

# Isobel A P Parkin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5175788/publications.pdf>

Version: 2024-02-01

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	Visualization Tools for Genomic Conservation. <i>Methods in Molecular Biology</i> , 2022, 2443, 285-308.	0.9	9
2	L-system models for image-based phenomics: case studies of maize and canola. <i>In Silico Plants</i> , 2022, 4, .	1.9	9
3	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
4	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
5	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
6	Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021, 7, 757-765.	9.3	31
7	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
8	Deep neural networks for genomic prediction do not estimate marker effects. <i>Plant Genome</i> , 2021, 14, e20147.	2.8	15
9	Gene expression profiling reveals transcription factor networks and subgenome bias during <i>Brassica napus</i> seed development. <i>Plant Journal</i> , 2021, 109, 477.	5.7	8
10	Exploiting High-Throughput Indoor Phenotyping to Characterize the Founders of a Structured <i>B. napus</i> Breeding Population. <i>Frontiers in Plant Science</i> , 2021, 12, 780250.	3.6	3
11	Characterization and Mapping of <i>retr04</i> , <i>retr05</i> and <i>retr06</i> Broad-Spectrum Resistances to Turnip Mosaic Virus in <i>Brassica juncea</i> , and the Development of Robust Methods for Utilizing Recalcitrant Genotyping Data. <i>Frontiers in Plant Science</i> , 2021, 12, 787354.	3.6	0
12	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
13	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
14	Characterization of B-Genome Specific High Copy hAT MITE Families in <i>Brassica nigra</i> Genome. <i>Frontiers in Plant Science</i> , 2020, 11, 1104.	3.6	1
15	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
16	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
17	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
18	Latent Space Phenotyping: Automatic Image-Based Phenotyping for Treatment Studies. <i>Plant Phenomics</i> , 2020, 2020, 5801869.	5.9	26

#	ARTICLE	IF	CITATIONS
19	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
20	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. <i>PLoS ONE</i> , 2019, 14, e0217692.	2.5	8
21	Clubroot resistance gene <i>Rcr6</i> in <i>Brassica nigra</i> resides in a genomic region homologous to chromosome A08 in <i>B. rapa</i> . <i>BMC Plant Biology</i> , 2019, 19, 224.	3.6	32
22	Field cress genome mapping: Integrating linkage and comparative maps with cytogenetic analysis for rDNA carrying chromosomes. <i>Scientific Reports</i> , 2019, 9, 17028.	3.3	5
23	Connecting genome structural variation with complex traits in crop plants. <i>Theoretical and Applied Genetics</i> , 2019, 132, 733-750.	3.6	97
24	Core and Differentially Abundant Bacterial Taxa in the Rhizosphere of Field Grown <i>Brassica napus</i> Genotypes: Implications for Canola Breeding. <i>Frontiers in Microbiology</i> , 2019, 10, 3007.	3.5	39
25	Crop Lodging Prediction From UAV-Acquired Images of Wheat and Canola Using a DCNN Augmented With Handcrafted Texture Features. , 2019, , .		34
26	Classification of Crop Lodging with Gray Level Co-occurrence Matrix. , 2018, , .		17
27	Re-exploration of Uâ€™s Triangle Brassica Species Based on Chloroplast Genomes and 45S nrDNA Sequences. <i>Scientific Reports</i> , 2018, 8, 7353.	3.3	36
28	Detecting de Novo Homoeologous Recombination Events in Cultivated <i>Brassica napus</i> Using a Genome-Wide SNP Array. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2673-2683.	1.8	33
29	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
30	A user guide to the Brassica 60K Illumina Infiniumâ„¢ SNP genotyping array. <i>Theoretical and Applied Genetics</i> , 2017, 130, 621-633.	3.6	90
31	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
32	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
33	Extensive homoeologous genome exchanges in allopolyploid crops revealed by <i>scp</i> mRNA-based visualization. <i>Plant Biotechnology Journal</i> , 2017, 15, 594-604.	8.3	96
34	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
35	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
36	Co-linearity and divergence of the A subgenome of <i>Brassica juncea</i> compared with other <i>Brassica</i> species carrying different A subgenomes. <i>BMC Genomics</i> , 2016, 17, 18.	2.8	32

#	ARTICLE	IF	CITATIONS
37	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
38	The developmental transcriptome atlas of the biofuel crop <i>Camelina sativa</i> . <i>Plant Journal</i> , 2016, 88, 879-894.	5.7	60
39	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	12.8	375
40	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
41	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
42	Hairy Canola ( <i>Brassica napus</i> ) re-visited: Down-regulating TTG1 in an AtGL3-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
43	Analysis of Genotyping-by-Sequencing (GBS) Data. <i>Methods in Molecular Biology</i> , 2016, 1374, 269-284.	0.9	6
44	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
45	Single-nucleotide polymorphism identification and genotyping in <i>Camelina sativa</i> . <i>Molecular Breeding</i> , 2015, 35, 35.	2.1	36
46	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
47	Quantitative and structural analyses of T-DNA tandem repeats in transgenic <i>Arabidopsis</i> SK mutant lines. <i>Plant Cell, Tissue and Organ Culture</i> , 2015, 123, 183-192.	2.3	7
48	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
49	Comparison of Five Major Trichome Regulatory Genes in <i>Brassica villosa</i> with Orthologues within the Brassicaceae. <i>PLoS ONE</i> , 2014, 9, e95877.	2.5	8
50	Species- and genome-wide dissection of the shoot ionome in <i>Brassica napus</i> and its relationship to seedling development. <i>Frontiers in Plant Science</i> , 2014, 5, 485.	3.6	35
51	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
52	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
53	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	12.6	2,089
54	Polyloid Evolution of the Brassicaceae during the Cenozoic Era. <i>Plant Cell</i> , 2014, 26, 2777-2791.	6.6	165

#	ARTICLE	IF	CITATIONS
55	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	12.8	918
56	The emerging biofuel crop Camelina sativa retains a highly undifferentiated hexaploid genome structure. Nature Communications, 2014, 5, 3706.	12.8	295
57	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid Brassica oleracea. Genome Biology, 2014, 15, R77.	9.6	456
58	Genome-Wide Delineation of Natural Variation for Pod Shatter Resistance in Brassica napus. PLoS ONE, 2014, 9, e101673.	2.5	182
59	Genetic Diversity and Population Structure in a World Collection of <i>Brassica napus</i> Accessions with Emphasis on South Korea, Japan, and Pakistan. Crop Science, 2013, 53, 1537-1545.	1.8	30
60	Arabidopsis cpSRP54 regulates carotenoid accumulation in Arabidopsis and Brassica napus. Journal of Experimental Botany, 2012, 63, 5189-5202.	4.8	28
61	Monolignol biosynthesis is associated with resistance to <i>Sclerotinia sclerotiorum</i> in <i>Camelina sativa</i> . Molecular Plant Pathology, 2012, 13, 887-899.	4.2	81
62	Revised Selection Criteria for Candidate Restriction Enzymes in Genome Walking. PLoS ONE, 2012, 7, e35117.	2.5	12
63	The <i>Arabidopsis</i> tt19 mutant differentially accumulates proanthocyanidin and anthocyanin through a 3 amino acid substitution in glutathione S-transferase. Plant, Cell and Environment, 2011, 34, 374-388.	5.7	43
64	The genome of the mesopolyploid crop species Brassica rapa. Nature Genetics, 2011, 43, 1035-1039.	21.4	1,893
65	Analysis of B-Genome Chromosome Introgression in Interspecific Hybrids of <i>Brassica napus</i> and <i>B. carinata</i> . Genetics, 2011, 187, 659-673.	2.9	48
66	saskPrimer &#x2014; An automated pipeline for design of intron-spanning PCR primers in non-model organisms. , 2011, , .		0
67	A new dominant Arabidopsis transparent testa mutant, sk21-D, and modulation of seed flavonoid biosynthesis by KAN4. Plant Biotechnology Journal, 2010, 8, 979-993.	8.3	22
68	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". Genome, 2010, 53, 929-938.	2.0	44
69	Forward and reverse genetics of rapid-cycling Brassica oleracea. Theoretical and Applied Genetics, 2009, 118, 953-961.	3.6	57
70	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. Planta, 2008, 228, 241-253.	3.2	45
71	Comparative genome organization reveals a single copy of CBF in the freezing tolerant crucifer Thlaspi arvense. Plant Molecular Biology, 2007, 65, 693-705.	3.9	13
72	Exploiting the wild crucifer Thlaspi arvense to identify conserved and novel genes expressed during a plant's response to cold stress. Plant Molecular Biology, 2006, 63, 171-184.	3.9	47

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	Maximizing the Efficacy of SAGE Analysis Identifies Novel Transcripts in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2004, 136, 3223-3233.	4.8	35
76	An auxin-responsive SCARECROW-like transcriptional activator interacts with histone deacetylase. <i>Plant Molecular Biology</i> , 2004, 55, 417-431.	3.9	78
77	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
78	A novel protein from <i>Brassica napus</i> has a putative KID domain and responds to low temperature. <i>Plant Journal</i> , 2003, 33, 1073-1086.	5.7	30
79	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
80	Detection and Effects of a Homeologous Reciprocal Transposition in <i>Brassica napus</i> . <i>Genetics</i> , 2003, 165, 1569-1577.	2.9	131
81	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
82	Mapping the <i>Brassica</i> Genome. <i>Outlook on Agriculture</i> , 1993, 22, 85-92.	3.4	45