

Frank M You

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

3,698
citations

185998

28
h-index

138251

58
g-index

77
all docs

77
docs citations

77
times ranked

4178
citing authors

#	ARTICLE	IF	CITATIONS
1	Inheritance of marsh spot disease resistance in cranberry common bean (<i>Phaseolus vulgaris</i> L.). <i>Crop Journal</i> , 2022, 10, 456-467.	2.3	2
2	Designing Genomic Solutions to Enhance Abiotic Stress Resistance in Flax. , 2022, , 251-283.		2
3	Fine-mapping of a putative glutathione S-transferase (GST) gene responsible for yellow seed colour in flax (<i>Linum usitatissimum</i>). <i>BMC Research Notes</i> , 2022, 15, 72.	0.6	2
4	Insights into the Genetic Architecture and Genomic Prediction of Powdery Mildew Resistance in Flax (<i>Linum usitatissimum</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 4960.	1.8	12
5	Quantitative Trait Locus Mapping of Marsh Spot Disease Resistance in Cranberry Common Bean (<i>Phaseolus vulgaris</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 7639.	1.8	3
6	Loci harboring genes with important role in drought and related abiotic stress responses in flax revealed by multiple GWAS models. <i>Theoretical and Applied Genetics</i> , 2021, 134, 191-212.	1.8	23
7	Genome Assembly of the Canadian two-row Malting Barley cultivar AAC Synergy. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	6
8	<i>Aegilops tauschii</i> genome assembly Aet v5.0 features greater sequence contiguity and improved annotation. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	19
9	Genome-wide signatures in flax pinpoint to adaptive evolution along its ecological gradient. <i>Frontiers in Bioscience</i> , 2021, 26, 1559-1571.	0.8	4
10	Dominant inhibition of awn development by a putative zincâ€finger transcriptional repressor expressed at the <i>B1</i> locus in wheat. <i>New Phytologist</i> , 2020, 225, 340-355.	3.5	58
11	A phenylpropanoid diglyceride associates with the leaf rust resistance <i>Lr34res</i> gene in wheat. <i>Phytochemistry</i> , 2020, 178, 112456.	1.4	12
12	Identification of New Leaf Rust Resistance Loci in Wheat and Wild Relatives by Array-Based SNP Genotyping and Association Genetics. <i>Frontiers in Plant Science</i> , 2020, 11, 583738.	1.7	29
13	Genome-wide identification of ATP binding cassette (ABC) transporter and heavy metal associated (HMA) gene families in flax (<i>Linum usitatissimum</i> L.). <i>BMC Genomics</i> , 2020, 21, 722.	1.2	42
14	Evaluation of variant calling tools for large plant genome re-sequencing. <i>BMC Bioinformatics</i> , 2020, 21, 360.	1.2	27
15	Genomic Prediction Accuracy of Seven Breeding Selection Traits Improved by QTL Identification in Flax. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1577.	1.8	21
16	Genome-wide introgression from a bread wheatâ€™s <i>Lophopyrum elongatum</i> amphiploid into wheat. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1227-1241.	1.8	7
17	Drought response of flax accessions and identification of quantitative trait nucleotides (QTNs) governing agronomic and root traits by genome-wide association analysis. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	12
18	Mapping Quantitative Trait Loci onto Chromosome-Scale Pseudomolecules in Flax. <i>Methods and Protocols</i> , 2020, 3, 28.	0.9	25

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19	Evaluation of Genomic Prediction for Pasm Resistance in Flax. <i>International Journal of Molecular Sciences</i> , 2019, 20, 359.	1.8	45
20	A fine-scale genetic linkage map reveals genomic regions associated with economic traits in walnut (<i>Juglans regia</i>). <i>Plant Breeding</i> , 2019, 138, 635-646.	1.0	10
21	Sequencing a <i>Juglans regia</i> microcarpa hybrid yields high-quality genome assemblies of parental species. <i>Horticulture Research</i> , 2019, 6, 55.	2.9	67
22	The genetic structure of flax illustrates environmental and anthropogenic selections that gave rise to its eco-geographical adaptation. <i>Molecular Phylogenetics and Evolution</i> , 2019, 137, 22-32.	1.2	22
23	The Complex Genetic Architecture of Early Root and Shoot Traits in Flax Revealed by Genome-Wide Association Analyses. <i>Frontiers in Plant Science</i> , 2019, 10, 1483.	1.7	24
24	Genome-wide regulatory gene-derived SSRs reveal genetic differentiation and population structure in fiber flax genotypes. <i>Journal of Applied Genetics</i> , 2019, 60, 13-25.	1.0	15
25	Flax (<i>Linum usitatissimum</i> L.) <i>Genomics and Breeding.</i> , 2019, , 277-317.		3
26	Linum Genetic Markers, Maps, and QTL Discovery. <i>Plant Genetics and Genomics: Crops and Models</i> , 2019, , 97-117.	0.3	3
27	Chromosome-scale pseudomolecules refined by optical, physical and genetic maps in flax. <i>Plant Journal</i> , 2018, 95, 371-384.	2.8	119
28	Genome-Wide Association Analysis of Mucilage and Hull Content in Flax (<i>Linum usitatissimum</i> L.) Seeds. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2870.	1.8	42
29	Structural variation and rates of genome evolution in the grass family seen through comparison of sequences of genomes greatly differing in size. <i>Plant Journal</i> , 2018, 95, 487-503.	2.8	31
30	Genome-Wide Association Study and Selection Signatures Detect Genomic Regions Associated with Seed Yield and Oil Quality in Flax. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2303.	1.8	49
31	Rht23 (5Dq ²) likely encodes a Q homeologue with pleiotropic effects on plant height and spike compactness. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1825-1834.	1.8	27
32	Genome-Wide Association Studies for Pasm Resistance in Flax (<i>Linum usitatissimum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1982.	1.7	56
33	Patterns of SSR variation in bread wheat (<i>Triticum aestivum</i> L.) seeds under ex situ genebank storage and accelerated ageing. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 277-290.	0.8	12
34	Genome sequence of the progenitor of the wheat D genome <i>Aegilops tauschii</i> . <i>Nature</i> , 2017, 551, 498-502.	13.7	563
35	UGT74S1 is the key player in controlling secoisolariciresinol diglucoside (SDG) formation in flax. <i>BMC Plant Biology</i> , 2017, 17, 35.	1.6	18
36	Highly predictive SNP markers for efficient selection of the wheat leaf rust resistance gene Lr16. <i>BMC Plant Biology</i> , 2017, 17, 45.	1.6	53

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37	PIECE 2.0: an update for the plant gene structure comparison and evolution database. <i>Nucleic Acids Research</i> , 2017, 45, 1015-1020.	6.5	24
38	Solar Radiation-Associated Adaptive SNP Genetic Differentiation in Wild Emmer Wheat, <i>Triticum dicoccoides</i> . <i>Frontiers in Plant Science</i> , 2017, 8, 258.	1.7	12
39	Genetic Variability of 27 Traits in a Core Collection of Flax (<i>Linum usitatissimum</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1636.	1.7	56
40	RGAugury: a pipeline for genome-wide prediction of resistance gene analogs (RGAs) in plants. <i>BMC Genomics</i> , 2016, 17, 852.	1.2	162
41	Pseudogenes and Their Genome-Wide Prediction in Plants. <i>International Journal of Molecular Sciences</i> , 2016, 17, 1991.	1.8	34
42	Accuracy of genomic selection in biparental populations of flax (<i>Linum usitatissimum</i> L.). <i>Crop Journal</i> , 2016, 4, 290-303.	2.3	26
43	Genetic mapping of SrCad and SNP marker development for marker-assisted selection of Ug99 stem rust resistance in wheat. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1373-1382.	1.8	33
44	Genetics and mapping of seedling resistance to Ug99 stem rust in winter wheat cultivar Triumph 64 and differentiation of SrTmp, SrCad, and Sr42. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2171-2177.	1.8	24
45	Pedigrees and genetic base of flax cultivars registered in Canada. <i>Canadian Journal of Plant Science</i> , 2016, 96, 837-852.	0.3	22
46	Validation and diagnostic marker development for a genetic region associated with wheat yellow mosaic virus resistance. <i>Euphytica</i> , 2016, 211, 91-101.	0.6	6
47	A saturated SNP linkage map for the orange wheat blossom midge resistance gene Sm1. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1507-1517.	1.8	15
48	GSP: a web-based platform for designing genome-specific primers in polyploids. <i>Bioinformatics</i> , 2016, 32, 2382-2383.	1.8	30
49	Estimation of genetic parameters and their sampling variances for quantitative traits in the type 2 modified augmented design. <i>Crop Journal</i> , 2016, 4, 107-118.	2.3	17
50	Synteny analysis in Rosids with a walnut physical map reveals slow genome evolution in long-lived woody perennials. <i>BMC Genomics</i> , 2015, 16, 707.	1.2	83
51	Disease Resistance Gene Analogs (RGAs) in Plants. <i>International Journal of Molecular Sciences</i> , 2015, 16, 19248-19290.	1.8	234
52	Development of Microsatellite Markers in Tung Tree (<i>Vernicia fordii</i>) Using Cassava Genomic Sequences. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 893-904.	1.0	4
53	QTL for fatty acid composition and yield in linseed (<i>Linum usitatissimum</i> L.). <i>Theoretical and Applied Genetics</i> , 2015, 128, 965-984.	1.8	47
54	Comparative analysis of codon usage patterns in chloroplast genomes of the Asteraceae family. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 828-840.	1.0	61

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55	Computational Identification and Comparative Analysis of miRNAs in Wheat Group 7 Chromosomes. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 487-500.	1.0	10
56	Genetic variation of six desaturase genes in flax and their impact on fatty acid composition. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2627-2641.	1.8	53
57	<i>Aegilops tauschii</i> single nucleotide polymorphisms shed light on the origins of wheat D genome genetic diversity and pinpoint the geographic origin of hexaploid wheat. <i>New Phytologist</i> , 2013, 198, 925-937.	3.5	243
58	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7940-7945.	3.3	214
59	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. <i>BMC Genomics</i> , 2012, 13, 354.	1.2	47
60	Genome wide SNP discovery in flax through next generation sequencing of reduced representation libraries. <i>BMC Genomics</i> , 2012, 13, 684.	1.2	82
61	Mapping and validation of quantitative trait loci associated with wheat yellow mosaic bymovirus resistance in bread wheat. <i>Theoretical and Applied Genetics</i> , 2012, 124, 177-188.	1.8	28
62	Characterizing the walnut genome through analyses of BAC end sequences. <i>Plant Molecular Biology</i> , 2012, 78, 95-107.	2.0	27
63	Annotation-based genome-wide SNP discovery in the large and complex <i>Aegilops tauschii</i> genome using next-generation sequencing without a reference genome sequence. <i>BMC Genomics</i> , 2011, 12, 59.	1.2	146
64	A new implementation of high-throughput five-dimensional clone pooling strategy for BAC library screening. <i>BMC Genomics</i> , 2010, 11, 692.	1.2	10
65	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	1.2	189
66	A BAC-based physical map of <i>Brachypodium distachyon</i> and its comparative analysis with rice and wheat. <i>BMC Genomics</i> , 2009, 10, 496.	1.2	42
67	High-throughput fingerprinting of bacterial artificial chromosomes using the snapshot labeling kit and sizing of restriction fragments by capillary electrophoresis. <i>Genomics</i> , 2003, 82, 378-389.	1.3	242