

Ian Bancroft

List of Publications by Year in descending order

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62
papers

11,277
citations

87888

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62
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all docs

64
docs citations

64
times ranked

7682
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome structural evolution in Brassica crops. <i>Nature Plants</i> , 2021, 7, 757-765.	9.3	31
2	Validation of a novel associative transcriptomics pipeline in Brassica oleracea: identifying candidates for vernalisation response. <i>BMC Genomics</i> , 2021, 22, 539.	2.8	6
3	Genomic signatures of vegetable and oilseed allopolyploid <i>Brassica juncea</i> and genetic loci controlling the accumulation of glucosinolates. <i>Plant Biotechnology Journal</i> , 2021, 19, 2619-2628.	8.3	30
4	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	8.3	44
5	The impact of reducing fatty acid desaturation on the composition and thermal stability of rapeseed oil. <i>Plant Biotechnology Journal</i> , 2020, 18, 983-991.	8.3	22
6	A high-contiguity Brassica nigra genome localizes active centromeres and defines the ancestral Brassica genome. <i>Nature Plants</i> , 2020, 6, 929-941.	9.3	94
7	A Brassica napus Reductase Gene Dissected by Associative Transcriptomics Enhances Plant Adaption to Freezing Stress. <i>Frontiers in Plant Science</i> , 2020, 11, 971.	3.6	11
8	QTL-seq identifies <i>BnaFT.A02</i> and <i>BnaFLC.A02</i> as candidates for variation in vernalization requirement and response in winter oilseed rape (<i>Brassica napus</i>). <i>Plant Biotechnology Journal</i> , 2020, 18, 2466-2481.	8.3	35
9	Validation of an Associative Transcriptomics platform in the polyploid crop species <i>Brassica juncea</i> by dissection of the genetic architecture of agronomic and quality traits. <i>Plant Journal</i> , 2020, 103, 1885-1893.	5.7	12
10	The WRKY6 transcription factor affects seed oil accumulation and alters fatty acid compositions in <i>Arabidopsis thaliana</i> . <i>Physiologia Plantarum</i> , 2020, 169, 612-624.	5.2	35
11	Data in support of genetic architecture of glucosinolate variations in Brassica napus. <i>Data in Brief</i> , 2019, 25, 104402.	1.0	4
12	Analysing the genetic architecture of clubroot resistance variation in Brassica napus by associative transcriptomics. <i>Molecular Breeding</i> , 2019, 39, 112.	2.1	40
13	Genetic architecture of glucosinolate variation in Brassica napus. <i>Journal of Plant Physiology</i> , 2019, 240, 152988.	3.5	38
14	Genome-wide selection footprints and deleterious variations in young Asian allotetraploid rapeseed. <i>Plant Biotechnology Journal</i> , 2019, 17, 1998-2010.	8.3	54
15	Cytonuclear interactions remain stable during allopolyploid evolution despite repeated whole-genome duplications in <i>Brassica</i> . <i>Plant Journal</i> , 2019, 98, 434-447.	5.7	32
16	Dissecting the complex regulation of lodging resistance in Brassica napus. <i>Molecular Breeding</i> , 2018, 38, 30.	2.1	28
17	Validation of an updated Associative Transcriptomics platform for the polyploid crop species <i>Brassica napus</i> by dissection of the genetic architecture of erucic acid and tocopherol isoform variation in seeds. <i>Plant Journal</i> , 2018, 93, 181-192.	5.7	75
18	Organization of the genome sequence of the polyploid crop species Brassica juncea. <i>Nature Genetics</i> , 2018, 50, 1496-1497.	21.4	14

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19	Species-Wide Variation in Shoot Nitrate Concentration, and Genetic Loci Controlling Nitrate, Phosphorus and Potassium Accumulation in <i>Brassica napus</i> L. <i>Frontiers in Plant Science</i> , 2018, 9, 1487.	3.6	22
20	Assembly and comparison of two closely related <i>Brassica napus</i> genomes. <i>Plant Biotechnology Journal</i> , 2017, 15, 1602-1610.	8.3	150
21	Carbohydrate microarrays and their use for the identification of molecular markers for plant cell wall composition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6860-6865.	7.1	35
22	Genome sequence and genetic diversity of European ash trees. <i>Nature</i> , 2017, 541, 212-216.	27.8	166
23	Extensive homoeologous genome exchanges in allopolyploid crops revealed by <i>scRNA-seq</i> -based visualization. <i>Plant Biotechnology Journal</i> , 2017, 15, 594-604.	8.3	96
24	Identification of Candidate Genes for Calcium and Magnesium Accumulation in <i>Brassica napus</i> L. by Association Genetics. <i>Frontiers in Plant Science</i> , 2017, 8, 1968.	3.6	39
25	Variation across a wheat genetic diversity panel for saccharification of hydrothermally pretreated straw. <i>Biotechnology for Biofuels</i> , 2017, 10, 227.	6.2	2
26	Elucidation of the genetic basis of variation for stem strength characteristics in bread wheat by Associative Transcriptomics. <i>BMC Genomics</i> , 2016, 17, 500.	2.8	44
27	Genome distribution of differential homoeologue contributions to leaf gene expression in bread wheat. <i>Plant Biotechnology Journal</i> , 2016, 14, 1207-1214.	8.3	41
28	Molecular markers for tolerance of European ash (<i>Fraxinus excelsior</i>) to dieback disease identified using Associative Transcriptomics. <i>Scientific Reports</i> , 2016, 6, 19335.	3.3	85
29	Effect of <i>Brassica napus</i> cultivar on cellulosic ethanol yield. <i>Biotechnology for Biofuels</i> , 2015, 8, 99.	6.2	10
30	Seedling development traits in <i>Brassica napus</i> examined by gene expression analysis and association mapping. <i>BMC Plant Biology</i> , 2015, 15, 136.	3.6	28
31	Collinearity analysis of Brassica A and C genomes based on an updated inferred unigene order. <i>Data in Brief</i> , 2015, 3, 51-55.	1.0	10
32	Identification of a gene controlling variation in the salt tolerance of rapeseed (<i>Brassica napus</i> L.). <i>Planta</i> , 2015, 242, 313-326.	3.2	45
33	Identification, evolution, and expression partitioning of miRNAs in allopolyploid <i>Brassica napus</i> . <i>Journal of Experimental Botany</i> , 2015, 66, 7241-7253.	4.8	44
34	Construction of Brassica 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
35	Dissection of the Control of Anion Homeostasis by Associative Transcriptomics in <i>Brassica napus</i> . <i>Plant Physiology</i> , 2014, 166, 442-450.	4.8	52
36	A Novel and Fast Approach for Population Structure Inference Using Kernel-PCA and Optimization. <i>Genetics</i> , 2014, 198, 1421-1431.	2.9	27

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37	Associative Transcriptomics Study Dissects the Genetic Architecture of Seed Glucosinolate Content in Brassica napus. DNA Research, 2014, 21, 613-625.	3.4	94
38	The control of seed oil polyunsaturate content in the polyploid crop species Brassica napus. Molecular Breeding, 2014, 33, 349-362.	2.1	69
39	Steam explosion of oilseed rape straw: Establishing key determinants of saccharification efficiency. Bioresource Technology, 2014, 162, 175-183.	9.6	31
40	Genome-Wide Association Study Dissects the Genetic Architecture of Seed Weight and Seed Quality in Rapeseed (Brassica napus L.). DNA Research, 2014, 21, 355-367.	3.4	247
41	Variation in the chemical composition of wheat straw: the role of tissue ratio and composition. Biotechnology for Biofuels, 2014, 7, 121.	6.2	56
42	Genome-wide investigation of genetic changes during modern breeding of Brassica napus. Theoretical and Applied Genetics, 2014, 127, 1817-1829.	3.6	60
43	Early allopolyploid evolution in the post-Neolithic Brassica napus oilseed genome. Science, 2014, 345, 950-953.	12.6	2,089
44	The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications, 2014, 5, 3930.	12.8	918
45	Oleaginous crops as integrated production platforms for food, feed, fuel and renewable industrial feedstock. OCL - Oilseeds and Fats, Crops and Lipids, 2014, 21, D606.	1.4	13
46	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid Brassica oleracea. Genome Biology, 2014, 15, R77.	9.6	456
47	Analysis of the bread wheat genome using whole-genome shotgun sequencing. Nature, 2012, 491, 705-710.	27.8	983
48	Rapid quantification of reducing sugars in biomass hydrolysates: Improving the speed and precision of the dinitrosalicylic acid assay. Biomass and Bioenergy, 2012, 44, 117-121.	5.7	106
49	Use of mRNA-seq to discriminate contributions to the transcriptome from the constituent genomes of the polyploid crop species Brassica napus. BMC Genomics, 2012, 13, 247.	2.8	91
50	Associative transcriptomics of traits in the polyploid crop species Brassica napus. Nature Biotechnology, 2012, 30, 798-802.	17.5	347
51	Dissecting the genome of the polyploid crop oilseed rape by transcriptome sequencing. Nature Biotechnology, 2011, 29, 762-766.	17.5	187
52	The genome of the mesopolyploid crop species Brassica rapa. Nature Genetics, 2011, 43, 1035-1039.	21.4	1,893
53	An association transcriptomics approach to the prediction of hybrid performance. Molecular Breeding, 2010, 26, 91-106.	2.1	26
54	Unraveling the Complex Trait of Crop Yield With Quantitative Trait Loci Mapping in Brassica napus. Genetics, 2009, 182, 851-861.	2.9	362

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55	Comparative Analysis between Homoeologous Genome Segments of <i>Brassica napus</i> and Its Progenitor Species Reveals Extensive Sequence-Level Divergence. <i>Plant Cell</i> , 2009, 21, 1912-1928.	6.6	194
56	A newly-developed community microarray resource for transcriptome profiling in Brassica species enables the confirmation of Brassica-specific expressed sequences. <i>BMC Plant Biology</i> , 2009, 9, 50.	3.6	55
57	Single nucleotide polymorphism (SNP) discovery in the polyploid <i>Brassica napus</i> using Solexa transcriptome sequencing. <i>Plant Biotechnology Journal</i> , 2009, 7, 334-346.	8.3	307
58	Characterization of the centromere and pericentromere retrotransposons in <i>Brassica rapa</i> and their distribution in related <i>Brassica</i> species. <i>Plant Journal</i> , 2007, 49, 173-183.	5.7	116
59	Comparative Genomics of <i>Brassica oleracea</i> and <i>Arabidopsis thaliana</i> Reveal Gene Loss, Fragmentation, and Dispersal after Polyploidy. <i>Plant Cell</i> , 2006, 18, 1348-1359.	6.6	374
60	Sequence-Level Analysis of the Diploidization Process in the Triplicated FLOWERING LOCUS C Region of <i>Brassica rapa</i> . <i>Plant Cell</i> , 2006, 18, 1339-1347.	6.6	223
61	Conservation of the microstructure of genome segments in <i>Brassica napus</i> and its diploid relatives. <i>Plant Journal</i> , 2004, 40, 725-733.	5.7	221
62	Comparative physical mapping of segments of the genome of <i>Brassica oleracea</i> var. <i>alboglabra</i> that are homoeologous to sequenced regions of chromosomes 4 and 5 of <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2000, 23, 233-243.	5.7	200