaments. <i>Antonie Van Leeuwenhoek</i> , <b>2002</b> , 81, 197-202	2.1	24

11	Identification of Transposon-Tagged Maize Genes Displaying Homology to Arrayed cDNA Clones with the Use of Mutator Insertion Display. <i>Journal of Genome Science and Technology</i> , <b>2002</b> , 1, 48-55		3
10	Transcriptome Profiling of the Shoot and Root Tips of S562L, a Soybean GmCLAVATA1A Mutant. <i>Atlas Journal of Biology</i> ,3, 183-205		2
9	Current progress in studying blackleg disease ( <i>Leptosphaeria maculans</i> and <i>L. biglobosa</i> ) of canola in Iran: Where do we stand now?. <i>Plant Pathology</i> ,	2.8	1
8	Genome-Wide Association Studies in Plants1-7		0
7	Speed breeding: a powerful tool to accelerate crop research and breeding		7
6	Two independent approaches converge to the cloning of a new <i>Leptosphaeria maculans</i> avirulence effector gene, AvrLmS-Lep2		7
5	Genomic rearrangements have consequences for introgression breeding as revealed by genome assemblies of wild and cultivated lentil species		4
4	Wheat Panache - a pangenome graph database representing presence/absence variation across 16 bread wheat genomes		1
3	Brassica napus genes Rlm4 and Rlm7, conferring resistance to <i>Leptosphaeria maculans</i> , are alleles of the Rlm9 wall-associated kinase-like resistance locus		1
2	Genetic structure and phylogenetic relationships of <i>Leptosphaeria maculans</i> and <i>L. biglobosa</i> in Northern regions of Iran. <i>Archives of Phytopathology and Plant Protection</i> ,1-20	1	0
1	Graph pangenomes find missing heritability. <i>Nature Genetics</i> ,	36.3	1