

François Belzile

List of Publications by Year in descending order

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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	An Improved Genotyping by Sequencing (GBS) Approach Offering Increased Versatility and Efficiency of SNP Discovery and Genotyping. PLoS ONE, 2013, 8, e54603.	2.5	406
2	Identification of loci governing eight agronomic traits using a GBS GWAS approach and validation by QTL mapping in soya bean. Plant Biotechnology Journal, 2015, 13, 211-221.	8.3	340
3	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
4	Random Chromosome Segregation without Meiotic Arrest in Both Male and Female Meocytes of a <i>dmc1</i> Mutant of Arabidopsis. Plant Cell, 1999, 11, 1623-1634.	6.6	302
5	Identification and functional characterization of silicon transporters in soybean using comparative genomics of major intrinsic proteins in Arabidopsis and rice. Plant Molecular Biology, 2013, 83, 303-315.	3.9	233
6	Cloning, functional characterization and heterologous expression of TaLsi1, a wheat silicon transporter gene. Plant Molecular Biology, 2012, 79, 35-46.	3.9	182
7	Mapping and identification of a potential candidate gene for a novel maturity locus, E10, in soybean. Theoretical and Applied Genetics, 2017, 130, 377-390.	3.6	162
8	Genome Wide Association Mapping of <i>Sclerotinia sclerotiorum</i> Resistance in Soybean with a Genotyping-by-Sequencing Approach. Plant Genome, 2014, 7, plantgenome2013.10.0030.	2.8	135
9	Highways as corridors and habitats for the invasive common reed <i>Phragmites australis</i> in Quebec, Canada. Journal of Applied Ecology, 2008, 45, 459-466.	4.0	130
10	Discovery of a multigene family of aquaporin silicon transporters in the primitive plant <i>Equisetum arvense</i> . Plant Journal, 2012, 72, 320-330.	5.7	111
11	Genome-Wide SNP Calling from Genotyping by Sequencing (GBS) Data: A Comparison of Seven Pipelines and Two Sequencing Technologies. PLoS ONE, 2016, 11, e0161333.	2.5	109
12	The impact of sequence divergence and DNA mismatch repair on homeologous recombination in Arabidopsis. Plant Journal, 2006, 45, 908-916.	5.7	99
13	Fast-GBS: a new pipeline for the efficient and highly accurate calling of SNPs from genotyping-by-sequencing data. BMC Bioinformatics, 2017, 18, 5.	2.6	99
14	Expansion pathways of the exotic common reed (<i>Phragmites australis</i>): a historical and genetic analysis. Diversity and Distributions, 2007, 13, 430-437.	4.1	88
15	Increased Genomic Prediction Accuracy in Wheat Breeding Through Spatial Adjustment of Field Trial Data. G3: Genes, Genomes, Genetics, 2013, 3, 2105-2114.	1.8	80
16	Silicon protects soybean plants against <i>Phytophthora sojae</i> by interfering with effector-receptor expression. BMC Plant Biology, 2018, 18, 97.	3.6	80
17	Identification and characterization of silicon efflux transporters in horsetail (<i>Equisetum arvense</i>). Journal of Plant Physiology, 2016, 200, 82-89.	3.5	73
18	Seeds contribute strongly to the spread of the invasive genotype of the common reed (<i>Phragmites</i>) Tj ETQq0 0 0 rgBJ /Overlock 10 Tf 5	2.4	69

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19	Insertional Mutagenesis of a Fungal Biocontrol Agent Led to Discovery of a Rare Cellobiose Lipid with Antifungal Activity. <i>Applied and Environmental Microbiology</i> , 2003, 69, 2595-2602.	3.1	64
20	Efficient genome-wide genotyping strategies and data integration in crop plants. <i>Theoretical and Applied Genetics</i> , 2018, 131, 499-511.	3.6	62
21	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
22	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
23	Population structure and linkage disequilibrium in barley assessed by DArT markers. <i>Theoretical and Applied Genetics</i> , 2009, 119, 43-52.	3.6	58
24	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
25	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
26	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
27	Microsatellite Instability in <i>Arabidopsis</i> Increases with Plant Development. <i>Plant Physiology</i> , 2010, 154, 1415-1427.	4.8	51
28	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
29	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
30	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
31	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
32	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
33	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
34	Pattern of somatic transposition in a high copy Ac tomato line.. <i>Plant Journal</i> , 1992, 2, 173-179.	5.7	38
35	A novel reporter for intrachromosomal homoeologous recombination in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2004, 40, 1007-1015.	5.7	38
36	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

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37	Genome-wide association study for resistance to the southern root-knot nematode (<i>Meloidogyne</i>) Tj ETQq1 1 0.784314 rgBT/Overlo	2.1	35
38	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
39	Inefficient and incorrect processing of the <i>Ac</i> transposase transcript in <i>iae1</i> and wild-type <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 1997, 11, 921-931.	5.7	32
40	The <i>Arabidopsis</i> DNA mismatch repair gene <i>PMS1</i> restricts somatic recombination between homeologous sequences. <i>Plant Molecular Biology</i> , 2009, 69, 675-684.	3.9	31
41	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
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	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
44	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
45	Visual markers for tomato derived from the anthocyanin biosynthetic pathway. <i>Euphytica</i> , 1994, 79, 163-167.	1.2	24
46	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
47	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
48	Validation of Genotyping-By-Sequencing Analysis in Populations of Tetraploid Alfalfa by 454 Sequencing. <i>PLoS ONE</i> , 2015, 10, e0131918.	2.5	22
49	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
50	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
51	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
52	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
53	Molecular tools for detecting <i>Pdh1</i> can improve soybean breeding efficiency by reducing yield losses due to pod shatter. <i>Molecular Breeding</i> , 2019, 39, 1.	2.1	19
54	Fast-GBS v2.0: an analysis toolkit for genotyping-by-sequencing data. <i>Genome</i> , 2020, 63, 577-581.	2.0	19

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55	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
56	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
57	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
58	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
59	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
60	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
61	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
62	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
63	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
64	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
65	Time for a paradigm shift in the use of plant genetic resources. <i>Genome</i> , 2020, 63, 189-194.	2.0	13
66	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
67	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
68	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
69	Identification of loci controlling mineral element concentration in soybean seeds. <i>BMC Plant Biology</i> , 2020, 20, 419.	3.6	12
70	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
71	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
72	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

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73	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
74	NanoGBS: A Miniaturized Procedure for GBS Library Preparation. <i>Frontiers in Genetics</i> , 2020, 11, 67.	2.3	11
75	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
76	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
77	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
78	Haplotype diversity underlying quantitative traits in Canadian soybean breeding germplasm. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1967-1976.	3.6	10
79	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
80	Genome-Wide Association Study Statistical Models: A Review. <i>Methods in Molecular Biology</i> , 2022, , 43-62.	0.9	10
81	Increased Ac excision (iae): <i>Arabidopsis thaliana</i> mutations affecting Ac transposition. <i>Plant Journal</i> , 1997, 11, 901-919.	5.7	9
82	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
83	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
84	DepthFinder: a tool to determine the optimal read depth for reduced-representation sequencing. <i>Bioinformatics</i> , 2020, 36, 26-32.	4.1	9
85	Population structure of Nepali spring wheat (<i>Triticum aestivum</i> L.) germplasm. <i>BMC Plant Biology</i> , 2020, 20, 530.	3.6	9
86	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
87	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
88	Improvement of key agronomical traits in soybean through genomic prediction of superior crosses. <i>Crop Science</i> , 2021, 61, 3908-3918.	1.8	7
89	Genetic Analysis of High Protein Content in AC Proteus™ Related Soybean Populations Using SSR, SNP, DArT and DArTseq Markers. <i>Scientific Reports</i> , 2019, 9, 19657.	3.3	6
90	Accurate Imputation of Untyped Variants from Deep Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2243, 271-281.	0.9	6

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91	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	6
92	Recombinant Protein Secretion in <i>Pseudozyma flocculosa</i> and <i>Pseudozyma antarctica</i> with a Novel Signal Peptide. Bioscience, Biotechnology and Biochemistry, 2008, 72, 3158-3166.	1.3	5
93	Comparison of genetic diversity between Canadian adapted genotypes and exotic germplasm of soybean. Genome, 2010, 53, 337-345.	2.0	5
94	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. Plant Direct, 2020, 4, e00289.	1.9	5
95	QTL mapping uncovers a semi-dwarf 1 (<i>sdw1</i>) allele in the barley (<i>Hordeum vulgare</i>) ND23049 line. Genome, 2018, 61, 429-436.	2.0	4
96	Genome-wide association study to identify soybean stem pushing resistance and lodging resistance loci. Canadian Journal of Plant Science, 2021, 101, 663-670.	0.9	4
97	A high-resolution consensus linkage map for barley based on GBS-derived genotypes. Genome, 2022, 65, 83-94.	2.0	2
98	SRG extractor: a skinny reference genome approach for reduced-representation sequencing. Bioinformatics, 2019, 35, 3160-3162.	4.1	1
99	The SoyaGen Project: Putting Genomics to Work for Soybean Breeders. Frontiers in Plant Science, 2022, 13, 887553.	3.6	1