

# Isobel A P Parkin

## List of Publications by Year in descending order

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82  
papers

10,496  
citations

81900

39  
h-index

66911

78  
g-index

84  
all docs

84  
docs citations

84  
times ranked

7545  
citing authors

#	ARTICLE	IF	CITATIONS
1	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
2	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	21.4	1,893
3	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	12.8	918
4	Segmental Structure of the <i>Brassica napus</i> Genome Based on Comparative Analysis With <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2005, 171, 765-781.	2.9	516
5	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid <i>Brassica oleracea</i> . <i>Genome Biology</i> , 2014, 15, R77.	9.6	456
6	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	12.8	375
7	The emerging biofuel crop <i>Camelina sativa</i> retains a highly undifferentiated hexaploid genome structure. <i>Nature Communications</i> , 2014, 5, 3706.	12.8	295
8	Molecular characterization of <i>Brassica napus</i> NAC domain transcriptional activators induced in response to biotic and abiotic stress. <i>Plant Molecular Biology</i> , 2003, 53, 383-397.	3.9	271
9	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.	8.3	217
10	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.	3.6	205
11	Genome-Wide Delineation of Natural Variation for Pod Shatter Resistance in <i>Brassica napus</i> . <i>PLoS ONE</i> , 2014, 9, e101673.	2.5	182
12	PCP-A1, a Defensin-like <i>Brassica</i> Pollen Coat Protein That Binds the S Locus Glycoprotein, Is the Product of Gametophytic Gene Expression. <i>Plant Cell</i> , 1998, 10, 1333-1347.	6.6	166
13	Polyloid Evolution of the Brassicaceae during the Cenozoic Era. <i>Plant Cell</i> , 2014, 26, 2777-2791.	6.6	165
14	Comparison of a <i>Brassica oleracea</i> Genetic Map With the Genome of <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2003, 164, 359-372.	2.9	139
15	Detection and Effects of a Homeologous Reciprocal Transposition in <i>Brassica napus</i> . <i>Genetics</i> , 2003, 165, 1569-1577.	2.9	131
16	The compact genome of the plant pathogen <i>Plasmodiophora brassicae</i> is adapted to intracellular interactions with host <i>Brassica</i> spp. <i>BMC Genomics</i> , 2016, 17, 272.	2.8	107
17	Connecting genome structural variation with complex traits in crop plants. <i>Theoretical and Applied Genetics</i> , 2019, 132, 733-750.	3.6	97
18	Extensive homoeologous genome exchanges in allopolyploid crops revealed by scRNA-seq based visualization. <i>Plant Biotechnology Journal</i> , 2017, 15, 594-604.	8.3	96

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19	A high-contiguity <i>Brassica nigra</i> genome localizes active centromeres and defines the ancestral <i>Brassica</i> genome. <i>Nature Plants</i> , 2020, 6, 929-941.	9.3	94
20	Mapping of homoeologous chromosome exchanges influencing quantitative trait variation in <i>Brassica napus</i> . <i>Plant Biotechnology Journal</i> , 2017, 15, 1478-1489.	8.3	93
21	A user guide to the <i>Brassica</i> 60K Illumina Infinium <sup>®</sup> SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2017, 130, 621-633.	3.6	90
22	Monolignol biosynthesis is associated with resistance to <i>Sclerotinia sclerotiorum</i> in <i>Camelina sativa</i> . <i>Molecular Plant Pathology</i> , 2012, 13, 887-899.	4.2	81
23	Complexities of Chromosome Landing in a Highly Duplicated Genome: Toward Map-Based Cloning of a Gene Controlling Blackleg Resistance in <i>Brassica napus</i> . <i>Genetics</i> , 2005, 171, 1977-1988.	2.9	80
24	An auxin-responsive SCARECROW-like transcriptional activator interacts with histone deacetylase. <i>Plant Molecular Biology</i> , 2004, 55, 417-431.	3.9	78
25	Agronomic and Seed Quality Traits Dissected by Genome-Wide Association Mapping in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 386.	3.6	78
26	Microsatellite markers used for genome-wide association mapping of partial resistance to <i>Sclerotinia sclerotiorum</i> in a world collection of <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2016, 36, 72.	2.1	64
27	The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . <i>Plant Journal</i> , 2016, 88, 879-894.	5.7	60
28	Construction of <i>Brassica</i> A and C genome-based ordered pan-transcriptomes for use in rapeseed genomic research. <i>Data in Brief</i> , 2015, 4, 357-362.	1.0	58
29	Forward and reverse genetics of rapid-cycling <i>Brassica oleracea</i> . <i>Theoretical and Applied Genetics</i> , 2009, 118, 953-961.	3.6	57
30	Association mapping of seed quality traits in <i>Brassica napus</i> L. using GWAS and candidate QTL approaches. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	51
31	The <i>Brassica napus</i> wall-associated kinase-like (WAKL) gene <i>Rlm9</i> provides race-specific blackleg resistance. <i>Plant Journal</i> , 2020, 104, 892-900.	5.7	51
32	Molecular cytogenetic identification of B genome chromosomes linked to blackleg disease resistance in <i>Brassica napus</i> × <i>B. carinata</i> interspecific hybrids. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1305-1318.	3.6	49
33	Analysis of B-Genome Chromosome Introgression in Interspecific Hybrids of <i>Brassica napus</i> × <i>B. carinata</i> . <i>Genetics</i> , 2011, 187, 659-673.	2.9	48
34	Exploiting the wild crucifer <i>Thlaspi arvense</i> to identify conserved and novel genes expressed during a plant's response to cold stress. <i>Plant Molecular Biology</i> , 2006, 63, 171-184.	3.9	47
35	Centromere Locations in <i>Brassica</i> A and C Genomes Revealed Through Half-Tetrad Analysis. <i>Genetics</i> , 2016, 202, 513-523.	2.9	47
36	Mapping the <i>Brassica</i> Genome. <i>Outlook on Agriculture</i> , 1993, 22, 85-92.	3.4	45

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37	Brassica napus possesses an expanded set of polygalacturonase inhibitor protein genes that are differentially regulated in response to Sclerotinia sclerotiorum infection, wounding and defense hormone treatment. <i>Planta</i> , 2008, 228, 241-253.	3.2	45
38	Long-read sequencing reveals widespread intragenic structural variants in a recent allopolyploid crop plant. <i>Plant Biotechnology Journal</i> , 2021, 19, 240-250.	8.3	45
39	Towards unambiguous transcript mapping in the allotetraploid Brassica napus 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, 929-938.	2.0	44
40	The <i>Arabidopsis</i> tt19 mutant differentially accumulates proanthocyanidin and anthocyanin through a 3 amino acid substitution in glutathione S-transferase. <i>Plant, Cell and Environment</i> , 2011, 34, 374-388.	5.7	43
41	Core and Differentially Abundant Bacterial Taxa in the Rhizosphere of Field Grown Brassica napus Genotypes: Implications for Canola Breeding. <i>Frontiers in Microbiology</i> , 2019, 10, 3007.	3.5	39
42	Single-nucleotide polymorphism identification and genotyping in Camelina sativa. <i>Molecular Breeding</i> , 2015, 35, 35.	2.1	36
43	Re-exploration of Ua™s Triangle Brassica Species Based on Chloroplast Genomes and 45S nrDNA Sequences. <i>Scientific Reports</i> , 2018, 8, 7353.	3.3	36
44	Maximizing the Efficacy of SAGE Analysis Identifies Novel Transcripts in Arabidopsis. <i>Plant Physiology</i> , 2004, 136, 3223-3233.	4.8	35
45	Species- and genome-wide dissection of the shoot ionome in Brassica napus and its relationship to seedling development. <i>Frontiers in Plant Science</i> , 2014, 5, 485.	3.6	35
46	A major quantitative trait locus on chromosome A9, <i>BnaPh1</i> , controls homoeologous recombination in <i>Brassica napus</i> . <i>New Phytologist</i> , 2021, 229, 3281-3293.	7.3	35
47	WheatCRISPR: a web-based guide RNA design tool for CRISPR/Cas9-mediated genome editing in wheat. <i>BMC Plant Biology</i> , 2019, 19, 474.	3.6	34
48	Crop Lodging Prediction From UAV-Acquired Images of Wheat and Canola Using a DCNN Augmented With Handcrafted Texture Features. , 2019, , .		34
49	Detecting de Novo Homoeologous Recombination Events in Cultivated Brassica napus Using a Genome-Wide SNP Array. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2673-2683.	1.8	33
50	Assessing Diversity in the <i>Camelina</i> Genus Provides Insights into the Genome Structure of <i>Camelina sativa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1297-1308.	1.8	33
51	Co-linearity and divergence of the A subgenome of Brassica juncea compared with other Brassica species carrying different A subgenomes. <i>BMC Genomics</i> , 2016, 17, 18.	2.8	32
52	Clubroot resistance gene Rcr6 in Brassica nigra resides in a genomic region homologous to chromosome A08 in B. rapa. <i>BMC Plant Biology</i> , 2019, 19, 224.	3.6	32
53	Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021, 7, 757-765.	9.3	31
54	A novel protein from Brassica napus has a putative KID domain and responds to low temperature. <i>Plant Journal</i> , 2003, 33, 1073-1086.	5.7	30

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55	Genetic Diversity and Population Structure in a World Collection of <i>Brassica napus</i> Accessions with Emphasis on South Korea, Japan, and Pakistan. <i>Crop Science</i> , 2013, 53, 1537-1545.	1.8	30
56	High-density single nucleotide polymorphism (SNP) array mapping in <i>Brassica oleracea</i> : identification of QTL associated with carotenoid variation in broccoli florets. <i>Theoretical and Applied Genetics</i> , 2014, 127, 2051-2064.	3.6	30
57	<i>Arabidopsis</i> cpSRP54 regulates carotenoid accumulation in <i>Arabidopsis</i> and <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 5189-5202.	4.8	28
58	Latent Space Phenotyping: Automatic Image-Based Phenotyping for Treatment Studies. <i>Plant Phenomics</i> , 2020, 2020, 5801869.	5.9	26
59	A new dominant <i>Arabidopsis</i> transparent testa mutant, <i>sk21-D</i> , and modulation of seed flavonoid biosynthesis by <i>KAN4</i> . <i>Plant Biotechnology Journal</i> , 2010, 8, 979-993.	8.3	22
60	Hairy Canola ( <i>Brassica napus</i> ) re-visited: Down-regulating <i>TTG1</i> in an <i>AtGL3</i> -enhanced hairy leaf background improves growth, leaf trichome coverage, and metabolite gene expression diversity. <i>BMC Plant Biology</i> , 2016, 16, 12.	3.6	18
61	Classification of Crop Lodging with Gray Level Co-occurrence Matrix. , 2018, , .		17
62	Korean <i>Brassica oleracea</i> germplasm offers a novel source of qualitative resistance to blackleg disease. <i>European Journal of Plant Pathology</i> , 2017, 149, 611-623.	1.7	16
63	UAV-Based Hyperspectral Imaging Technique to Estimate Canola ( <i>Brassica napus</i> L.) Seedpods Maturity. <i>Canadian Journal of Remote Sensing</i> , 2021, 47, 33-47.	2.4	15
64	Deep neural networks for genomic prediction do not estimate marker effects. <i>Plant Genome</i> , 2021, 14, e20147.	2.8	15
65	Comparative genome organization reveals a single copy of <i>CBF</i> in the freezing tolerant crucifer <i>Thlaspi arvense</i> . <i>Plant Molecular Biology</i> , 2007, 65, 693-705.	3.9	13
66	Narrow genetic base shapes population structure and linkage disequilibrium in an industrial oilseed crop, <i>Brassica carinata</i> A. Braun. <i>Scientific Reports</i> , 2020, 10, 12629.	3.3	13
67	Mid-infrared spectroscopy is a fast screening method for selecting <i>Arabidopsis</i> genotypes with altered leaf cuticular wax. <i>Plant, Cell and Environment</i> , 2020, 43, 662-674.	5.7	12
68	Revised Selection Criteria for Candidate Restriction Enzymes in Genome Walking. <i>PLoS ONE</i> , 2012, 7, e35117.	2.5	12
69	Multi-trait and multi-environment QTL analysis reveals the impact of seed colour on seed composition traits in <i>Brassica napus</i> . <i>Molecular Breeding</i> , 2016, 36, 1.	2.1	11
70	Phenotyping Flowering in Canola ( <i>Brassica napus</i> L.) and Estimating Seed Yield Using an Unmanned Aerial Vehicle-Based Imagery. <i>Frontiers in Plant Science</i> , 2021, 12, 686332.	3.6	11
71	Visualization Tools for Genomic Conservation. <i>Methods in Molecular Biology</i> , 2022, 2443, 285-308.	0.9	9
72	L-system models for image-based phenomics: case studies of maize and canola. <i>In Silico Plants</i> , 2022, 4, .	1.9	9

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73	Comparison of Five Major Trichome Regulatory Genes in <i>Brassica villosa</i> with Orthologues within the Brassicaceae. PLoS ONE, 2014, 9, e95877.	2.5	8
74	Genes associated with chloroplasts and hormone-signaling, and transcription factors other than CBFs are associated with differential survival after low temperature treatments of <i>Camelina sativa</i> biotypes. PLoS ONE, 2019, 14, e0217692.	2.5	8
75	Gene expression profiling reveals transcription factor networks and subgenome bias during <i>Brassica napus</i> seed development. Plant Journal, 2021, 109, 477.	5.7	8
76	Quantitative and structural analyses of T-DNA tandem repeats in transgenic <i>Arabidopsis</i> SK mutant lines. Plant Cell, Tissue and Organ Culture, 2015, 123, 183-192.	2.3	7
77	Analysis of Genotyping-by-Sequencing (GBS) Data. Methods in Molecular Biology, 2016, 1374, 269-284.	0.9	6
78	Field cress genome mapping: Integrating linkage and comparative maps with cytogenetic analysis for rDNA carrying chromosomes. Scientific Reports, 2019, 9, 17028.	3.3	5
79	Exploiting High-Throughput Indoor Phenotyping to Characterize the Founders of a Structured <i>B. napus</i> Breeding Population. Frontiers in Plant Science, 2021, 12, 780250.	3.6	3
80	Characterization of B-Genome Specific High Copy hAT MITE Families in <i>Brassica nigra</i> Genome. Frontiers in Plant Science, 2020, 11, 1104.	3.6	1
81	saskPrimer &#x2014; An automated pipeline for design of intron-spanning PCR primers in non-model organisms. , 2011, , .		0
82	Characterization and Mapping of retr04, retr05 and retr06 Broad-Spectrum Resistances to Turnip Mosaic Virus in <i>Brassica juncea</i> , and the Development of Robust Methods for Utilizing Recalcitrant Genotyping Data. Frontiers in Plant Science, 2021, 12, 787354.	3.6	0