

François Belzile

List of Publications by Year in descending order

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Version: 2024-02-01

99
papers

4,826
citations

117625

34
h-index

106344

65
g-index

110
all docs

110
docs citations

110
times ranked

4835
citing authors

#	ARTICLE	IF	CITATIONS
1	A high-resolution consensus linkage map for barley based on GBS-derived genotypes. <i>Genome</i> , 2022, 65, 83-94.	2.0	2
2	RXLR effector gene <i>Avr3a</i> from <i>Phytophthora sojae</i> is recognized by <i>Rps8</i> in soybean. <i>Molecular Plant Pathology</i> , 2022, 23, 693-706.	4.2	9
3	Combined use of Oxford Nanopore and Illumina sequencing yields insights into soybean structural variation biology. <i>BMC Biology</i> , 2022, 20, 53.	3.8	10
4	Mapping of partial resistance to <i>Phytophthora sojae</i> in soybean PIs using whole-genome sequencing reveals a major QTL. <i>Plant Genome</i> , 2022, 15, e20184.	2.8	11
5	The SoyaGen Project: Putting Genomics to Work for Soybean Breeders. <i>Frontiers in Plant Science</i> , 2022, 13, 887553.	3.6	1
6	Genome-Wide Association Study Statistical Models: A Review. <i>Methods in Molecular Biology</i> , 2022, , 43-62.	0.9	10
7	Soybean (<i>Glycine max</i>) Haplotype Map (GmHapMap): a universal resource for soybean translational and functional genomics. <i>Plant Biotechnology Journal</i> , 2021, 19, 324-334.	8.3	48
8	Accurate Imputation of Untyped Variants from Deep Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2243, 271-281.	0.9	6
9	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	6
10	A bumper crop of SNPs in soybean through high-density genotyping-by-sequencing (HD-GBS). <i>Plant Biotechnology Journal</i> , 2021, 19, 860-862.	8.3	13
11	Genome-wide association study to identify soybean stem pushing resistance and lodging resistance loci. <i>Canadian Journal of Plant Science</i> , 2021, 101, 663-670.	0.9	4
12	Improvement of key agronomical traits in soybean through genomic prediction of superior crosses. <i>Crop Science</i> , 2021, 61, 3908-3918.	1.8	7
13	The pan-genome of the cultivated soybean (PanSoy) reveals an extraordinarily conserved gene content. <i>Plant Biotechnology Journal</i> , 2021, 19, 1852-1862.	8.3	41
14	Omics advances and integrative approaches for the simultaneous improvement of seed oil and protein content in soybean (<i>Glycine max</i> L.). <i>Critical Reviews in Plant Sciences</i> , 2021, 40, 398-421.	5.7	17
15	GWAS identifies an ortholog of the rice D11 gene as a candidate gene for grain size in an international collection of hexaploid wheat. <i>Scientific Reports</i> , 2021, 11, 19483.	3.3	8
16	Genome-wide association study for resistance to the <i>Meloidogyne javanica</i> causing root-knot nematode in soybean. <i>Theoretical and Applied Genetics</i> , 2021, 134, 777-792.	3.6	15
17	DepthFinder: a tool to determine the optimal read depth for reduced-representation sequencing. <i>Bioinformatics</i> , 2020, 36, 26-32.	4.1	9
18	Genome-wide association analyses reveal the genetic basis of biomass accumulation under symbiotic nitrogen fixation in African soybean. <i>Theoretical and Applied Genetics</i> , 2020, 133, 665-676.	3.6	21

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19	Integrated QTL mapping, gene expression and nucleotide variation analyses to investigate complex quantitative traits: a case study with the soybean– <i>Phytophthora sojae</i> interaction. <i>Plant Biotechnology Journal</i> , 2020, 18, 1492-1494.	8.3	18
20	Time for a paradigm shift in the use of plant genetic resources. <i>Genome</i> , 2020, 63, 189-194.	2.0	13
21	Fast-GBS v2.0: an analysis toolkit for genotyping-by-sequencing data. <i>Genome</i> , 2020, 63, 577-581.	2.0	19
22	Population structure of Nepali spring wheat (<i>Triticum aestivum</i> L.) germplasm. <i>BMC Plant Biology</i> , 2020, 20, 530.	3.6	9
23	Comprehensive Genome-Wide Association Analysis Reveals the Genetic Basis of Root System Architecture in Soybean. <i>Frontiers in Plant Science</i> , 2020, 11, 590740.	3.6	17
24	Identification of loci controlling mineral element concentration in soybean seeds. <i>BMC Plant Biology</i> , 2020, 20, 419.	3.6	12
25	Genome-wide association identifies several QTLs controlling cysteine and methionine content in soybean seed including some promising candidate genes. <i>Scientific Reports</i> , 2020, 10, 21812.	3.3	12
26	The commitment of barley microspores into embryogenesis correlates with miRNA-directed regulation of members of the SPL, GRF and HD-ZIP III transcription factor families. <i>Plant Direct</i> , 2020, 4, e00289.	1.9	5
27	Genome-wide association mapping of <i>Sclerotinia sclerotiorum</i> resistance in soybean using whole-genome resequencing data. <i>BMC Plant Biology</i> , 2020, 20, 195.	3.6	25
28	Haplotype diversity underlying quantitative traits in Canadian soybean breeding germplasm. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1967-1976.	3.6	10
29	Discriminant haplotypes of avirulence genes of <i>Phytophthora sojae</i> lead to a molecular assay to predict phenotypes. <i>Molecular Plant Pathology</i> , 2020, 21, 318-329.	4.2	12
30	NanoGBS: A Miniaturized Procedure for GBS Library Preparation. <i>Frontiers in Genetics</i> , 2020, 11, 67.	2.3	11
31	Characterizing resistance to soybean cyst nematode in PI 494182, an early maturing soybean accession. <i>Crop Science</i> , 2020, 60, 2053-2069.	1.8	15
32	Screening populations for copy number variation using genotyping-by-sequencing: a proof of concept using soybean fast neutron mutants. <i>BMC Genomics</i> , 2019, 20, 634.	2.8	20
33	Genome-wide genetic diversity is maintained through decades of soybean breeding in Canada. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3089-3100.	3.6	19
34	Association mapping of a locus that confers southern stem canker resistance in soybean and SNP marker development. <i>BMC Genomics</i> , 2019, 20, 798.	2.8	13
35	A Systematic Gene-Centric Approach to Define Haplotypes and Identify Alleles on the Basis of Dense Single Nucleotide Polymorphism Datasets. <i>Plant Genome</i> , 2019, 12, 1-11.	2.8	15
36	Comparing Single-SNP, Multi-SNP, and Haplotype-Based Approaches in Association Studies for Major Traits in Barley. <i>Plant Genome</i> , 2019, 12, 1-14.	2.8	48

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37	SRG extractor: a skinny reference genome approach for reduced-representation sequencing. <i>Bioinformatics</i> , 2019, 35, 3160-3162.	4.1	1
38	Molecular tools for detecting Pdh1 can improve soybean breeding efficiency by reducing yield losses due to pod shatter. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	19
39	Genetic Analysis of High Protein Content in <i>Proteus</i> ™ Related Soybean Populations Using SSR, SNP, DArT and DArTseq Markers. <i>Scientific Reports</i> , 2019, 9, 19657.	3.3	6
40	QTL mapping uncovers a semi-dwarf 1 (<i>sdw1</i>) allele in the barley (<i>Hordeum vulgare</i>) ND23049 line. <i>Genome</i> , 2018, 61, 429-436.	2.0	4
41	Efficient genome-wide genotyping strategies and data integration in crop plants. <i>Theoretical and Applied Genetics</i> , 2018, 131, 499-511.	3.6	62
42	Exploring the potential and limitations of genotyping-by-sequencing for SNP discovery and genotyping in tetraploid potato. <i>Genome</i> , 2018, 61, 449-456.	2.0	31
43	Differential Expression Profiling of Microspores During the Early Stages of Isolated Microspore Culture Using the Responsive Barley Cultivar Gobernadora. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1603-1614.	1.8	22
44	Comprehensive description of genomewide nucleotide and structural variation in short-season soya bean. <i>Plant Biotechnology Journal</i> , 2018, 16, 749-759.	8.3	46
45	Identification of QTLs Associated with Biological Nitrogen Fixation Traits in Soybean Using a Genotyping-by-Sequencing Approach. <i>Crop Science</i> , 2018, 58, 2523-2532.	1.8	9
46	Identification of candidate domestication-related genes with a systematic survey of loss-of-function mutations. <i>Plant Journal</i> , 2018, 96, 1218-1227.	5.7	11
47	When less can be better: How can we make genomic selection more cost-effective and accurate in barley?. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1873-1890.	3.6	45
48	Silicon protects soybean plants against <i>Phytophthora sojae</i> by interfering with effector-receptor expression. <i>BMC Plant Biology</i> , 2018, 18, 97.	3.6	80
49	Fast-GBS: a new pipeline for the efficient and highly accurate calling of SNPs from genotyping-by-sequencing data. <i>BMC Bioinformatics</i> , 2017, 18, 5.	2.6	99
50	Genome-wide association study for resistance to the southern root-knot nematode (<i>Meloidogyne</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	2.1	33
51	Mapping and identification of a potential candidate gene for a novel maturity locus, E10, in soybean. <i>Theoretical and Applied Genetics</i> , 2017, 130, 377-390.	3.6	162
52	Genotyping-by-Sequencing on Pooled Samples and its Use in Measuring Segregation Bias during the Course of Androgenesis in Barley. <i>Plant Genome</i> , 2016, 9, plantgenome2014.10.0073.	2.8	21
53	Genome-Wide SNP Calling from Genotyping by Sequencing (GBS) Data: A Comparison of Seven Pipelines and Two Sequencing Technologies. <i>PLoS ONE</i> , 2016, 11, e0161333.	2.5	109
54	The geographic distribution and complex evolutionary history of the NX-2 trichothecene chemotype from <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2016, 95, 39-48.	2.1	55

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55	Identification and characterization of silicon efflux transporters in horsetail (<i>Equisetum arvense</i>). <i>Journal of Plant Physiology</i> , 2016, 200, 82-89.	3.5	73
56	Extent and overlap of segregation distortion regions in 12 barley crosses determined via a Pool-GBS approach. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1393-1404.	3.6	15
57	Strategies for a successful plant invasion: the reproduction of <i>Phragmites australis</i> in north-eastern North America. <i>Journal of Ecology</i> , 2015, 103, 1529-1537.	4.0	52
58	Scanning and Filling: Ultra-Dense SNP Genotyping Combining Genotyping-By-Sequencing, SNP Array and Whole-Genome Resequencing Data. <i>PLoS ONE</i> , 2015, 10, e0131533.	2.5	60
59	A new method for studying population genetics of cyst nematodes based on Pool-Seq and genome-wide allele frequency analysis. <i>Molecular Ecology Resources</i> , 2015, 15, 1356-1365.	4.8	31
60	Identification of loci governing eight agronomic traits using a GBS-GWAS approach and validation by QTL mapping in soya bean. <i>Plant Biotechnology Journal</i> , 2015, 13, 211-221.	8.3	340
61	Validation of Genotyping-By-Sequencing Analysis in Populations of Tetraploid Alfalfa by 454 Sequencing. <i>PLoS ONE</i> , 2015, 10, e0131918.	2.5	22
62	Rapid Identification of Alleles at the Soybean Maturity Gene E3 using genotyping by Sequencing and a Haplotype-Based Approach. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0034.	2.8	45
63	Genome Wide Association Mapping of <i>Sclerotinia sclerotiorum</i> Resistance in Soybean with a Genotyping-by-Sequencing Approach. <i>Plant Genome</i> , 2014, 7, plantgenome2013.10.0030.	2.8	135
64	A Zoospore Inoculation Method with <i>Phytophthora sojae</i> to Assess the Prophylactic Role of Silicon on Soybean Cultivars. <i>Plant Disease</i> , 2014, 98, 1632-1638.	1.4	24
65	Genomic characterization of the <i>Hordeum vulgare</i> DEP1 (HvDEP1) gene and its diversity in a collection of barley accessions. <i>Euphytica</i> , 2014, 198, 29-41.	1.2	10
66	Improving the efficiency of isolated microspore culture in six-row spring barley: I-optimization of key physical factors. <i>Plant Cell Reports</i> , 2014, 33, 993-1001.	5.6	15
67	Improving the efficiency of isolated microspore culture in six-row spring barley: II-exploring novel growth regulators to maximize embryogenesis and reduce albinism. <i>Plant Cell Reports</i> , 2014, 33, 871-879.	5.6	30
68	Sexual reproduction of Japanese knotweed (<i>Fallopia japonica</i> s.l.) at its northern distribution limit: New evidence of the effect of climate warming on an invasive species. <i>American Journal of Botany</i> , 2014, 101, 459-466.	1.7	37
69	Comparative analysis of genetic diversity in Canadian barley assessed by SSR, DarT, and pedigree data. <i>Genome</i> , 2013, 56, 351-358.	2.0	13
70	Identification and functional characterization of silicon transporters in soybean using comparative genomics of major intrinsic proteins in Arabidopsis and rice. <i>Plant Molecular Biology</i> , 2013, 83, 303-315.	3.9	233
71	The Transition from a Phytopathogenic Smut Ancestor to an Anamorphic Biocontrol Agent Deciphered by Comparative Whole-Genome Analysis. <i>Plant Cell</i> , 2013, 25, 1946-1959.	6.6	59
72	Increased Genomic Prediction Accuracy in Wheat Breeding Through Spatial Adjustment of Field Trial Data. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 2105-2114.	1.8	80

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73	Characterization of Populations of Turf-Type Perennial Ryegrass Recurrently Selected for Superior Freezing Tolerance. <i>Crop Science</i> , 2013, 53, 2225-2238.	1.8	9
74	An Improved Genotyping by Sequencing (GBS) Approach Offering Increased Versatility and Efficiency of SNP Discovery and Genotyping. <i>PLoS ONE</i> , 2013, 8, e54603.	2.5	406
75	A reproducible assay for measuring partial resistance to <i>Sclerotinia sclerotiorum</i> in soybean. <i>Canadian Journal of Plant Science</i> , 2012, 92, 279-288.	0.9	12
76	Discovery of a multigene family of aquaporin silicon transporters in the primitive plant <i>Equisetum arvense</i> . <i>Plant Journal</i> , 2012, 72, 320-330.	5.7	111
77	Cloning, functional characterization and heterologous expression of TaLsi1, a wheat silicon transporter gene. <i>Plant Molecular Biology</i> , 2012, 79, 35-46.	3.9	182
78	Seeds contribute strongly to the spread of the invasive genotype of the common reed (<i>Phragmites</i>) in Quebec, Canada. <i>Journal of Applied Ecology</i> , 2008, 45, 459-466.	2.4	69
79	Identification of QTLs Associated with Partial Resistance to White Mold in Soybean Using Field-Based Inoculation. <i>Crop Science</i> , 2010, 50, 969-979.	1.8	33
80	Comparison of genetic diversity between Canadian adapted genotypes and exotic germplasm of soybean. <i>Genome</i> , 2010, 53, 337-345.	2.0	5
81	Microsatellite Instability in <i>Arabidopsis</i> Increases with Plant Development. <i>Plant Physiology</i> , 2010, 154, 1415-1427.	4.8	51
82	The <i>Arabidopsis</i> DNA mismatch repair gene PMS1 restricts somatic recombination between homeologous sequences. <i>Plant Molecular Biology</i> , 2009, 69, 675-684.	3.9	31
83	Population structure and linkage disequilibrium in barley assessed by DArT markers. <i>Theoretical and Applied Genetics</i> , 2009, 119, 43-52.	3.6	58
84	Highways as corridors and habitats for the invasive common reed (<i>Phragmites australis</i>) in Quebec, Canada. <i>Journal of Applied Ecology</i> , 2008, 45, 459-466.	4.0	130
85	Recombinant Protein Secretion in <i>Pseudozyma flocculosa</i> and <i>Pseudozyma antarctica</i> with a Novel Signal Peptide. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 3158-3166.	1.3	5
86	Usefulness of Heterologous Promoters in the <i>Pseudozyma flocculosa</i> Gene Expression System. <i>Bioscience, Biotechnology and Biochemistry</i> , 2008, 72, 456-462.	1.3	11
87	An <i>Arabidopsis</i> MLH1 mutant exhibits reproductive defects and reveals a dual role for this gene in mitotic recombination. <i>Plant Journal</i> , 2007, 51, 431-440.	5.7	51
88	Expansion pathways of the exotic common reed (<i>Phragmites australis</i>): a historical and genetic analysis. <i>Diversity and Distributions</i> , 2007, 13, 430-437.	4.1	88
89	The <i>Pseudozyma flocculosa</i> actin promoter allows the strong expression of a recombinant protein in the <i>Pseudozyma</i> species. <i>Applied Microbiology and Biotechnology</i> , 2007, 74, 1300-1307.	3.6	12
90	Cloning of the glyceraldehyde-3-phosphate dehydrogenase gene from <i>Pseudozyma flocculosa</i> and functionality of its promoter in two <i>Pseudozyma</i> species. <i>Antonie Van Leeuwenhoek</i> , 2007, 92, 245-255.	1.7	10

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91	The impact of sequence divergence and DNA mismatch repair on homeologous recombination in Arabidopsis. Plant Journal, 2006, 45, 908-916.	5.7	99
92	The protective role of silicon in the Arabidopsis-powdery mildew pathosystem. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17554-17559.	7.1	303
93	A novel reporter for intrachromosomal homoeologous recombination in Arabidopsis thaliana. Plant Journal, 2004, 40, 1007-1015.	5.7	38
94	Insertional Mutagenesis of a Fungal Biocontrol Agent Led to Discovery of a Rare Cellobiose Lipid with Antifungal Activity. Applied and Environmental Microbiology, 2003, 69, 2595-2602.	3.1	64
95	Random Chromosome Segregation without Meiotic Arrest in Both Male and Female Meicytes of a <i>dmc1</i> Mutant of Arabidopsis. Plant Cell, 1999, 11, 1623-1634.	6.6	302
96	Increased Ac excision (<i>iae</i>): Arabidopsis thaliana mutations affecting Ac transposition. Plant Journal, 1997, 11, 901-919.	5.7	9
97	Inefficient and incorrect processing of the Ac transposase transcript in <i>iae1</i> and wild-type Arabidopsis thaliana. Plant Journal, 1997, 11, 921-931.	5.7	32
98	Visual markers for tomato derived from the anthocyanin biosynthetic pathway. Euphytica, 1994, 79, 163-167.	1.2	24
99	Pattern of somatic transposition in a high copy Ac tomato line.. Plant Journal, 1992, 2, 173-179.	5.7	38