

Frédéric Marsolais

List of Publications by Year in descending order

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70
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#	ARTICLE	IF	CITATIONS
1	<i>Pectin acetyltransferase 8</i> influences pectin acetylation in the seed coat, seed imbibition, and dormancy in common bean (<sc><i>Phaseolus vulgaris</i></sc> L.). , 2022, 4, e130.		4
2	Common bean (<sc><i>Phaseolus vulgaris</i></sc> L.) with increased cysteine and methionine concentration. , 2021, 3, e103.		7
3	LEAFY COTYLEDON1 expression in the endosperm enables embryo maturation in Arabidopsis. Nature Communications, 2021, 12, 3963.	5.8	24
4	Patterns of Genetic Variation in a Soybean Germplasm Collection as Characterized with Genotyping-by-Sequencing. Plants, 2021, 10, 1611.	1.6	6
5	Development of a Csy4-processed guide RNA delivery system with soybean-infecting virus ALSV for genome editing. BMC Plant Biology, 2021, 21, 419.	1.6	16
6	Evidence that class I glutamine amidotransferase, GAT1_2.1, acts as a glutaminase in roots of Arabidopsis thaliana. Plant Science, 2021, 312, 111033.	1.7	7
7	Evaluation of beneficial and inhibitory effects of nitrate on nodulation and nitrogen fixation in common bean (Phaseolus vulgaris). , 2020, 2, e45.		15
8	Label-free quantitative proteomic analysis of alfalfa in response to microRNA156 under high temperature. BMC Genomics, 2020, 21, 758.	1.2	8
9	Effects of Nitrogen Application on Nitrogen Fixation in Common Bean Production. Frontiers in Plant Science, 2020, 11, 1172.	1.7	49
10	Postharvest seed coat darkening in pinto bean (<i>Phaseolus vulgaris</i>) is regulated by <i>P^{sd}</i>, an allele of the basic helixâ€loopâ€helix transcription factor <i>P</i>. Plants People Planet, 2020, 2, 663-677.	1.6	13
11	Agronomic Performance and Nitrogen Fixation of Heirloom and Conventional Dry Bean Varieties Under Low-Nitrogen Field Conditions. Frontiers in Plant Science, 2019, 10, 952.	1.7	39
12	Distribution and possible biosynthetic pathway of non-protein sulfur amino acids in legumes. Journal of Experimental Botany, 2019, 70, 4115-4121.	2.4	6
13	RNA polymerase II-independent recruitment of SPT6L at transcription start sites in Arabidopsis. Nucleic Acids Research, 2019, 47, 6714-6725.	6.5	24
14	Common Bean (Phaseolus vulgaris L.) Accumulates Most S-Methylcysteine as Its $\hat{3}$ -Glutamyl Dipeptide. Plants, 2019, 8, 126.	1.6	6
15	Deciphering <i>S</i>-methylcysteine biosynthesis in common bean by isotopic tracking with mass spectrometry. Plant Journal, 2019, 100, 176-186.	2.8	4
16	Agrobacterium â€mediated inoculation of asymptomatic Apple latent spherical virus as gene silencing vector in pea (Pisum sativum L.). , 2019, 1, e14.		3
17	Structural basis of potassium activation in plant asparaginases. FEBS Journal, 2018, 285, 1528-1539.	2.2	14
18	Slow darkening of pinto bean seed coat is associated with significant metabolite and transcript differences related to proanthocyanidin biosynthesis. BMC Genomics, 2018, 19, 260.	1.2	16

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19	Cytosolic acetyl-CoA promotes histone acetylation predominantly at H3K27 in Arabidopsis. <i>Nature Plants</i> , 2017, 3, 814-824.	4.7	85
20	Advances in Asparagine Metabolism. <i>Progress in Botany Fortschritte Der Botanik</i> , 2017, , 49-74.	0.1	5
21	Comparison of Gene Families: Seed Storage and Other Seed Proteins. <i>Compendium of Plant Genomes</i> , 2017, , 201-217.	0.3	9
22	Combining Isotope Labelling with High Resolution Liquid Chromatography-Tandem Mass Spectrometry to Study Sulfur Amino Acid Metabolism in Seeds of Common Bean (<i>Phaseolus vulgaris</i>). <i>Proceedings of the International Plant Sulfur Workshop</i> , 2017, , 135-144.	0.1	2
23	Prospects: The Importance of Common Bean as a Model Crop. <i>Compendium of Plant Genomes</i> , 2017, , 289-295.	0.3	1
24	Nitric Oxide and Reactive Oxygen Species Mediate Metabolic Changes in Barley Seed Embryo during Germination. <i>Frontiers in Plant Science</i> , 2016, 7, 138.	1.7	67
25	Genomic Analysis of Storage Protein Deficiency in Genetically Related Lines of Common Bean (<i>Phaseolus vulgaris</i>). <i>Frontiers in Plant Science</i> , 2016, 7, 389.	1.7	10
26	Higher endogenous methionine in transgenic Arabidopsis seeds affects the composition of storage proteins and lipids. <i>Amino Acids</i> , 2016, 48, 1413-1422.	1.2	19
27	Physicochemical characterization of a navy bean (<i>Phaseolus vulgaris</i>) protein fraction produced using a solvent-free method. <i>Food Chemistry</i> , 2016, 208, 35-41.	4.2	53
28	Characterization of aromatic aminotransferases from <i>Ephedra sinica</i> Stapf. <i>Amino Acids</i> , 2016, 48, 1209-1220.	1.2	16
29	Glyoxylate cycle and metabolism of organic acids in the scutellum of barley seeds during germination. <i>Plant Science</i> , 2016, 248, 37-44.	1.7	33
30	Soybean seeds overexpressing asparaginase exhibit reduced nitrogen concentration. <i>Physiologia Plantarum</i> , 2015, 155, 126-137.	2.6	7
31	Differential response to sulfur nutrition of two common bean genotypes differing in storage protein composition. <i>Frontiers in Plant Science</i> , 2015, 6, 92.	1.7	26
32	Transcriptome Profiling of Khat (<i>Catha edulis</i>) and <i>Ephedra sinica</i> Reveals Gene Candidates Potentially Involved in Amphetamine-Type Alkaloid Biosynthesis. <i>PLoS ONE</i> , 2015, 10, e0119701.	1.1	25
33	Determining Sulfur-Limiting Conditions for Studies of Seed Composition in Common Bean (<i>Phaseolus</i>) Tj ETQq1 1 0,784314 1gBT /Over	0.1	1
34	Na ⁺ /K ⁺ exchange switches the catalytic apparatus of potassium-dependent plant asparaginase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1854-1872.	2.5	23
35	Genome-wide single nucleotide polymorphism and Insertion-Deletion discovery through next-generation sequencing of reduced representation libraries in common bean. <i>Molecular Breeding</i> , 2014, 33, 769-778.	1.0	29
36	Identification and characterization of omega-amidase as an enzyme metabolically linked to asparagine transamination in Arabidopsis. <i>Phytochemistry</i> , 2014, 99, 36-43.	1.4	28

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37	Genetic transformation and full recovery of alfalfa plants via secondary somatic embryogenesis. In <i>In Vitro Cellular and Developmental Biology - Plant</i> , 2013, 49, 17-23.	0.9	16
38	Characterization of Arabidopsis serine:glyoxylate aminotransferase, AGT1, as an asparagine aminotransferase. <i>Phytochemistry</i> , 2013, 85, 30-35.	1.4	51
39	Transcriptome Profiling Identifies Candidate Genes Associated with the Accumulation of Distinct Sulfur ¹³ -Glutamyl Dipeptides in Phaseolus vulgaris and Vigna mungo Seeds. <i>Frontiers in Plant Science</i> , 2013, 4, 60.	1.7	21
40	Characterization of a Cruciferin Deficient Mutant of Arabidopsis and Its Utility for Overexpression of Foreign Proteins in Plants. <i>PLoS ONE</i> , 2013, 8, e64980.	1.1	20
41	Relationship between asparagine metabolism and protein concentration in soybean seed. <i>Journal of Experimental Botany</i> , 2012, 63, 3173-3184.	2.4	64
42	Transcripts of sulphur metabolic genes are co-ordinately regulated in developing seeds of common bean lacking phaseolin and major lectins. <i>Journal of Experimental Botany</i> , 2012, 63, 6283-6295.	2.4	25
43	Benzaldehyde is a precursor of phenylpropylamino alkaloids as revealed by targeted metabolic profiling and comparative biochemical analyses in Ephedra spp.. <i>Phytochemistry</i> , 2012, 81, 71-79.	1.4	20
44	Biosynthesis of amphetamine analogs in plants. <i>Trends in Plant Science</i> , 2012, 17, 404-412.	4.3	30
45	Transcriptomics of Legume Seed: Soybean a Model Grain Legume. , 2012, , 129-142.		2
46	Role of asparaginase variable loop at the carboxyl terminal of the alpha subunit in the determination of substrate preference in plants. <i>Planta</i> , 2012, 235, 1013-1022.	1.6	21
47	Arabidopsis mutants lacking asparaginases develop normally but exhibit enhanced root inhibition by exogenous asparagine. <i>Amino Acids</i> , 2012, 42, 2307-2318.	1.2	33
48	Expressed sequence tag analysis of khat (Catha edulis) provides a putative molecular biochemical basis for the biosynthesis of phenylpropylamino alkaloids. <i>Genetics and Molecular Biology</i> , 2011, 34, 640-646.	0.6	25
49	Analysis of common bean expressed sequence tags identifies sulfur metabolic pathways active in seed and sulfur-rich proteins highly expressed in the absence of phaseolin and major lectins. <i>BMC Genomics</i> , 2011, 12, 268.	1.2	33
50	Proteomic analysis of common bean seed with storage protein deficiency reveals up-regulation of sulfur-rich proteins and starch and raffinose metabolic enzymes, and down-regulation of the secretory pathway. <i>Journal of Proteomics</i> , 2010, 73, 1587-1600.	1.2	63
51	A single-repeat MYB transcription factor, GmMYB176, regulates CHS8 gene expression and affects isoflavonoid biosynthesis in soybean. <i>Plant Journal</i> , 2010, 62, no-no.	2.8	129
52	Functional Genomicsâ€™ Transcriptomics in Soybean. , 2010, , 199-222.		0
53	Seed Storage Protein Deficiency Improves Sulfur Amino Acid Content in Common Bean (<i>Phaseolus</i>) Tj ETQq1 1 0.784314 rgBT /Over and Food Chemistry, 2008, 56, 5647-5654.	2.4	53
54	Sulfotransferases from Plants, Algae and Phototrophic Bacteria. <i>Advances in Photosynthesis and Respiration</i> , 2008, , 111-130.	1.0	12

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55	Molecular and biochemical characterization of two brassinosteroid sulfotransferases from Arabidopsis, AtST4a (At2g14920) and AtST1 (At2g03760). <i>Planta</i> , 2007, 225, 1233-1244.	1.6	85
56	Co-occurrence of both l-asparaginase subtypes in Arabidopsis: At3g16150 encodes a K ⁺ -dependent l-asparaginase. <i>Planta</i> , 2006, 224, 668-679.	1.6	74
57	Free amino acid profiles suggest a possible role for asparagine in the control of storage-product accumulation in developing seeds of low- and high-protein soybean lines. <i>Journal of Experimental Botany</i> , 2005, 56, 1951-1963.	2.4	83
58	Molecular and biochemical characterization of BNST4, an ethanol-inducible steroid sulfotransferase from <i>Brassica napus</i> , and regulation of BNST genes by chemical stress and during development. <i>Plant Science</i> , 2004, 166, 1359-1370.	1.7	30
59	Plant Soluble Sulfotransferases: Structural and Functional Similarity with Mammalian Enzymes. <i>Recent Advances in Phytochemistry</i> , 2000, 34, 433-456.	0.5	16
60	Inactivation of Brassinosteroid Biological Activity by a Salicylate-inducible Steroid Sulfotransferase from <i>Brassica napus</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 20925-20930.	1.6	114
61	³ â€-Phosphoadenosine 5â€-Phosphosulfate Binding Site of Flavonol 3-Sulfotransferase Studied by Affinity Chromatography and ³¹ P NMRâ€. <i>Biochemistry</i> , 1999, 38, 4066-4071.	1.2	22
62	Recent developments in the study of the structure-function relationship of flavonol sulfotransferases. <i>Chemico-Biological Interactions</i> , 1998, 109, 117-122.	1.7	15
63	Biochemistry and molecular biology of plant sulfotransferases. <i>FASEB Journal</i> , 1997, 11, 517-525.	0.2	105
64	Mutational Analysis of Domain II of Flavonol 3-Sulfotransferase. <i>FEBS Journal</i> , 1997, 247, 1056-1062.	0.2	25
65	Chimeric Flavonol Sulfotransferases Define a Domain Responsible for Substrate and Position Specificities. <i>Journal of Biological Chemistry</i> , 1995, 270, 12498-12502.	1.6	44
66	Identification of Amino Acid Residues Critical for Catalysis and Cosubstrate Binding in the Flavonol 3-Sulfotransferase. <i>Journal of Biological Chemistry</i> , 1995, 270, 30458-30463.	1.6	67
67	AAC Argosy navy dry bean. <i>Canadian Journal of Plant Science</i> , 0, , .	0.3	0
68	AAC Shock navy dry bean. <i>Canadian Journal of Plant Science</i> , 0, , .	0.3	0
69	Development of germplasm lines of edible bean with improved cysteine and methionine concentration. , 0, , .		0
70	A fast and efficient method to introduce apple latent spherical virus to legume plants via <sc>Agrobacterium rhizogenes</sc>-mediated transformation of hairy roots. , 0, , .		0