

Supporting Information

Spatial Protein Expression of *Panax Ginseng* by In-depth Proteomic Analysis for Ginsenoside Biosynthesis and Transportation

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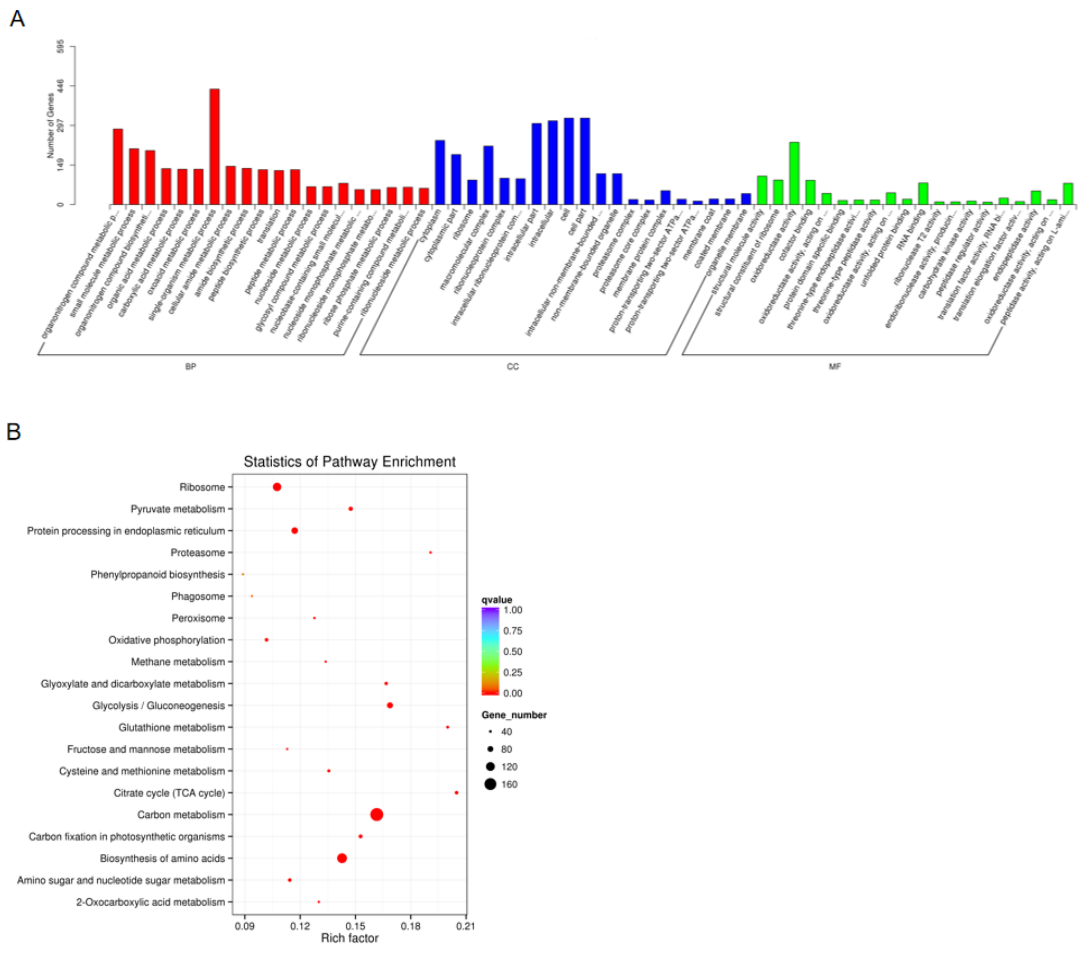


Figure S1. GO (A) and KEGG (B) analysis of commonly contained proteins.

Table S1. Comparison of sample preparation protocols for ginseng cauline leaf and root.

	No.	Lysis buffer	Depletion method	Number of identified proteins
cauline leaf	1	GdnHCl Lysate	Methanol-chloroform precipitation	1366
	2	GdnHCl Lysate	N/A	1019
	3	Tris-HCl Lysate	Acetone precipitation	529
	4	Tris-HCl Lysate	N/A	361
Root	5	GdnHCl Lysate	N/A	929
	6	Tris-HCl Lysate	N/A	439

Table S2. The top20 of ginseng cauline leaf protein based on the abundance of MS analysis.

protein name	Coverage [%]	Peptides	PSMs	Molecular function	Biological process
Ribulose biphosphate carboxylase large chain	33	16	81	Catalysis of the reaction: D-ribulose-1,5-biphosphate + CO ₂ + H ₂ O = 2,3-phospho-D-glycerate	incorporate carbon into organic compounds
Ribulose biphosphate carboxylase large chain (Fragment)	29	11	48	Catalysis of the reaction: D-ribulose-1,5-biphosphate + CO ₂ + H ₂ O = 2,3-phospho-D-glycerate	incorporate carbon into organic compounds
Ribonuclease-like storage protein	58	10	42	Interacting selectively and non-covalently with RNA molecule; Catalysis of the two-stage endonucleolytic cleavage	
ATP synthase subunit β, chloroplastic	43	16	34	Interacting selectively and non-covalently with ATP, ADP + H ₂ O + phosphate + H ⁺ (in) = ATP + H ⁺ (out), by a rotational mechanism	result in the formation of ATP;The directed movement of a proton across a membrane
ATP synthase subunit β, chloroplastic	55	15	34	Interacting selectively and non-covalently with ATP	result in the formation of ATP;The directed movement of a proton across a membrane
Catalase	24	19	34	Catalysis of the reaction: 2 hydrogen peroxide = O ₂ + 2 H ₂ O	Any process that results in a change in state or activity of a cell or an organism; A metabolic process that results in electrons transfer
Ribulose biphosphate carboxylase/oxygenase activase 1	36	15	33	Interacting selectively and non-covalently with ATP	
ATP synthase subunit β, mitochondrial	42	17	31	Interacting selectively and non-covalently with ATP; ADP + H ₂ O + phosphate + H ⁺ (in) = ATP + H ⁺ (out), by a rotational mechanism	result in the formation of ATP;The directed movement of a proton across a membrane
ATP synthase subunit β, mitochondrial	43	17	30	Interacting selectively and non-covalently with ATP; ADP + H ₂ O + phosphate + H ⁺ (in) = ATP + H ⁺ (out), by a rotational mechanism	result in the formation of ATP;The directed movement of a proton across a membrane
Glyceraldehyde-3-phosphate dehydrogenase GAPB, chloroplastic	25	14	30	Interacting selectively and non-covalently with nicotinamide adenine dinucleotide; Catalysis of an oxidation-reduction (redox) reaction	The chemical reactions and pathways involving glucose; A metabolic process that results in electrons transfer
Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	30	13	29	Interacting selectively and non-covalently with nicotinamide adenine dinucleotide; Catalysis of an oxidation-reduction (redox) reaction	The chemical reactions and pathways involving glucose; A metabolic process that results in electrons transfer
Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	31	13	29	Interacting selectively and non-covalently with nicotinamide adenine dinucleotide; Catalysis of an oxidation-reduction (redox) reaction	The chemical reactions and pathways involving glucose; A metabolic process that results in electrons transfer
Catalase isozyme 2	34	15	28	Catalysis of the reaction: 2 hydrogen peroxide = O ₂ + 2 H ₂ O	Any process that results in a change in state or activity of a cell or an organism; A metabolic process that results in electrons transfer
Glycine dehydrogenase (decarboxylating) 1, mitochondrial	29	20	27	Catalysis of the reaction: glycine + lipoylprotein = S-aminomethylidihydrolypoylprotein + CO ₂	The chemical reactions and pathways resulting in the breakdown of glycine, aminoethanoic acid; A metabolic process that results in electrons transfer
Heat shock cognate 70 kDa protein	25	16	26		
ATP-dependent Clp protease					
ATP-binding subunit ClpA homolog CD4B, chloroplastic	26	21	25	Interacting selectively and non-covalently with ATP, and any protein or protein complex	The chemical reactions and pathways involving a protein, includes protein modification.
Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	29	9	23	Catalysis of an oxidation-reduction (redox) reaction	A metabolic process that results in electrons transfer
Serine hydroxymethyltransferase 1, mitochondrial	46	19	23	Catalysis of the reaction: 5,10-methylenetetrahydrofolate + glycine + H ₂ O = tetrahydrofolate + L-serine	one-carbon (C1) units are transferred between tetrahydrofolate molecules, to synthesise other tetrahydrofolate molecules
Chaperonin 60 subunit β 2, chloroplastic	37	19	22	Interacting selectively and non-covalently with ATP	restores the biological activity of an unfolded or misfolded protein.
Serine hydroxymethyltransferase, mitochondrial	46	19	22	Catalysis of the reaction: 5,10-methylenetetrahydrofolate + glycine + H ₂ O = tetrahydrofolate + L-serine	one-carbon (C1) units are transferred between tetrahydrofolate molecules, to synthesise other tetrahydrofolate molecules

Table S3. The top20 ginseng root proteins based on the abundance by MS analysis.

protein name	Coverage [%]	Peptides	PSMs	Molecular function	Biological process
Ribonuclease-like storage protein	61	22	178	Interacting selectively and non-covalently with RNA molecule; Catalysis of the two-stage endonucleolytic cleavage	
Ribonuclease-like storage protein	63	23	167	Interacting selectively and non-covalently with RNA molecule; Catalysis of the two-stage endonucleolytic cleavage	
Ribonuclease-like storage protein	76	19	166	Interacting selectively and non-covalently with RNA molecule; Catalysis of the two-stage endonucleolytic cleavage	
Ribonuclease-like storage protein	58	19	157	Interacting selectively and non-covalently with RNA molecule; Catalysis of the two-stage endonucleolytic cleavage	
β -amylase	27	24	108	Catalysis of the reaction: (1,4-alpha-D-glucosyl)(n+1) + H ₂ O = (1,4-alpha-D-glucosyl)(n-1) + alpha-maltose	The chemical reactions and pathways resulting in the breakdown of a polysaccharide
Heat shock cognate 70 kDa protein	35	28	53		
Ribonuclease-like storage protein	60	27	40	Interacting selectively and non-covalently with RNA molecule; Catalysis of the two-stage endonucleolytic cleavage	
Heat shock cognate 70 kDa protein	28	19	37		
α -1,4 glucan phosphorylase L-1 isozyme, chloroplastic/amyloplastic	35	24	35	Catalysis of the reaction: glycogen + phosphate = maltodextrin + alpha-D-glucose 1-phosphate	The chemical reactions and pathways involving carbohydrates
Heat shock cognate 70 kDa protein 2 Probable mediator of RNA polymerase II transcription subunit 37c	26	19	35		
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	28	26	34	Catalysis of the reaction: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = L-methionine + tetrahydropteroyltri-L-glutamate; Interacting selectively and non-covalently with zinc (Zn) ions.	The chemical reactions and pathways resulting in the formation of methionine
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	28	23	33	Catalysis of the reaction: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = L-methionine + tetrahydropteroyltri-L-glutamate; Interacting selectively and non-covalently with zinc (Zn) ions.	The chemical reactions and pathways resulting in the formation of methionine
ATP synthase subunit β , mitochondrial	45	18	32	Interacting selectively and non-covalently with ATP; ADP + H ₂ O + phosphate + H ⁺ (in) = ATP + H ⁺ (out), by a rotational mechanism	result in the formation of ATP; The directed movement of a proton across a membrane
Enolase 2	52	22	32	Catalysis of the reaction: 2-phospho-D-glycerate = phosphoenolpyruvate + H ₂ O; Interacting selectively and non-covalently with any metal ion.	The chemical reactions and pathways resulting in the breakdown of a carbohydrate into pyruvate
1,4-alpha-glucan-branching enzyme	32	22	31	Catalysis of the hydrolysis of any O-glycosyl bond	The chemical reactions and pathways involving carbohydrates, and result in the formation of glycogen
Enolase 2	53	22	31	Catalysis of the reaction: 2-phospho-D-glycerate = phosphoenolpyruvate + H ₂ O; Interacting selectively and non-covalently with any metal ion.	The chemical reactions and pathways resulting in the breakdown of a carbohydrate into pyruvate
Fructose-bisphosphate aldolase 6, cytosolic	58	21	31	Catalysis of the reaction: D-fructose 1,6-bisphosphate = glyceraldehyde 3-phosphate + D-glyceraldehyde-3-phosphate	The chemical reactions and pathways to catalysis glycolysis resulting in the breakdown of a carbohydrate into pyruvate
ATP synthase subunit β , mitochondrial	44	18	30	Interacting selectively and non-covalently with ATP; ADP + H ₂ O + phosphate + H ⁺ (in) = ATP + H ⁺ (out), by a rotational mechanism	result in the formation of ATP; The directed movement of a proton across a membrane
Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	64	14	29	Catalysis of an oxidation-reduction (redox) reaction	A metabolic process that results in electrons transfer

Table S4. The UGTs and CYPs identified from ginseng cauline leaf and root.

Gene ID	Swissprot description	leaf	root		Gene ID	Swissprot description	leaf	root	
PG08475	7-deoxygluconate glucosyltransferase OS = periwinkle OX = 4058 GN = UGT709C2 PE = 1 SV = 1	Y	N	UGT70	PG15945	UDP-glycosyltransferase 76B1 OS = Arabidopsis OX = 3702 GN = UGT76B1 PE = 2 SV = 1	Y	N	UGT76
PG36439	7-deoxygluconate glucosyltransferase OS = periwinkle OX = 4058 GN = UGT709C2 PE = 1 SV = 1	Y	N	UGT70	PG00517	Kaempferol 3-O- β -D-galactosyltransferase OS = Petunia OX = 4102 PE = 1 SV = 1	Y	N	UGT78
PG23742	UDP-glycosyltransferase 71E1 OS =	Y	N	UGT71	PG00083	UDP-glycosyltransferase 79B30 OS =	Y	N	UGT79

	Stevia rebaudiana OX = 55670 GN = UGT71E1 PE = 2 SV = 1					soybean maximum OX = 3847 GN = FG3 PE = 1 SV = 2			
PG30324	UDP-glucoside flavonoid 3-O-glucosyltransferase 6 OS = strawberry (Fragariaananassa) OX = 3747 GN = GT6 PE = 1 SV = 1	Y	Y	UGT71	PG03287	UDP-glycosyltransferase 84B1 OS = Arabidopsis OX = 3702 GN = UGT84B1 PE = 2 SV = 1	Y	N	UGT84
PG34795	UDP-glucoside flavonoid 3-O-glucosyltransferase 6 OS = strawberry (Fragariaananassa) OX = 3747 GN = GT6 PE = 1 SV = 1	Y	Y	UGT71	PG34278	Linamarin synthase 1 OS = Manihotesculenta OX = 3983 GN = UGT85K4 PE = 1 SV = 1	Y	N	UGT85
PG05151	UDP-glucoside flavonoid 3-O-glucosyltransferase 6 OS = strawberry (Fragariaananassa) OX = 3747 GN = GT6 PE = 1 SV = 1	N	Y	UGT71	PG19859	Linamarin synthase 2 OS = Manihotesculenta OX = 3983 GN = UGT85K5 PE = 1 SV = 1	Y	N	UGT85
PG34796	UDP-glucoside flavonoid 3-O-glucosyltransferase 6 OS = strawberry (Fragariaananassa) OX = 3747 GN = GT6 PE = 1 SV = 1	Y	N	UGT71	PG18416	UDP-glycosyltransferase 88A1 OS = Arabidopsis OX = 3702 GN = UGT88A1 PE = 2 SV = 1	N	Y	UGT88
PG21124	Hydroquinone glucosyltransferase OS = Rauwolfiaserpentina OX = 4060 GN = AS PE = 1 SV = 1	Y	Y	UGT72	PG02224	UDP-glycosyltransferase 89B2 OS = Stevia rebaudiana OX = 55670 GN = UGT89B2 PE = 2 SV = 1	Y	N	UGT89
PG30450	Hydroquinone glucosyltransferase OS = Rauwolfiaserpentina OX = 4060 GN = AS PE = 1 SV = 1	Y	N	UGT72	PG34647	UDP-glycosyltransferase 91A1 OS = Arabidopsis OX = 3702 GN = UGT91A1 PE = 2 SV = 1	Y	Y	UGT91
PG16259	East glucosyltransferase OS = Tobacco OX = 4097 GN = TOGT1 PE = 1 SV = 1	Y	N	UGT73	PG05454	UDP-glycosyltransferase 91A1 OS = Arabidopsis OX = 3702 GN = UGT91A1 PE = 2 SV = 1	N	Y	UGT91
PG29012	East glucosyltransferase OS = Tobacco OX = 4097 GN = TOGT1 PE = 1 SV = 1	Y	N	UGT73	PG03173	UDP-glycosyltransferase 91C1 OS = Arabidopsis OX = 3702 GN = UGT91C1 PE = 2 SV = 1	Y	N	UGT91
PG14163	UDP-glycosyltransferase 74F2 OS = Arabidopsis OX = 3702 GN = UGT74F2 PE = 1 SV = 1	Y	N	UGT74	PG13029	UDP-glycosyltransferase 92A1 OS = Arabidopsis OX = 3702 GN = UGT92A1 PE = 2 SV = 1	Y	N	UGT92
PG17964	UDP-glycosyltransferase 74E2 OS = Arabidopsis OX = 3702 GN = UGT74E2 PE = 1 SV = 1	Y	N	UGT74	PG22997	β -D-glucosylcroctin β -1,6-glucosyltransferase OS = scorpion scorpion OX = 114476 GN = UGT94E5 PE = 1 SV = 1	Y	Y	UGT94
PG31437	UDP-glycosyltransferase 74E2 OS = Arabidopsis OX = 3702 GN = UGT74E2 PE = 1 SV = 1	Y	N	UGT74	PG35394	β -D-glucosylcroctin β -1,6-glucosyltransferase OS = scorpion scorpion OX = 114476 GN = UGT94E5 PE = 1 SV = 1	Y	N	UGT94
PG30551	UDP-glycosyltransferase 74E2 OS = Arabidopsis OX = 3702 GN = UGT74E2 PE = 1 SV = 1	Y	Y	UGT74	PG11440	β -D-glucosylcroctin β -1,6-glucosyltransferase OS = scorpion scorpion OX = 114476 GN = UGT94E5	Y	N	UGT94

						PE = 1 SV = 1			
PG14160	UDP-glycosyltransferase 74E1 OS = Arabidopsis OX = 3702 GN = UGT74E1 PE = 3 SV = 1	Y	N	UGT74	PG07945	Protein HOTHREAD OS = Arabidopsis OX = 3702 GN = HTH PE = 1 SV = 1	Y	N	UGT??
PG34073	Croctetin glucosyltransferase, chloroplast OS = scorpion scorpion OX = 114476 GN = UGT75L6 PE = 1 SV = 1	Y	N	UGT75	PG23330	Linoleic acid 13S-lipoxygenase 2-1, chloroplast OS = Solanum tuberosum OX = 4113 GN = LOX2.1 PE = 1 SV = 1	Y	N	UGT??
PG05721	Cytochrome P450 704B1 OS=Arabidopsis thaliana OX=3702 GN=CYP704B1 PE=1 SV=1	Y	N	CYP704B1	PG09699	Geraniol 8-hydroxylase OS=Catharanthusroseus OX=4058 GN=CYP76B6 PE=1 SV=1	Y	N	CYP76B6
PG25870	Cytochrome P450 704B1 OS=Arabidopsis thaliana OX=3702 GN=CYP704B1 PE=1 SV=1	Y	Y	CYP704B1	PG01467	Geraniol 8-hydroxylase OS=Catharanthusroseus OX=4058 GN=CYP76B6 PE=1 SV=1	Y	Y	CYP76B6
PG10057	Cytochrome P450 704C1 OS=Pinustaeda OX=3352 GN=CYP704C1 PE=2 SV=1	Y	N	CYP704C1	PG30778	Cytochrome P450 81E8 OS=Medicago truncatula OX=3880 GN=CYP81E8 PE=2 SV=1	Y	N	CYP81E8
PG40294	Cytochrome P450 71A8 OS=Menthapiperita OX=34256 GN=CYP71A8 PE=3 SV=1	Y	N	CYP71A8	PG29120	Cytochrome P450 82A3 OS=Glycine max OX=3847 GN=CYP82A3 PE=2 SV=1	Y	N	CYP82A3
PG16874	Cytochrome P450 CYP71D312 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP71D312	PG11378	Cytochrome P450 82A3 OS=Glycine max OX=3847 GN=CYP82A3 PE=2 SV=1	N	Y	CYP82A3
PG21495	Cytochrome P450 CYP71D313 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP71D313	PG32345	Cytochrome P450 82C4 OS=Arabidopsis thaliana OX=3702 GN=CYP82C4 PE=2 SV=1	Y	N	CYP82C4
PG26653	Cytochrome P450 CYP71D313 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP71D313	PG23797	Cytochrome P450 CYP82D47 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP82D47
PG32259	Cytochrome P450 CYP71D313 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP71D313	PG29513	Cytochrome P450 CYP82D47 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	Y	CYP82D47
PG04084	Cytochrome P450 71D8 OS=Glycine max OX=3847 GN=CYP71D8 PE=2 SV=1	N	Y	CYP71D8	PG02439	Cytochrome P450 83B1 OS=Arabidopsis thaliana OX=3702 GN=CYP83B1 PE=1 SV=1	Y	N	CYP83B1
PG01300	Cytochrome P450 CYP72A219 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP72A219	PG34334	Cytochrome P450 83B1 OS=Arabidopsis thaliana OX=3702 GN=CYP83B1 PE=1 SV=1	Y	N	CYP83B1
PG40963	Cytochrome P450 CYP72A219 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP72A219	PG34924	Cytochrome P450 89A9 OS=Arabidopsis thaliana OX=3702 GN=CYP89A9 PE=2 SV=1	Y	N	CYP89A9
PG03240	Cytochrome P450 CYP72A219 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP72A219	PG27129	Cytochrome P450 94A1 OS=Vicia sativa OX=3908 GN=CYP94A1 PE=2 SV=2	Y	N	CYP94A1
PG23478	Cytochrome P450 CYP72A219 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP72A219	PG23358	Cytochrome P450 94A2 OS=Vicia sativa OX=3908 GN=CYP94A2 PE=2 SV=1	Y	N	CYP94A2
PG09274	Cytochrome P450 CYP72A219 OS=Panax ginseng OX=4054 PE=2 SV=1	N	Y	CYP72A219	PG27467	Cytochrome P450 94A2 OS=Vicia sativa OX=3908 GN=CYP94A2 PE=2 SV=1	Y	N	CYP94A2
PG28769	Trans-cinnamate 4-monoxygenase	Y	Y	CYP73A1	PG16781	Cytochrome P450 97B2, chloroplastic	Y	N	CYP97B2

	OS=Helianthus tuberosus OX=4233 GN=CYP73A1 PE=1 SV=1					OS=Glycine max OX=3847 GN=CYP97B2 PE=2 SV=1			
PG13617	Cytochrome P450 CYP736A12 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP736A12	PG35257	Carotene epsilon-monooxygenase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CYP97C1 PE=1 SV=1	Y	N	CYP97C1
PG33495	Cytochrome P450 CYP736A12 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP736A12	PG24387	Cytochrome P450 98A2 OS=Glycine max OX=3847 GN=CYP98A2 PE=2 SV=1	Y	N	CYP98A2
PG36905	Cytochrome P450 CYP736A12 OS=Panax ginseng OX=4054 PE=2 SV=1	Y	N	CYP736A12	PG41871	Cytochrome P450 98A2 OS=Glycine max OX=3847 GN=CYP98A2 PE=2 SV=1	Y	Y	CYP98A2

Table S5. Proteins involved in ginsenoside biosynthesis.

Protein (Gene ID)	Biosynthetic pathway	Swissprot description	Cauline leaf	Root
AACT(PG11912)	MVA	Probable acetyl-CoA acetyltransferase, cytosolic 2 OS=Arabidopsis thaliana OX=3702 GN=At5g47720 PE=2 SV=1	Y	Y
HMGS (PG38955)	MVA	Hydroxymethylglutaryl-CoA synthase OS=Arabidopsis thaliana OX=3702 GN=HMGS PE=1 SV=2	N	Y
MVK(PG20228)	MVA	Mevalonate kinase OS=Arabidopsis thaliana OX=3702 GN=At5g27450 PE=2 SV=1	N	Y
PMK(PG25943)	MVA	Phosphomevalonate kinase, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=PMK PE=1 SV=1	Y	N
MVD1(PG37213)	MVA	Diphosphomevalonate decarboxylase MVD2, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=MVD2 PE=1 SV=1	Y	Y
MVD2(PG02263)	MVA	Diphosphomevalonate decarboxylase MVD2, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=MVD2 PE=1 SV=1	N	Y
IDI1(PG19600)	MVA	Isopentenyl-diphosphate Delta-isomerase I OS=Camptothecaacuminata OX=16922 GN=IPI1 PE=2 SV=1	Y	Y
IDI2(PG03104)	MVA	Isopentenyl-diphosphate Delta-isomerase II OS=Camptothecaacuminata OX=16922 GN=IPI2 PE=2 SV=1	Y	N
FPS(PG34283)		Farnesyl pyrophosphate synthase OS=Artemisia annua OX=35608 GN=FPS1 PE=2 SV=1	Y	Y
PPDS(PG37358)		Dammarenydiol 12-hydroxylase OS=Panax ginseng OX=4054 GN=PPDS PE=1 SV=2	Y	Y
PPTS(PG26599)		Protopanaxadiol 6-hydroxylase OS=Panax ginseng OX=4054 PE=1 SV=1	Y	Y
CAS(PG03815)		Cycloartenol Synthase OS=Panax ginseng OX=4054 GN=OSCPNX1 PE=1 SV=1	Y	N
DXS(PG31496)	MEP	Protease 2 OS=Escherichia coli (strain K12) OX=83333 GN=ptrB PE=1 SV=2	N	Y
DXR1(PG36148)	MEP	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=DXR PE=2 SV=2	Y	Y
DXR2(PG34876)	MEP	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=DXR PE=2 SV=2	Y	Y
IspE(PG20660)	MEP	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplastic OS=Menthapiperita OX=34256 GN=ISPE PE=1 SV=1	N	Y
IspF(PG27983)	MEP	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, chloroplastic OS=Catharanthusroseus OX=4058 GN=ISPF PE=2 SV=1	Y	Y
IspG/gcpE1(PG25816)	MEP	4-hydroxy-3-methyl-2-lbutenyl diphosphate synthase	Y	N

		(ferredoxin), chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ISPG PE=1 SV=1 4-hydroxy-3-methy-2-lbutenyl diphosphate synthase		
IspG/gcpE2(PG34415)	MEP	(ferredoxin), chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ISPG PE=1 SV=1 4-hydroxy-3-methy-2-lbutenyl diphosphate reductase,	Y	Y
IspH(PG19130)	MEP	chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=ISPH PE=2 SV=1	Y	N
