# Jacqueline Batley

## List of Publications by Citations

**Source:** https://exaly.com/author-pdf/4976989/jacqueline-batley-publications-by-citations.pdf
**Version:** 2024-04-25

| 244 | 15,143 | 53 | 119 |
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| papers | citations | h-index | g-index |
| 266 | 20,084 | 7.2 | 6.38 |
| ext. papers | ext. citations | avg, IF | L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 244 | The genome of the mesopolyploid crop species Brassica rapa. *Nature Genetics*, **2011**, 43, 1035-9 | 36.3 | 1490 |
| 243 | Plant genetics. Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. *Science*, **2014**, 345, 950-3 | 33.3 | 1348 |
| 242 | Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, **2018**, 361, | 33.3 | 1296 |
| 241 | A chromosome-based draft sequence of the hexaploid bread wheat (Triticum aestivum) genome. *Science*, **2014**, 345, 1251788 | 33.3 | 1129 |
| 240 | The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. *Nature Communications*, **2014**, 5, 3930 | 17.4 | 676 |
| 239 | Speed breeding is a powerful tool to accelerate crop research and breeding. *Nature Plants*, **2018**, 4, 23-29 | 11.5 | 448 |
| 238 | Ancient hybridizations among the ancestral genomes of bread wheat. *Science*, **2014**, 345, 1250092 | 33.3 | 419 |
| 237 | Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid Brassica oleracea. *Genome Biology*, **2014**, 15, R77 | 18.3 | 306 |
| 236 | The pangenome of an agronomically important crop plant Brassica oleracea. *Nature Communications*, **2016**, 7, 13390 | 17.4 | 240 |
| 235 | Mining for single nucleotide polymorphisms and insertions/deletions in maize expressed sequence tag data. *Plant Physiology*, **2003**, 132, 84-91 | 6.6 | 230 |
| 234 | Plant genome sequencing: applications for crop improvement. *Plant Biotechnology Journal*, **2010**, 8, 2-9 | 11.6 | 218 |
| 233 | Accessing complex crop genomes with next-generation sequencing. *Theoretical and Applied Genetics*, **2013**, 126, 1-11 | 6 | 210 |
| 232 | The pangenome of hexaploid bread wheat. *Plant Journal*, **2017**, 90, 1007-1013 | 6.9 | 206 |
| 231 | Towards CRISPR/Cas crops - bringing together genomics and genome editing. *New Phytologist*, **2017**, 216, 682-698 | 9.8 | 165 |
| 230 | Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. *Frontiers in Plant Science*, **2015**, 6, 563 | 6.2 | 161 |
| 229 | Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. *Plant Biotechnology Journal*, **2017**, 15, 149-161 | 11.6 | 159 |
| 228 | A reference genome for pea provides insight into legume genome evolution. *Nature Genetics*, **2019**, 51, 1411-1422 | 36.3 | 157 |

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| 227 | The reference genetic linkage map for the multinational Brassica rapa genome sequencing project. *Theoretical and Applied Genetics*, **2007**, 115, 777-92 | 6 | 144 |
| 226 | Redundancy based detection of sequence polymorphisms in expressed sequence tag data using autoSNP. *Bioinformatics*, **2003**, 19, 421-2 | 7.2 | 142 |
| 225 | A high-density SNP genotyping array for Brassica napus and its ancestral diploid species based on optimised selection of single-locus markers in the allotetraploid genome. *Theoretical and Applied Genetics*, **2016**, 129, 1887-99 | 6 | 138 |
| 224 | Global agricultural intensification during climate change: a role for genomics. *Plant Biotechnology Journal*, **2016**, 14, 1095-8 | 11.6 | 138 |
| 223 | Genome-wide delineation of natural variation for pod shatter resistance in Brassica napus. *PLoS ONE*, **2014**, 9, e101673 | 3.7 | 133 |
| 222 | Towards plant pangenomics. *Plant Biotechnology Journal*, **2016**, 14, 1099-105 | 11.6 | 130 |
| 221 | Homoeologous exchange is a major cause of gene presence/absence variation in the amphidiploid Brassica napus. *Plant Biotechnology Journal*, **2018**, 16, 1265-1274 | 11.6 | 130 |
| 220 | Plant pan-genomes are the new reference. *Nature Plants*, **2020**, 6, 914-920 | 11.5 | 129 |
| 219 | INTRASPECIFIC GENETIC DIVERSITY IN THE MARINE COCCOLITHOPHORE EMILIANIA HUXLEYI (PRYMNESIOPHYCEAE): THE USE OF MICROSATELLITE ANALYSIS IN MARINE PHYTOPLANKTON POPULATION STUDIES1. *Journal of Phycology*, **2006**, 42, 526-536 | 3 | 112 |
| 218 | Discovering genetic polymorphisms in next-generation sequencing data. *Plant Biotechnology Journal*, **2009**, 7, 312-7 | 11.6 | 107 |
| 217 | Assembly and comparison of two closely related Brassica napus genomes. *Plant Biotechnology Journal*, **2017**, 15, 1602-1610 | 11.6 | 103 |
| 216 | Prioritization of candidate genes in "QTL-hotspot" region for drought tolerance in chickpea (Cicer arietinum L.). *Scientific Reports*, **2015**, 5, 15296 | 4.9 | 96 |
| 215 | Molecular Genetic Markers: Discovery, Applications, Data Storage and Visualisation. *Current Bioinformatics*, **2009**, 4, 16-27 | 4.7 | 95 |
| 214 | Sequencing and assembly of low copy and genic regions of isolated Triticum aestivum chromosome arm 7DS. *Plant Biotechnology Journal*, **2011**, 9, 768-75 | 11.6 | 91 |
| 213 | New technologies for ultra-high throughput genotyping in plants. *Methods in Molecular Biology*, **2009**, 513, 19-39 | 1.4 | 89 |
| 212 | Simple sequence repeat marker loci discovery using SSR primer. *Bioinformatics*, **2004**, 20, 1475-6 | 7.2 | 86 |
| 211 | Plant bioinformatics: from genome to phenome. *Trends in Biotechnology*, **2004**, 22, 232-7 | 15.1 | 85 |
| 210 | BioNano genome mapping of individual chromosomes supports physical mapping and sequence assembly in complex plant genomes. *Plant Biotechnology Journal*, **2016**, 14, 1523-31 | 11.6 | 82 |

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| 209 | Single nucleotide polymorphism discovery from wheat next-generation sequence data. *Plant Biotechnology Journal*, **2012**, 10, 743-9 | 11.6 | 80 |
| 208 | Genetic and physical mapping of flowering time loci in canola (Brassica napus L.). *Theoretical and Applied Genetics*, **2013**, 126, 119-32 | 6 | 80 |
| 207 | Sequencing wheat chromosome arm 7BS delimits the 7BS/4AL translocation and reveals homoeologous gene conservation. *Theoretical and Applied Genetics*, **2012**, 124, 423-32 | 6 | 79 |
| 206 | Molecular mapping of qualitative and quantitative loci for resistance to Leptosphaeria maculans causing blackleg disease in canola (Brassica napus L.). *Theoretical and Applied Genetics*, **2012**, 125, 405-18 | 6 | 75 |
| 205 | AutoSNPdb: an annotated single nucleotide polymorphism database for crop plants. *Nucleic Acids Research*, **2009**, 37, D951-3 | 20.1 | 73 |
| 204 | Investigating Drought Tolerance in Chickpea Using Genome-Wide Association Mapping and Genomic Selection Based on Whole-Genome Resequencing Data. *Frontiers in Plant Science*, **2018**, 9, 190 | 6.2 | 69 |
| 203 | The development of multiplex simple sequence repeat (SSR) markers to complement distinctness, uniformity and stability testing of rape (Brassica napus L.) varieties. *Theoretical and Applied Genetics* , **2003**, 106, 1091-101 | 6 | 69 |
| 202 | Genome sequence data: management, storage, and visualization. *BioTechniques*, **2009**, 46, 333-4, 336 | 2.5 | 65 |
| 201 | Genetic map construction and QTL mapping of resistance to blackleg (Leptosphaeria maculans) disease in Australian canola (Brassica napus L.) cultivars. *Theoretical and Applied Genetics*, **2009**, 120, 71-83 | 6 | 60 |
| 200 | Variation in abundance of predicted resistance genes in the Brassica oleracea pangenome. *Plant Biotechnology Journal*, **2019**, 17, 789-800 | 11.6 | 60 |
| 199 | Pangenomics Comes of Age: From Bacteria to Plant and Animal Applications. *Trends in Genetics*, **2020**, 36, 132-145 | 8.5 | 57 |
| 198 | A user guide to the Brassica 60K Illumina Infinium SNP genotyping array. *Theoretical and Applied Genetics*, **2017**, 130, 621-633 | 6 | 56 |
| 197 | SNP markers-based map construction and genome-wide linkage analysis in Brassica napus. *Plant Biotechnology Journal*, **2014**, 12, 851-60 | 11.6 | 55 |
| 196 | Dispersion and domestication shaped the genome of bread wheat. *Plant Biotechnology Journal*, **2013**, 11, 564-71 | 11.6 | 55 |
| 195 | Current Status and Challenges in Identifying Disease Resistance Genes in. *Frontiers in Plant Science*, **2017**, 8, 1788 | 6.2 | 53 |
| 194 | Discovery of Single Nucleotide Polymorphisms in Complex Genomes Using SGSautoSNP. *Biology*, **2012**, 1, 370-82 | 4.9 | 53 |
| 193 | Sequence and structure of Brassica rapa chromosome A3. *Genome Biology*, **2010**, 11, R94 | 18.3 | 53 |
| 192 | SSRPrimer and SSR Taxonomy Tree: Biome SSR discovery. *Nucleic Acids Research*, **2006**, 34, W656-9 | 20.1 | 53 |

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| 191 | High-resolution skim genotyping by sequencing reveals the distribution of crossovers and gene conversions in Cicer arietinum and Brassica napus. *Theoretical and Applied Genetics*, **2015**, 128, 1039-47 | 6 | 52 |
| 190 | Capturing the biofuel wellhead and powerhouse: the chloroplast and mitochondrial genomes of the leguminous feedstock tree Pongamia pinnata. *PLoS ONE*, **2012**, 7, e51687 | 3.7 | 52 |
| 189 | The loss of vernalization requirement in narrow-leafed lupin is associated with a deletion in the promoter and de-repressed expression of a Flowering Locus T (FT) homologue. *New Phytologist*, **2017**, 213, 220-232 | 9.8 | 51 |
| 188 | Improvements in Genomic Technologies: Application to Crop Genomics. *Trends in Biotechnology*, **2017**, 35, 547-558 | 15.1 | 50 |
| 187 | Investigation of the diversity of effector genes in the banana pathogen, Fusarium oxysporum f. sp. cubense, reveals evidence of horizontal gene transfer. *Molecular Plant Pathology*, **2018**, 19, 1155-1171 | 5.7 | 50 |
| 186 | Genomic distribution of simple sequence repeats in Brassica rapa. *Molecules and Cells*, **2007**, 23, 349-56 | 3.5 | 50 |
| 185 | A consensus map of rapeseed (Brassica napus L.) based on diversity array technology markers: applications in genetic dissection of qualitative and quantitative traits. *BMC Genomics*, **2013**, 14, 277 | 4.5 | 49 |
| 184 | A chromosomal genomics approach to assess and validate the desi and kabuli draft chickpea genome assemblies. *Plant Biotechnology Journal*, **2014**, 12, 778-86 | 11.6 | 48 |
| 183 | Identification of Putative Candidate Genes for Water Stress Tolerance in Canola (Brassica napus). *Frontiers in Plant Science*, **2015**, 6, 1058 | 6.2 | 48 |
| 182 | Single nucleotide polymorphism discovery in barley using autoSNPdb. *Plant Biotechnology Journal*, **2009**, 7, 326-33 | 11.6 | 48 |
| 181 | SNPServer: a real-time SNP discovery tool. *Nucleic Acids Research*, **2005**, 33, W493-5 | 20.1 | 46 |
| 180 | Characterization of the flanking regions of Zea mays microsatellites reveals a large number of useful sequence polymorphisms. *Theoretical and Applied Genetics*, **2002**, 105, 532-543 | 6 | 46 |
| 179 | Future tools for association mapping in crop plants. *Genome*, **2010**, 53, 1017-23 | 2.4 | 42 |
| 178 | Creating new interspecific hybrid and polyploid crops. *Trends in Biotechnology*, **2015**, 33, 436-41 | 15.1 | 41 |
| 177 | The Genome of a Southern Hemisphere Seagrass Species (Zostera muelleri). *Plant Physiology*, **2016**, 172, 272-83 | 6.6 | 41 |
| 176 | Characterization of disease resistance genes in the Brassica napus pangenome reveals significant structural variation. *Plant Biotechnology Journal*, **2020**, 18, 969-982 | 11.6 | 41 |
| 175 | Genome-wide Association Study Identifies New Loci for Resistance to in Canola. *Frontiers in Plant Science*, **2016**, 7, 1513 | 6.2 | 41 |
| 174 | The application of genomics and bioinformatics to accelerate crop improvement in a changing climate. *Current Opinion in Plant Biology*, **2016**, 30, 78-81 | 9.9 | 40 |

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| 173 | SNP Applications in Plants **2007**, 95-102 | | 39 |
| 172 | Genome-Wide Association Study of Genetic Control of Seed Fatty Acid Biosynthesis in. *Frontiers in Plant Science*, **2016**, 7, 2062 | 6.2 | 38 |
| 171 | Rapid divergence of repetitive DNAs in Brassica relatives. *Genomics*, **2011**, 97, 173-85 | 4.3 | 38 |
| 170 | Genome-wide identification and comparative analysis of NBS-LRR resistance genes in Brassica napus. *Crop and Pasture Science*, **2018**, 69, 72 | 2.2 | 37 |
| 169 | Comparison of transcription of multiple genes at three developmental stages of the plant pathogen Sclerotinia sclerotiorum. *FEMS Microbiology Letters*, **2006**, 258, 150-60 | 2.9 | 37 |
| 168 | Trait associations in the pangenome of pigeon pea (Cajanus cajan). *Plant Biotechnology Journal*, **2020**, 18, 1946-1954 | 11.6 | 36 |
| 167 | A high-throughput SNP array in the amphidiploid species Brassica napus shows diversity in resistance genes. *Functional and Integrative Genomics*, **2014**, 14, 643-55 | 3.8 | 36 |
| 166 | Degradation of the benzoxazolinone class of phytoalexins is important for virulence of Fusarium pseudograminearum towards wheat. *Molecular Plant Pathology*, **2015**, 16, 946-62 | 5.7 | 36 |
| 165 | High-throughput genotyping for species identification and diversity assessment in germplasm collections. *Molecular Ecology Resources*, **2015**, 15, 1091-101 | 8.4 | 36 |
| 164 | A complex recombination pattern in the genome of allotetraploid Brassica napus as revealed by a high-density genetic map. *PLoS ONE*, **2014**, 9, e109910 | 3.7 | 36 |
| 163 | DNA Methylation: Toward Crop Disease Resistance Improvement. *Trends in Plant Science*, **2019**, 24, 1137-1150 | 13.1 | 34 |
| 162 | A high-throughput SNuPE assay for genotyping SNPs in the flanking regions of Zea mays sequence tagged simple sequence repeats. *Molecular Breeding*, **2003**, 11, 111-120 | 3.4 | 34 |
| 161 | Copy number variation and disease resistance in plants. *Theoretical and Applied Genetics*, **2017**, 130, 2479-2490 | 6 | 33 |
| 160 | Identification and characterization of more than 4 million intervarietal SNPs across the group 7 chromosomes of bread wheat. *Plant Biotechnology Journal*, **2015**, 13, 97-104 | 11.6 | 32 |
| 159 | Construction and comparison of three reference-quality genome assemblies for soybean. *Plant Journal*, **2019**, 100, 1066-1082 | 6.9 | 32 |
| 158 | Identification and characterization of candidate Rlm4 blackleg resistance genes in Brassica napus using next-generation sequencing. *Plant Biotechnology Journal*, **2012**, 10, 709-15 | 11.6 | 32 |
| 157 | Wild Origins of Macadamia Domestication Identified Through Intraspecific Chloroplast Genome Sequencing. *Frontiers in Plant Science*, **2019**, 10, 334 | 6.2 | 31 |
| 156 | Genome-wide survey of the seagrass Zostera muelleri suggests modification of the ethylene signalling network. *Journal of Experimental Botany*, **2015**, 66, 1489-98 | 7 | 31 |

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| 155 | Polymorphic microsatellite loci in global populations of the marine coccolithophorid Emiliania huxleyi. *Molecular Ecology Notes*, **2002**, 2, 495-497 | | 31 |
| 154 | SNP discovery and applications in Brassica napus. *Journal of Plant Biotechnology*, **2012**, 39, 49-61 | 0.6 | 31 |
| 153 | Gene loss in the fungal canola pathogen Leptosphaeria maculans. *Functional and Integrative Genomics*, **2015**, 15, 189-96 | 3.8 | 30 |
| 152 | Bias in resistance gene prediction due to repeat masking. *Nature Plants*, **2018**, 4, 762-765 | 11.5 | 30 |
| 151 | Genome Analysis Identified Novel Candidate Genes for Ascochyta Blight Resistance in Chickpea Using Whole Genome Re-sequencing Data. *Frontiers in Plant Science*, **2017**, 8, 359 | 6.2 | 29 |
| 150 | Targeted identification of genomic regions using TAGdb. *Plant Methods*, **2010**, 6, 19 | 5.8 | 29 |
| 149 | Genetic maps and the use of synteny. *Methods in Molecular Biology*, **2009**, 513, 41-55 | 1.4 | 29 |
| 148 | Identification and characterization of simple sequence repeat (SSR) markers from Fragaria□nanassa expressed sequences. *Molecular Ecology Notes*, **2006**, 6, 319-322 | | 29 |
| 147 | Molecular marker applications in plants. *Methods in Molecular Biology*, **2015**, 1245, 13-27 | 1.4 | 29 |
| 146 | Type B Heterotrimeric G Protein □Subunit Regulates Auxin and ABA Signaling in Tomato. *Plant Physiology*, **2016**, 170, 1117-34 | 6.6 | 27 |
| 145 | The fate of chromosomes and alleles in an allohexaploid Brassica population. *Genetics*, **2014**, 197, 273-83 | 4 | 27 |
| 144 | Sixteen new simple sequence repeat markers from Brassica juncea expressed sequences and their cross-species amplification. *Molecular Ecology Notes*, **2007**, 7, 697-700 | | 27 |
| 143 | What Are SNPs? **2007**, 41-52 | | 27 |
| 142 | Single Nucleotide Polymorphism Discovery **2007**, 53-76 | | 27 |
| 141 | Single Nucleotide Polymorphism Genotyping in Plants **2007**, 77-94 | | 27 |
| 140 | Identification and characterization of simple sequence repeat (SSR) markers derived in silico from Brassica oleracea genome shotgun sequences. *Molecular Ecology Notes*, **2006**, 6, 1191-1194 | | 27 |
| 139 | Identification and characterization of simple sequence repeat markers from Brassica napus expressed sequences. *Molecular Ecology Notes*, **2007**, 7, 886-889 | | 26 |
| 138 | High-resolution molecular karyotyping uncovers pairing between ancestrally related Brassica chromosomes. *New Phytologist*, **2014**, 202, 964-974 | 9.8 | 25 |

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| 137 | Genomic advances will herald new insights into the Brassica: Leptosphaeria maculans pathosystem. *Plant Biology*, **2012**, 14 Suppl 1, 1-10 | 3.7 | 25 |
| 136 | Genetic diversity within populations of cyanobacteria assessed by analysis of single filaments. *Antonie Van Leeuwenhoek*, **2002**, 81, 197-202 | 2.1 | 24 |
| 135 | Epigenetics: Potentials and Challenges in Crop Breeding. *Molecular Plant*, **2019**, 12, 1309-1311 | 14.4 | 23 |
| 134 | Centromere Locations in Brassica A and C Genomes Revealed Through Half-Tetrad Analysis. *Genetics*, **2016**, 202, 513-23 | 4 | 23 |
| 133 | Molecular Marker-Based Genetic Analysis of Pasture and Turf Grasses **2004**, 197-238 | | 23 |
| 132 | Genetic and Molecular Regulation of Seed Storage Proteins (SSPs) to Improve Protein Nutritional Value of Oilseed Rape () Seeds. *Frontiers in Plant Science*, **2018**, 9, 890 | 6.2 | 23 |
| 131 | RNA-Seq and metabolic flux analysis of Tetraselmis sp. M8 during nitrogen starvation reveals a two-stage lipid accumulation mechanism. *Bioresource Technology*, **2017**, 244, 1281-1293 | 11 | 22 |
| 130 | Genome sequencing approaches and successes. *Methods in Molecular Biology*, **2009**, 513, 345-58 | 1.4 | 22 |
| 129 | Genome wide analysis of flowering time trait in multiple environments via high-throughput genotyping technique in Brassica napus L. *PLoS ONE*, **2015**, 10, e0119425 | 3.7 | 22 |
| 128 | Brassica ASTRA: an integrated database for Brassica genomic research. *Nucleic Acids Research*, **2005** , 33, D656-9 | 20.1 | 21 |
| 127 | Inherited allelic variants and novel karyotype changes influence fertility and genome stability in Brassica allohexaploids. *New Phytologist*, **2019**, 223, 965-978 | 9.8 | 20 |
| 126 | Characterization of simple sequence repeat markers derived in silico from Brassica rapa bacterial artificial chromosome sequences and their application in Brassica napus. *Molecular Ecology Notes*, **2007**, 7, 273-277 | | 20 |
| 125 | A comparative map viewer integrating genetic maps for Brassica and Arabidopsis. *BMC Plant Biology*, **2007**, 7, 40 | 5.3 | 20 |
| 124 | New computational tools for brassica genome research. *Comparative and Functional Genomics*, **2004**, 5, 276-80 | | 20 |
| 123 | Molecular breeding for resistance to black rot [Xanthomonas campestris pv. campestris (Pammel) Dowson] in Brassicas: recent advances. *Euphytica*, **2018**, 214, 1 | 2.1 | 20 |
| 122 | A □lactamase from cereal infecting Fusarium spp. catalyses the first step in the degradation of the benzoxazolinone class of phytoalexins. *Fungal Genetics and Biology*, **2015**, 83, 1-9 | 3.9 | 19 |
| 121 | Mining for SNPs and SSRs using SNPServer, dbSNP and SSR taxonomy tree. *Methods in Molecular Biology*, **2009**, 537, 303-21 | 1.4 | 19 |
| 120 | Microspore culture reveals complex meiotic behaviour in a trigenomic Brassica hybrid. *BMC Plant Biology*, **2015**, 15, 173 | 5.3 | 18 |

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| 119 | High-throughput FACS-based mutant screen identifies a gain-of-function allele of the Fusarium graminearum adenylyl cyclase causing deoxynivalenol over-production. *Fungal Genetics and Biology*, **2016**, 90, 1-11 | 3.9 | 18 |
| 118 | An advanced reference genome of Trifolium subterraneum L. reveals genes related to agronomic performance. *Plant Biotechnology Journal*, **2017**, 15, 1034-1046 | 11.6 | 17 |
| 117 | Transcriptomic comparison between developing seeds of yellow- and black-seeded Brassica napus reveals that genes influence seed quality. *BMC Plant Biology*, **2019**, 19, 203 | 5.3 | 17 |
| 116 | Exploring the application of wild species for crop improvement in a changing climate. *Current Opinion in Plant Biology*, **2020**, 56, 218-222 | 9.9 | 17 |
| 115 | Predicting polymorphic EST-SSRs in silico. *Molecular Ecology Resources*, **2013**, 13, 538-45 | 8.4 | 17 |
| 114 | CMap3D: a 3D visualization tool for comparative genetic maps. *Bioinformatics*, **2010**, 26, 273-4 | 7.2 | 17 |
| 113 | BASC: an integrated bioinformatics system for Brassica research. *Nucleic Acids Research*, **2007**, 35, D870-3 | 20.1 | 17 |
| 112 | Amplification and detection of transposon insertion flanking sequences using fluorescent muAFLP. *BioTechniques*, **2002**, 32, 1090-2, 1094, 1096-7 | 2.5 | 17 |
| 111 | CropSNPdb: a database of SNP array data for Brassica crops and hexaploid bread wheat. *Plant Journal*, **2019**, 98, 142-152 | 6.9 | 16 |
| 110 | Segregation for fertility and meiotic stability in novel Brassica allohexaploids. *Theoretical and Applied Genetics*, **2017**, 130, 767-776 | 6 | 15 |
| 109 | DEVELOPMENT OF HIGH THROUGHPUT SINGLE NUCLEOTIDE POLYMORPHISM GENOTYPING FOR THE ANALYSIS OF NODULARIA (CYANOBACTERIA) POPULATION GENETICS1. *Journal of Phycology*, **2003**, 39, 248-252 | 3 | 15 |
| 108 | Resistance Gene Analogs in the Brassicaceae: Identification, Characterization, Distribution, and Evolution. *Plant Physiology*, **2020**, 184, 909-922 | 6.6 | 15 |
| 107 | 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 Brassica napus. *BMC Genomics*, **2015**, 16, 409 | 4.5 | 14 |
| 106 | Identifying genetic diversity of avirulence genes in Leptosphaeria maculans using whole genome sequencing. *Functional and Integrative Genomics*, **2013**, 13, 295-308 | 3.8 | 14 |
| 105 | Can genomics assist the phenological adaptation of canola to new and changing environments?. *Crop and Pasture Science*, **2016**, 67, 284 | 2.2 | 14 |
| 104 | Second-generation sequencing for gene discovery in the Brassicaceae. *Plant Biotechnology Journal*, **2012**, 10, 750-9 | 11.6 | 13 |
| 103 | Integration of metabolome and transcriptome reveals flavonoid accumulation in the intergeneric hybrid between Brassica rapa and Raphanus sativus. *Scientific Reports*, **2019**, 9, 18368 | 4.9 | 13 |
| 102 | Understanding Host-Pathogen Interactions in in the Omics Era. *Plants*, **2020**, 9, | 4.5 | 12 |

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| 101 | Whole Genome Diversity, Population Structure, and Linkage Disequilibrium Analysis of Chickpea ( L.) Genotypes Using Genome-Wide DArTseq-Based SNP Markers. *Genes*, **2019**, 10, | 4.2 | 11 |
| 100 | Assessing Variations in Host Resistance to f sp. Race 4 in Species, With a Focus on the Subtropical Race 4. *Frontiers in Microbiology*, **2019**, 10, 1062 | 5.7 | 11 |
| 99 | Next generation characterisation of cereal genomes for marker discovery. *Biology*, **2013**, 2, 1357-77 | 4.9 | 11 |
| 98 | Identification and QTL mapping of resistance to Turnip yellows virus (TuYV) in oilseed rape, Brassica napus. *Theoretical and Applied Genetics*, **2020**, 133, 383-393 | 6 | 11 |
| 97 | Induced Methylation in Plants as a Crop Improvement Tool: Progress and Perspectives. *Agronomy*, **2020**, 10, 1484 | 3.6 | 11 |
| 96 | Sequencing the USDA core soybean collection reveals gene loss during domestication and breeding. *Plant Genome*, **2021**, e20109 | 4.4 | 11 |
| 95 | Targeted Knockout of Homologues for Yellow-Seeded with Reduced Flavonoids and Improved Fatty Acid Composition. *Journal of Agricultural and Food Chemistry*, **2020**, 68, 5676-5690 | 5.7 | 10 |
| 94 | An efficient approach to BAC based assembly of complex genomes. *Plant Methods*, **2016**, 12, 2 | 5.8 | 10 |
| 93 | Neodiversification of homeologous CLAVATA1-like receptor kinase genes in soybean leads to distinct developmental outcomes. *Scientific Reports*, **2017**, 7, 8878 | 4.9 | 10 |
| 92 | Scanning the effects of ethyl methanesulfonate on the whole genome of Lotus japonicus using second-generation sequencing analysis. *G3: Genes, Genomes, Genetics*, **2015**, 5, 559-67 | 3.2 | 10 |
| 91 | Genome-wide identification and comparative analysis of resistance genes in Brassica juncea. *Molecular Breeding*, **2020**, 40, 1 | 3.4 | 10 |
| 90 | Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. *Theoretical and Applied Genetics*, **2021**, 134, 1677-1690 | 6 | 10 |
| 89 | The pangenome of banana highlights differences between genera and genomes. *Plant Genome*, **2021**, e20100 | 4.4 | 10 |
| 88 | Molecular-cytogenetic characterization of C-genome chromosome substitution lines in Brassica juncea (L.) Czern and Coss. *Theoretical and Applied Genetics*, **2016**, 129, 1153-66 | 6 | 10 |
| 87 | Molecular characterization of disease resistance in Brassica juncea The current status and the way forward. *Plant Pathology*, **2021**, 70, 13-34 | 2.8 | 10 |
| 86 | Germin-like protein 2 gene promoter from rice is responsive to fungal pathogens in transgenic potato plants. *Functional and Integrative Genomics*, **2016**, 16, 19-27 | 3.8 | 9 |
| 85 | Genoproteomics-assisted improvement of Andrographis paniculata: toward a promising molecular and conventional breeding platform for autogamous plants affecting the pharmaceutical industry. *Critical Reviews in Biotechnology*, **2017**, 37, 803-816 | 9.4 | 9 |
| 84 | Mapping QTLs of resistance to head splitting in cabbage (Brassica oleracea L.var. capitata L.). *Molecular Breeding*, **2015**, 35, 1 | 3.4 | 9 |

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| 83 | Genomic comparison of two independent seagrass lineages reveals habitat-driven convergent evolution. *Journal of Experimental Botany*, **2018**, 69, 3689-3702 | 7 | 9 |
| 82 | Cytogenetic and Molecular Characterization of B-Genome Introgression Lines of Brassica napus L. *G3: Genes, Genomes, Genetics*, **2017**, 7, 77-86 | 3.2 | 9 |
| 81 | Next-generation genome sequencing can be used to rapidly characterise sequences flanking T-DNA insertions in random insertional mutants of. *Fungal Biology and Biotechnology*, **2014**, 1, 10 | 7.5 | 9 |
| 80 | Automated discovery of single nucleotide polymorphism and simple sequence repeat molecular genetic markers. *Methods in Molecular Biology*, **2007**, 406, 473-94 | 1.4 | 9 |
| 79 | Genome-Wide Identification and Evolution of Receptor-Like Kinases (RLKs) and Receptor like Proteins (RLPs) in. *Biology*, **2020**, 10, | 4.9 | 9 |
| 78 | First report of genome size and ploidy of the underutilized leguminous tuber crop Yam Bean (Pachyrhizus erosus and P. tuberosus) by flow cytometry. *Plant Genetic Resources: Characterisation and Utilisation*, **2019**, 17, 456-459 | 1 | 8 |
| 77 | Revolution in Genotyping Platforms for Crop Improvement. *Advances in Biochemical Engineering/Biotechnology*, **2018**, 164, 37-52 | 1.7 | 8 |
| 76 | Computational Identification and Comparative Analysis of miRNAs in Wheat Group 7 Chromosomes. *Plant Molecular Biology Reporter*, **2014**, 32, 487-500 | 1.7 | 8 |
| 75 | Advances in plant genotyping: where the future will take us. *Methods in Molecular Biology*, **2015**, 1245, 1-11 | 1.4 | 8 |
| 74 | Genomics Armed With Diversity Leads the Way in Improvement in a Changing Global Environment. *Frontiers in Genetics*, **2021**, 12, 600789 | 4.5 | 8 |
| 73 | Genome-Wide Analysis of the Lateral Organ Boundaries Domain Gene Family in Brassica Napus. *Genes*, **2020**, 11, | 4.2 | 7 |
| 72 | Speed breeding: a powerful tool to accelerate crop research and breeding | | 7 |
| 71 | Two independent approaches converge to the cloning of a new Leptosphaeria maculans avirulence effector gene, AvrLmS-Lep2 | | 7 |
| 70 | Genotype-Environment mismatch of kelp forests under climate change. *Molecular Ecology*, **2021**, 30, 3730-3746 | 5.7 | 7 |
| 69 | Current status of structural variation studies in plants. *Plant Biotechnology Journal*, **2021**, 19, 2153-2163 | 11.6 | 7 |
| 68 | Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. *Plant Biotechnology Journal*, **2021**, 19, 2488-2500 | 11.6 | 7 |
| 67 | The Fdb3 transcription factor of the Fusarium Detoxification of Benzoxazolinone gene cluster is required for MBOA but not BOA degradation in Fusarium pseudograminearum. *Fungal Genetics and Biology*, **2016**, 88, 44-53 | 3.9 | 6 |
| 66 | Molecular Marker Discovery and Genetic Map Visualisation **2009**, 165-189 | | 6 |

| | | | |
|---|---|---|---|
| 65 | A comparative study of interspecies mating of Phratora vulgatissima and P. vitellinae using behavioural tests and molecular markers. *Entomologia Experimentalis Et Applicata*, **2004**, 110, 231-241 | 2.1 | 6 |
| 64 | Frontiers in Dissecting and Managing Diseases: From Reference-Based RGA Candidate Identification to Building Pan-RGAomes. *International Journal of Molecular Sciences*, **2020**, 21, | 6.3 | 6 |
| 63 | Integrated physical map of bread wheat chromosome arm 7DS to facilitate gene cloning and comparative studies. *New Biotechnology*, **2019**, 48, 12-19 | 6.4 | 6 |
| 62 | Agricultural selection and presence▯bsence variation in spring-type canola germplasm. *Crop and Pasture Science*, **2018**, 69, 55 | 2.2 | 6 |
| 61 | "Doubled-haploid" allohexaploid Brassica lines lose fertility and viability and accumulate genetic variation due to genomic instability. *Chromosoma*, **2019**, 128, 521-532 | 2.8 | 5 |
| 60 | Population structure of the beetle pests Phyllodecta vulgatissima and P. vitellinae on UK willow plantations. *Insect Molecular Biology*, **2004**, 13, 413-21 | 3.4 | 5 |
| 59 | Fertile allohexaploid Brassica hybrids obtained from crosses between B. oleracea and B. juncea via ovule rescue and colchicine treatment of cuttings. *Plant Cell, Tissue and Organ Culture*, **2020**, 140, 301-313 | 2.7 | 5 |
| 58 | Regulation of a novel Fusarium cytokinin in Fusarium pseudograminearum. *Fungal Biology*, **2019**, 123, 255-266 | 2.8 | 5 |
| 57 | Modeling first order additive ▯additive epistasis improves accuracy of genomic prediction for sclerotinia stem rot resistance in canola. *Plant Genome*, **2021**, 14, e20088 | 4.4 | 5 |
| 56 | Chromosomal genomics facilitates fine mapping of a Russian wheat aphid resistance gene. *Theoretical and Applied Genetics*, **2015**, 128, 1373-83 | 6 | 4 |
| 55 | Microsatellite cross-amplification in coccolithophores: application in population diversity studies. *Hereditas*, **2006**, 143, 99-102 | 2.4 | 4 |
| 54 | The importance of plant pan-genomes in breeding. **2020**, 27-32 | | 4 |
| 53 | Effect of Leptosphaeria maculans Infection on Promoter DNA Methylation of Defence Genes in Brassica napus. *Agronomy*, **2020**, 10, 1072 | 3.6 | 4 |
| 52 | Candidate Rlm6 resistance genes against Leptosphaeria. maculans identified through a genome-wide association study in Brassica juncea (L.) Czern. *Theoretical and Applied Genetics*, **2021**, 134, 2035-2050 | 6 | 4 |
| 51 | The application of pangenomics and machine learning in genomic selection in plants. *Plant Genome*, **2021**, 14, e20112 | 4.4 | 4 |
| 50 | Genomic rearrangements have consequences for introgression breeding as revealed by genome assemblies of wild and cultivated lentil species | | 4 |
| 49 | QTL Genetic Mapping Study for Traits Affecting Meal Quality in Winter Oilseed Rape ( L.). *Genes*, **2021**, 12, | 4.2 | 4 |
| 48 | Population Diversity of Leptosphaeria maculans in Australia. *International Journal of Biology*, **2015**, 7, | 1.1 | 3 |

| | | | |
|---|---|---|---|
| 47 | Identification of Transposon-Tagged Maize Genes Displaying Homology to Arrayed cDNA Clones with the Use of Mutator Insertion Display. *Journal of Genome Science and Technology*, **2002**, 1, 48-55 | | 3 |
| 46 | The Use of Genetic and Gene Technologies in Shaping Modern Rapeseed Cultivars ( L.). *Genes*, **2020**, 11, | 4.2 | 3 |
| 45 | Linkage mapping and QTL analysis of flowering time using ddRAD sequencing with genotype error correction in Brassica napus. *BMC Plant Biology*, **2020**, 20, 546 | 5.3 | 3 |
| 44 | Stable, fertile lines produced by hybridization between allotetraploids Brassica juncea (AABB) and Brassica carinata (BBCC) have merged the A and C genomes. *New Phytologist*, **2021**, 230, 1242-1257 | 9.8 | 3 |
| 43 | The Gene, a New Player of - Interaction Maps on Chromosome C03 in Canola. *Frontiers in Plant Science*, **2021**, 12, 654604 | 6.2 | 3 |
| 42 | Amborella gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. *New Phytologist*, **2021**, | 9.8 | 3 |
| 41 | Using Genomics to Adapt Crops to Climate Change **2019**, 91-109 | | 2 |
| 40 | New technologies for ultrahigh-throughput genotyping in plant taxonomy. *Methods in Molecular Biology*, **2014**, 1115, 151-75 | 1.4 | 2 |
| 39 | Genetic Diversity in the Perennial Ryegrass Fungal Endophyte Neotyphodium lolii. *Developments in Plant Breeding*, **2004**, 155-164 | | 2 |
| 38 | Quantitative Trait Locus Mapping of Resistance to Turnip Yellows Virus in and and Introgression of These Resistances by Resynthesis Into Allotetraploid Plants for Deployment in .. *Frontiers in Plant Science*, **2021**, 12, 781385 | 6.2 | 2 |
| 37 | Transcriptome Profiling of the Shoot and Root Tips of S562L, a Soybean GmCLAVATA1A Mutant. *Atlas Journal of Biology*,3, 183-205 | | 2 |
| 36 | Recent Findings Unravel Genes and Genetic Factors Underlying Resistance in and Its Relatives. *International Journal of Molecular Sciences*, **2020**, 22, | 6.3 | 2 |
| 35 | Plant Genomics and Climate Change **2016**, | | 2 |
| 34 | Comparison and evolutionary analysis of Brassica nucleotide binding site leucine rich repeat (NLR) genes and importance for disease resistance breeding. *Plant Genome*, **2021**, 14, e20060 | 4.4 | 2 |
| 33 | Draft Genome Assembly and Transcriptome Dataset for European Turnip ( L. ssp. ), ECD4 Carrying Clubroot Resistance. *Frontiers in Genetics*, **2021**, 12, 651298 | 4.5 | 2 |
| 32 | Genotyping for Species Identification and Diversity Assessment Using Double-Digest Restriction Site-Associated DNA Sequencing (ddRAD-Seq). *Methods in Molecular Biology*, **2020**, 2107, 159-187 | 1.4 | 2 |
| 31 | Brassica napus genes Rlm4 and Rlm7, conferring resistance to Leptosphaeria maculans, are alleles of the Rlm9 wall-associated kinase-like resistance locus.. *Plant Biotechnology Journal*, **2022**, | 11.6 | 2 |
| 30 | Pangenomics in crop improvement-from coding structural variations to finding regulatory variants with pangenome graphs.. *Plant Genome*, **2021**, e20177 | 4.4 | 2 |

| | | | |
|---|---|---|---|
| 29 | Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus cqProt-003.. *Theoretical and Applied Genetics*, **2022**, 135, 1443 | 6 | 1 |
| 28 | Current progress in studying blackleg disease ( Leptosphaeria maculans and L. biglobosa ) of canola in Iran: Where do we stand now?. *Plant Pathology*, | 2.8 | 1 |
| 27 | Studying the Genetic Diversity of Yam Bean Using a New Draft Genome Assembly. *Agronomy*, **2021**, 11, 953 | 3.6 | 1 |
| 26 | Status and advances in mining for blackleg (Leptosphaeria maculans) quantitative resistance (QR) in oilseed rape (Brassica napus). *Theoretical and Applied Genetics*, **2021**, 134, 3123-3145 | 6 | 1 |
| 25 | De Novo SNP Discovery and Genotyping of Iranian Pimpinella Species Using ddRAD Sequencing. *Agronomy*, **2021**, 11, 1342 | 3.6 | 1 |
| 24 | SNP analysis ofMacadamia integrifoliachloroplast genomes to determine the genetic structure of wild populations. *Acta Horticulturae*, **2016**, 175-180 | 0.3 | 1 |
| 23 | A differential k-mer analysis pipeline for comparing RNA-Seq transcriptome and meta-transcriptome datasets without a reference. *Functional and Integrative Genomics*, **2019**, 19, 363-371 | 3.8 | 1 |
| 22 | Immunoassays and diagnostic antibodies for Perkinsus spp. pathogens of marine molluscs. *Diseases of Aquatic Organisms*, **2021**, 147, 13-23 | 1.7 | 1 |
| 21 | Genome-Wide Mining of Disease Resistance Gene Analogs Using Conserved Domains. *Methods in Molecular Biology*, **2020**, 2107, 365-375 | 1.4 | 1 |
| 20 | Wheat Panache - a pangenome graph database representing presence/absence variation across 16 bread wheat genomes | | 1 |
| 19 | Expanding Gene-Editing Potential in Crop Improvement with Pangenomes.. *International Journal of Molecular Sciences*, **2022**, 23, | 6.3 | 1 |
| 18 | Brassica napus genes Rlm4 and Rlm7, conferring resistance to Leptosphaeria maculans, are alleles of the Rlm9 wall-associated kinase-like resistance locus | | 1 |
| 17 | Molecular Markers for Identifying Resistance Genes in Brassica napus. *Agronomy*, **2022**, 12, 985 | 3.6 | 1 |
| 16 | Allele segregation analysis of F hybrids between independent Brassica allohexaploid lineages.. *Chromosoma*, **2022**, 1 | 2.8 | 1 |
| 15 | Graph pangenomes find missing heritability. *Nature Genetics*, | 36.3 | 1 |
| 14 | Virulence/avirulence patterns among Leptosphaeria maculans isolates determines expression of resistance, senescence and yellowing in cotyledons of Brassica napus. *European Journal of Plant Pathology*, **2020**, 156, 1077-1089 | 2.1 | 0 |
| 13 | Genome-Wide Association Studies in Plants1-7 | | 0 |
| 12 | Formulation and efficacy testing of bio-organic fertilizer produced through solid-state fermentation of agro-waste by Burkholderia cenocepacia. *Chemosphere*, **2021**, 132762 | 8.4 | 0 |

| | | | |
|---|---|---|---|
| 11 | Detection of Epistasis for Seed and Some Phytochemical Traits in Coriander under Different Irrigation Regimes. *Agronomy*, **2021**, 11, 1891 | 3.6 | 0 |
| 10 | Machine learning models outperform deep learning models, provide interpretation and facilitate feature selection for soybean trait prediction.. *BMC Plant Biology*, **2022**, 22, 180 | 5.3 | 0 |
| 9 | Systematic trait dissection in oilseed rape provides a comprehensive view, further insight, and exact roadmap for yield determination. **2022**, 15, 38 | | 0 |
| 8 | Advancing designer crops for climate resilience through an integrated genomics approach.. *Current Opinion in Plant Biology*, **2022**, 67, 102220 | 9.9 | 0 |
| 7 | Mining of Cloned Disease Resistance Gene Homologs (CDRHs) in Brassica Species and Arabidopsis thaliana. *Biology*, **2022**, 11, 821 | 4.9 | 0 |
| 6 | Genetic structure and phylogenetic relationships of Leptosphaeria maculans and L. biglobosa in Northern regions of Iran. *Archives of Phytopathology and Plant Protection*,1-20 | 1 | 0 |
| 5 | Next Generation Sequencing and Germplasm Resources **2014**, 369-390 | | |
| 4 | Case Study for Trait-Related Gene Evolution: Disease Resistance Genes in Brassica napus. *Compendium of Plant Genomes*, **2018**, 223-232 | 0.8 | |
| 3 | Genome Analysis of the Broad Host Range Necrotroph Highlights Genes Associated With Virulence.. *Frontiers in Plant Science*, **2022**, 13, 811152 | 6.2 | |
| 2 | Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. *Agronomy*, **2021**, 11, 2587 | 3.6 | |
| 1 | Development of monoclonal antibodies against Perkinsus olseni using whole cells. *Aquaculture Reports*, **2022**, 24, 101179 | 2.3 | |