

Supplementary Materials

Mass Spectrometry-Based Identification of Bioactive Bee Pollen Proteins: Evaluation of Allergy Risk After Bee Pollen Supplementation

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Table S2. Results of BLAST analysis including the highest sequence alignments to characterised proteins. [1] - *Vitis vinifera*; [2] - *Arabidopsis lyrata* subsp. *lyrata*; [3] - *Glycine max*; [4] - *Brachypodium distachyon*; [5] - *Arabidopsis thaliana*; [6] - *Brassica rapa*; [7] - *Zea mays*; [8] - *Solanum tuberosum*; [9] - *Vitis riparia*; [10] - *Capsella rubella*; [11] - *Oryza sativa Japonica Group*; [12] - *Glycine soja*; [13] - *Solanum verrucosum*.

Accession	Protein Name	Significant Alignment Sequence	Query Coverage	Percent Identity	E-Value
gi 14778089 8	Hypothetical protein VITISV_007504 [1]	polyprotein [1]	57%	79%	0.0
gi 14781560 9	hypothetical protein VITISV_036160 [1]	PREDICTED: UDP-arabinopyranose mutase 3 [1]	90%	100%	0.0
gi 14782110 7	hypothetical protein VITISV_018473 [1]	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase [9]	100%	95%	0.0
gi 29779604 9	hypothetical protein ARALYDRAFT_495305 [2]	actin-depolymerizing factor 12 [10]	100%	100%	2 x 10 ⁻⁹⁶
gi 29780493 2	hypothetical protein ARALYDRAFT_915516 [2]	adenosylhomocysteinase 1 [2]	100%	100%	0.0
gi 29780582 2	hypothetical protein ARALYDRAFT_916391 [2]	UDP-glucose 6-dehydrogenase 4 [2]	100%	100%	0.0
gi 29781168 9	hypothetical protein ARALYDRAFT_488394 [2]	UDP-glucose 6-dehydrogenase 3 [2]	100%	100%	0.0
gi 29781213 9	hypothetical protein ARALYDRAFT_488852 [2]	aldehyde oxidase GLOX1 [2]	100%	100%	0.0
gi 29782002 0	hypothetical protein ARALYDRAFT_906673 [2]	fructose-bisphosphate aldolase 8, cytosolic [2]	100%	100%	0.0
gi 29782712 5	hypothetical protein ARALYDRAFT_482625 [2]	fructose-bisphosphate aldolase 6, cytosolic [2]	100%	100%	0.0
gi 29782923 0	hypothetical protein ARALYDRAFT_478006 [2]	peroxisomal fatty acid beta-oxidation multifunctional protein MFP2 isoform X2 [2]	100%	100%	0.0
gi 29783126 4	hypothetical protein ARALYDRAFT_898993 [2]	late embryogenesis abundant protein 1 [2]	100%	95%	2 x 10 ⁻⁵²
gi 29783283 6	hypothetical protein ARALYDRAFT_896165 [2]	UDP-glucose 6-dehydrogenase 3 [2]	100%	100%	0.0

gi 29783357 4	hypothetical protein ARALYDRAFT_478121 [2]	polygalacturonase isoform X1 [2]	100%	100%	0.0
gi 29783416 4	hypothetical protein ARALYDRAFT_478720 [2]	L-ascorbate oxidase homolog [2]	100%	100%	0.0
gi 29783961 3	hypothetical protein ARALYDRAFT_476916 [2]	protein disulfide isomerase-like 1-2 [2]	97%	100%	0.0
gi 29784141 1	hypothetical protein ARALYDRAFT_475824 [2]	aldehyde oxidase GLOX1 [2]	100%	97%	0.0
gi 35172069 7	uncharacterized protein LOC100499870 [3]	NAD(P)H dehydrogenase (quinone) FQR1-like isoform 1 [3]	100%	100%	1×10^{-133}
gi 35657448 9	PREDICTED: uncharacterized protein LOC100783153 [3]	mediator of DNA damage checkpoint protein 1 isoform X2 [3]	77%	96%	0.0
gi 35711739 9	PREDICTED: uncharacterized protein LOC100827223 [4]	hapless 2 isoform X2 [11]	100%	64%	6×10^{-54}
gi 36380714 0	uncharacterized protein LOC100795446 [3]	Fructose-bisphosphate aldolase 6, cytosolic-like [3]	100%	100%	0.0
gi 11683134 5	unknown [5]	pfkB-like carbohydrate kinase family protein [5]	99%	100%	0.0
gi 11972082 2	unknown [6]	late embryogenesis abundant protein 2 [6]	100%	100%	5×10^{-71}
gi 23801518 6	unknown [7]	glyceraldehyde-3-phosphate dehydrogenase 1, cytosolic isoform X2 [7]	100%	100%	0.0
gi 25562903 1	unknown [3]	Monodehydroascorbate reductase isoform B [12]	100%	100%	3×10^{-120}
gi 25563873 3	unknown [3]	UDP-glucose 6-dehydrogenase 1 [3]	100%	100%	0.0
gi 25563899 1	unknown [3]	probable UDP-arabinopyranose mutase 1 [3]	98%	100%	0.0
gi 77999255	unknown [8]	fructose-bisphosphate aldolase 6, cytosolic [13]	100%	100%	0.0