

Additional File 3. Results of BLASTX search and functional classification of *L. albus* phloem exudate ESTs.

Accession number of closest match	Annotation	Score (bits)	E-value	ESTs per contig
Energy metabolism				
ABB46862.2	Enolase, putative, expressed [Oryza sativa (japonica cultivar-group)]	543	1.00E-153	1
BAC77064.1	NADP-specific isocitrate dehydrogenase [Lupinus albus]	528	1.00E-148	1
BAA77604.1	plastidic aldolase NPALDP1 [Nicotiana paniculata]	514	1.00E-144	1
AAL66290.1 AF452450_1	adenosine 5'-phosphosulfate reductase [Glycine max]	500	1.00E-140	1
NP_001078275.1	pyruvate kinase, putative [Arabidopsis thaliana]	473	1.00E-132	1
O65735	Fructose-bisphosphate aldolase, cytoplasmic isozyme [Cicer arietinum]	471	1.00E-131	2
CAA56354.1	NADP dependent malic enzyme [Phaseolus vulgaris]	465	1.00E-129	1
O24301	Sucrose synthase 2 (Sucrose-UDP glucosyltransferase 2) [Pisum sativum]	461	1.00E-128	1
AAO15574.1	malate dehydrogenase [Lupinus albus]	394	1.00E-123	1
ABA86966.1	triosephosphate isomerase [Glycine max]	424	1.00E-117	2
CAI83772.1	glyceraldehyde-3-phosphate-dehydrogenase [Lupinus albus]	413	1.00E-114	2
P80269	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor (NADH-ubiquinone oxidoreductase 23 kDa subunit) [Solanum tuberosum]	363	5.00E-99	1
AAF01037.1	NADH ubiquinone oxidoreductase PSST subunit [Lupinus luteus]	337	4.00E-91	1
ABA07956.1	glyceraldehyde-3-dehydrogenase C subunit [Glycine max]	311	2.00E-83	1
ABD28700.1	ATP binding , related [Medicago truncatula]	306	1.00E-81	1
BAC81652.1	short-chain alcohol dehydrogenase A [Pisum sativum]	297	4.00E-79	2
Q42961.1	Phosphoglycerate kinase, chloroplast precursor [Nicotiana tabacum]	248	3.00E-64	3
AAY85660.1	cytosolic glucose-6-phosphate isomerase [Helianthus annuus]	220	4.00E-56	1
AAT46998.1	triosephosphate isomerase [Glycine max]	202	1.00E-50	1
CAI53675.1	pyruvate kinase [Glycine max]	147	5.00E-34	1
1F3Y A	Chain A, Solution Structure Of The Nudix Enzyme Diadenosine Tetrphosphate Hydrolase From Lupinus Angustifolius L.	102	1.00E-20	1
General metabolism				
AAL33919.1	UDP-glucose pyrophosphorylase [Amorpha fruticosa]	523	1.00E-147	3
AAA98603.1	mitochondrial aspartate aminotransferase [Glycine max]	525	1.00E-147	1
BAB40967.1	UDP-D-glucuronate carboxy-lyase [Pisum sativum]	514	1.00E-144	1
ABO77438.1	S-adenosyl-L-methionine synthetase [Medicago sativa subsp. falcata]	503	1.00E-141	2
CAJ01707.1	putative S-adenosylhomocystein hydrolase 2 [Hordeum vulgare subsp. vulgare]	504	1.00E-141	1
Q9SP37	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) [Lupinus luteus]	495	1.00E-138	2
AAA74441.1	phosphatidylinositol-specific phospholipase C [Glycine max]	478	1.00E-136	1
Q43785	Glutamine synthetase nodule isozyme (Glutamate--ammonia ligase) [Medicago sativa]	477	1.00E-133	1
CAC05439.1	glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]	463	6.00E-129	1
P51850	Pyruvate decarboxylase isozyme 1 (PDC) [Pisum sativum]	461	1.00E-128	1
ABO80948.1	S-adenosylmethionine synthetase [Medicago truncatula]	456	1.00E-127	3

AAO23063.1	ent-kaurenoic acid oxidase [Pisum sativum]	410	1.00E-122	1
1803516A	glycolate oxidase	437	1.00E-121	1
AAW21273.1	glutamine synthetase [Saccharum officinarum]	434	1.00E-120	1
ABO61376.1	serine hydroxymethyltransferase [Populus tremuloides]	434	1.00E-120	1
ABC74567.1	acetoacetyl-CoA thiolase [Picrohiza kurroa]	435	1.00E-120	1
CAA53078.1	3-ketoacyl-CoA thiolase B; acetyl-CoA C-acyltransferase [Mangifera indica]	432	1.00E-119	1
NP_188498.1	aspartate/glutamate/uridylate kinase family protein [Arabidopsis thaliana]	430	1.00E-119	1
AAT58365.1	GMPase [Medicago sativa]	427	1.00E-118	1
AAC50014.1	aspartate aminotransferase glyoxysomal isozyme AAT1 precursor [Glycine max]	407	1.00E-115	1
AAK52082.1	nuclease [Nicotiana tabacum]	416	1.00E-114	1
Q9FR44.1	Phosphoethanolamine N-methyltransferase 1 (PEAMT 1) (AtNMT1) [Arabidopsis thaliana]	408	1.00E-112	1
	Trans-cinnamate 4-monooxygenase (Cinnamic acid 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73)			
Q96423	[Glycyrrhiza echinata]	397	1.00E-109	1
ABD33275.2	progesterone 5-beta-reductase, putative [Medicago truncatula]	398	1.00E-109	1
ABN08096.1	Galactose mutarotase-like [Medicago truncatula]	377	1.00E-103	1
CAC10212.1	putative mitochondrial glyoxalase II [Cicer arietinum]	375	1.00E-102	1
AAR13305.1	phytochelatin synthetase-like protein [Phaseolus vulgaris]	372	1.00E-101	1
BAA25187.1	ARG10 [Vigna radiata]	368	1.00E-100	2
AAM60857.1	dihydrolipoamide S-acetyltransferase, putative [Arabidopsis thaliana]	365	2.00E-99	2
ABB29942.1	S-adenosyl methionine synthase-like [Solanum tuberosum]	360	5.00E-98	2
AAX84672.1	aldo/keto reductase AKR [Manihot esculenta]	353	5.00E-96	1
CAO48819.1	unnamed protein product [Vitis vinifera]	350	8.00E-95	1
ABC94943.1	squalene epoxidase [Medicago sativa]	316	8.00E-85	1
BAB33421.1	putative senescence-associated protein [Pisum sativum]	307	4.00E-82	4
AAL74418.2	ATP sulfurylase [Glycine max]	306	1.00E-81	1
CAA74101.1	laccase [Populus trichocarpa]	301	4.00E-80	1
ABD28680.1	Rubber elongation factor [Medicago truncatula]	301	2.00E-80	1
BAC10552.1	nine-cis-epoxycarotenoid dioxygenase4 [Pisum sativum]	288	2.00E-76	1
ABW34717.1	acireductone dioxygenase [Solanum tuberosum]	281	4.00E-74	1
	Caffeic acid 3-O-methyltransferase (S-adenosyl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT)			
P28002	[Medicago sativa]	268	2.00E-70	1
AAB03852.1	alpha-carboxyltransferase aCT-1 precursor [Glycine max]	257	6.00E-67	1
NP_187342.1	MFP2 (MULTIFUNCTIONAL PROTEIN); enoyl-CoA hydratase [Arabidopsis thaliana]	241	2.00E-62	1
NP_195242.1	O-methyltransferase family 2 protein [Arabidopsis thaliana]	241	4.00E-62	3
BAA88226.1	thiamin biosynthetic enzyme [Glycine max]	239	6.00E-62	2
P43280	S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1) (AdoMet synthetase 1) [Solanum lycopersicum]	238	2.00E-61	1
AAK63009.1 AF320025_1	heme oxygenase 3 [Glycine max]	238	1.00E-61	1
Q04593	Phenylalanine ammonia-lyase 2 [Pisum sativum]	238	2.00E-61	1
BAD94178.1	putative myo-inositol 1-phosphate synthase [Arabidopsis thaliana]	219	8.00E-56	2
BAF49299.1	putative glycosyltransferase [Clitoria ternatea]	195	1.00E-48	1

NP_194843.1	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	192	2.00E-47	1
AAL91002.1	asparagine synthetase [Securigera parviflora]	179	4.00E-44	1
BAB33422.1	putative senescence-associated protein [Pisum sativum]	175	2.00E-42	2
NP_565701.1	lipase class 3 family protein [Arabidopsis thaliana]	169	9.00E-41	1
NP_190412.1	hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	160	4.00E-38	1
CAA63598.1	glyoxysomal beta-ketoacyl-thiolase [Brassica napus]	156	5.00E-37	1
AAY86360.1	cinnamoyl-CoA reductase [Acacia mangium x Acacia auriculiformis]	149	9.00E-35	1
ABU62755.1	4,5-DOPA dioxygenase extradiol [Nicotiana benthamiana]	147	2.00E-34	1
AAS79665.1	cryptochrome 2A apoprotein [Pisum sativum]	137	5.00E-31	1
AAL89723.1	S-adenosylmethionine decarboxylase [Glycine max]	136	4.00E-31	2
AAC70779.1	granule-bound glycogen (starch) synthase [Astragalus membranaceus]	128	2.00E-28	1
ABW89464.1	glutamine synthetase [Gossypium hirsutum]	119	8.00E-26	1
ABN06032.1	Galactose-binding like [Medicago truncatula]	111	2.00E-23	1
ABO77440.1	S-adenosylmethionine decarboxylase [Medicago sativa subsp. falcata]	72.4	2.00E-11	2
AAB96761.1	ferredoxin-dependent glutamate synthase [Glycine max]	72.8	1.00E-11	1
AAT40304.1	S-adenosylmethionine synthase; SAM synthase [Medicago sativa]	402	1.00E-110	1
Photosynthesis				
AAA50172.1	photosystem II type I chlorophyll a/b-binding protein [Glycine max]	514	1.00E-144	6
AAR10886.1	chlorophyll a/b binding protein [Trifolium pratense]	442	1.00E-122	3
AAD27878.1	chlorophyll a/b binding protein CP29 [Vigna radiata]	432	1.00E-119	1
P27521.1	Chlorophyll a-b binding protein 4, chloroplast precursor [Arabidopsis thaliana]	357	7.00E-97	1
ABQ63097.1	photosystem I subunit PsdA [Glycine max]	342	1.00E-92	1
AAA33866.1	ribulose 1,5-bisphosphate carboxylase small subunit [Malus x domestica x Pyrus communis]	300	5.00E-80	1
P08927	RuBisCO large subunit-binding protein subunit beta, chloroplast precursor (60 kDa chaperonin subunit beta) (CPN-60 beta) [Pisum sativum]	298	3.00E-79	1
O65100 FRI3_VIGUN	Ferritin-3, chloroplast precursor	283	8.00E-75	1
BAD97359.1	PsbQ [Nicotiana tabacum]	204	3.00E-51	1
ABI84258.1	photosystem I psaH protein [Arachis hypogaea]	202	2.00E-50	1
P10690	Photosystem II 10 kDa polypeptide, chloroplast precursor [Spinacia oleracea]	156	5.00E-37	1
CAB53034.1	photosystem I subunit XI precursor [Arabidopsis thaliana]	153	4.00E-36	1
CAA96570.1	CP12 [Pisum sativum]	148	3.00E-34	1
P14226 PSBO_PEA	Oxygen-evolving enhancer protein 1, chloroplast precursor (OEE1)	89.7	5.00E-17	1
Cell structural components				
Q39445	Tubulin beta chain (Beta-tubulin) [Cicer arietinum]	546	1.00E-154	1
AAF03692.1	actin [Picea rubens]	487	1.00E-136	1
P37392	Tubulin beta-1 chain (Beta-1-tubulin) [Lupinus albus]	469	1.00E-134	1
NP_187818.1	ACT11 (ACTIN-11); structural constituent of cytoskeleton [Arabidopsis thaliana]	451	1.00E-125	1
AAB40079.1	actin [Glycine max]	429	1.00E-119	1
ABN08645.1	Tubulin binding cofactor C [Medicago truncatula]	405	1.00E-111	1
P12459.1	Tubulin beta-1 chain (Beta-1-tubulin) [Glycine max]	394	3.00E-108	1

BAD29243.1	dTDP-D-glucose 4,6-dehydratase-like [Oryza sativa]	390	1.00E-107	1
AAV83799.1	putative actin 1 [Chorispora bungeana]	367	1.00E-100	3
ABX57816.1	alpha tubulin [Picea wilsonii]	306	6.00E-82	1
ABB16985.1	profilin-like protein [Solanum tuberosum]	248	2.00E-64	1
AAU81921.1	profilin [Arachis hypogaea]	221	4.00E-56	1
CAD33929.1	microtubule associated protein [Cicer arietinum]	208	2.00E-52	1
ABA81885.1	profilin-like [Solanum tuberosum]	207	5.00E-52	1
Q941H7	Profilin (Minor allergen Lit c 1) [Litchi chinensis]	158	1.00E-37	1
ABV55999.1	alpha-tubulin 7 [Populus tremuloides]	151	2.00E-35	1
NP_566316.1	kelch repeat-containing protein [Arabidopsis thaliana]	73.6	6.00E-12	1
Protein modification/turnover				
ABA12220.1	translation elongation factor 1A-4 [Gossypium hirsutum]	518	1.00E-145	1
ABA12221.1	translation elongation factor 1A-5 [Gossypium hirsutum]	497	1.00E-139	1
ABE91931.1	Proteasome component region PCI [Medicago truncatula]	485	1.00E-135	1
CAC20221.1	ribosomal protein L2 [Glycine max]	466	1.00E-130	2
AAV67798.1	14-3-3 protein [Manihot esculenta]	468	1.00E-130	1
AAB36545.1	ubiquitin-like protein [Phaseolus vulgaris]	444	1.00E-123	2
P35100	ATP-dependent Clp protease ATP-binding subunit clpC homolog chloroplast precursor [Pisum sativum]	435	1.00E-120	2
ABD32840.1	Peptidase C1A, papain; Somatotropin hormone; Peptidase C1, propeptide [Medicago truncatula]	430	1.00E-119	1
ABF18679.1	cysteine protease [Medicago sativa]	415	1.00E-114	1
AAN72085.1	putative aminopeptidase [Arabidopsis thaliana]	391	1.00E-107	1
CAA83548.1	PsHSC71.0 [Pisum sativum]	371	1.00E-103	1
NP_178234.1	60S ribosomal protein L7 (RPL7B) [Arabidopsis thaliana]	370	1.00E-101	1
AAD56020.1	elongation factor-1 alpha 3 [Lilium longiflorum]	369	1.00E-101	2
ABE79560.1	Chaperone DnaK [Medicago truncatula]	358	3.00E-97	1
ABA46772.1	RUB1-conjugating enzyme-like protein [Solanum tuberosum]	353	9.00E-96	2
O65731	40S ribosomal protein S5 [Cicer arietinum]	347	3.00E-94	1
ABE80155.1	Peptidylprolyl isomerase, FKBP-type [Medicago truncatula]	342	2.00E-92	1
CAA04447.1	DnaJ-like protein [Medicago sativa]	335	2.00E-90	2
NP_565477.1	AtRPN1a/RPN1A (26S proteasome regulatory subunit S2 1A); binding [Arabidopsis thaliana]	227	4.00E-90	1
AAR83877	60S ribosomal protein L19 [Capsicum annuum]	330	5.00E-89	2
ABD28502.1	Cyclin-like F-box [Medicago truncatula]	329	1.00E-88	1
CAD29823.2	putative ubiquitin-conjugating enzyme [Populus x canadensis]	325	2.00E-87	1
AAK02067.1	cyclophilin-40 [Arabidopsis thaliana]	322	1.00E-86	1
ABA40437.1	40S ribosomal protein S7-like protein [Solanum tuberosum]	311	3.00E-83	2
O49886	Peptidyl-prolyl cis-trans isomerase (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) [Lupinus luteus]	312	1.00E-83	5
ABM53472.1	eIF5A [Rosa chinensis]	307	5.00E-82	2
NP_564011.1	UBC36; ubiquitin-protein ligase [Arabidopsis thaliana]	309	2.00E-82	1
AAR83868.1	60S ribosomal protein L12 [Capsicum annuum]	279	2.00E-73	1
P48724	Eukaryotic translation initiation factor 5 (eIF-5) [Phaseolus vulgaris]	275	3.00E-72	1

AAD34458.1	Skp1 [Medicago sativa]	266	8.00E-70	1
CAA80333.1	ubiquitin extension protein [Lupinus albus]	264	4.00E-69	1
ABR25690.1	60S ribosomal protein l7a [Oryza sativa (indica cultivar-group)]	257	3.00E-67	1
ABN08266.1	Poly(ADP-ribose) polymerase, catalytic region [Medicago truncatula]	254	5.00E-66	1
ABF93903.1	60S ribosomal protein L21, putative, expressed [Oryza sativa (japonica cultivar-group)]	245	2.00E-63	1
NP_565053.1	SNF7 family protein [Arabidopsis thaliana]	240	6.00E-62	1
ABG27020.1	SKP1-like b [Medicago truncatula]	234	7.00E-60	1
AAS57912.1	70 kDa heat shock cognate protein 1 [Vigna radiata]	228	3.00E-58	1
O22584	40S ribosomal protein S14 [Lupinus luteus]	223	8.00E-57	1
NP_173692.1	PFL (POINTED FIRST LEAVES); structural constituent of ribosome [Arabidopsis thaliana]	222	2.00E-56	1
Q9M5L0	60S ribosomal protein L35 [Euphorbia esula]	219	7.00E-56	2
NP_195162.2	protease-related [Arabidopsis thaliana]	145	7.00E-54	1
ABJ91230.1	CBL-interacting protein kinase 24 [Populus trichocarpa]	202	6.00E-51	1
ABB55398.1	40S ribosomal protein S10-like [Solanum tuberosum]	206	2.00E-51	1
1909359A	ribosomal protein S19 [Solanum tuberosum]	194	3.00E-48	1
AAP72960.1	putative ribosomal protein L31 [Lactuca sativa]	188	2.00E-46	4
Q06445	Cysteine proteinase inhibitor (Cystatin) [Vigna unguiculata]	171	2.00E-41	1
CAA10612.1	ribosomal protein S14 [Pisum sativum]	156	1.00E-36	1
ABA46751.1	eukaryotic initiation factor 5A4-like protein [Solanum tuberosum]	141	2.00E-32	1
ABY60454.1	putative polyubiquitin [Adonis aestivalis var. palaestina]	133	3.00E-30	1
O04287	Peptidyl-prolyl isomerase FKBP12 (PPIase) (Rotamase) [Vicia faba]	127	2.00E-28	1
O22518	40S ribosomal protein SA (p40) [Glycine max]	111	1.00E-23	1
AAC15418.1	14-3-3 protein homolog [Maackia amurensis]	109	6.00E-23	1
AAL91663.1	60s acidic ribosomal protein [Prunus dulcis]	100	5.00E-20	1
NP_187595.1	CDC48 (CELL DIVISION CYCLE 48); ATPase [Arabidopsis thaliana]	101	1.00E-20	1
AAB88458.1	ribosomal protein S12 [Lupinus albus]	98.6	4.00E-19	1
P25866	Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier protein) [Triticum aestivum]	94.4	4.00E-18	1
ABY56104.1	ribosomal protein [Cucumis sativus]	92.8	6.00E-18	1
ABC69274.2	putative DnaJ protein [Camellia sinensis]	89.7	1.00E-16	1
ABD32395.1	Histone-fold/TFIID-TAF/NF-Y [Medicago truncatula]	80.9	4.00E-14	1
Redox regulation				
ABQ41114.1	monodehydroascorbate reductase [Vitis vinifera]	507	1.00E-142	1
CAI56334.1	TPA: isoflavone reductase-like protein 5 [Vitis vinifera]	450	1.00E-125	1
AAO13838.1	peroxidase 2 [Lupinus albus]	420	1.00E-116	1
AAG22740.1	allergenic isoflavone reductase-like protein Bet v 6.0102 [Betula pendula]	414	1.00E-114	2
ABM45856.1	cytosolic ascorbate peroxidase [Arachis hypogaea]	382	1.00E-104	1
NP_181836.1	AT-P4H-1 (A. THALIANA P4H ISOFORM 1); oxidoreductase [Arabidopsis thaliana]	370	1.00E-101	1
P32110	Probable glutathione S-transferase (Heat shock protein 26A) (G2-4) [Glycine max]	347	5.00E-94	2
CAM57107.1	Rieske iron-sulphur protein precursor [Glycine max]	345	2.00E-93	1
CAE12168.2	formate dehydrogenase [Quercus robur]	343	8.00E-93	1

ABX79343.1	dehydroascorbate reductase [Vitis vinifera]	340	5.00E-92	1
ABD32912.1	Ferric reductase-like transmembrane component [Medicago truncatula]	341	2.00E-92	1
ABI84254.1	thioredoxin fold [Arachis hypogaea]	291	2.00E-77	2
CAD31838.1	putative quinone oxidoreductase [Cicer arietinum]	290	5.00E-77	1
ABF51006.1	Cu-Zn superoxide dismutase [Arachis hypogaea]	259	1.00E-67	1
AAC83463.1	cationic peroxidase 2 [Glycine max]	236	1.00E-60	2
P49332	Probable glutathione S-transferase parC (Auxin-regulated protein parC) [Nicotiana tabacum]	235	2.00E-60	1
CAM57109.1	Rieske iron-sulphur protein precursor [Zantedeschia aethiopica]	231	2.00E-59	1
BAA10929.1	cytochrome P450 like_TBP [Nicotiana tabacum]	187	6.00E-46	4
T02955	probable cytochrome P450 monooxygenase - maize (fragment) [Zea mays]	144	3.00E-41	1
BAA76419.1	ascorbate peroxidase [Cicer arietinum]	144	2.00E-33	1
CAJ43614.1	monodehydroascorbate reductase [Plantago major]	141	4.00E-32	2
CAA10132.1	superoxide dismutase [Cicer arietinum]	125	2.00E-27	1
BAD18377.1	type 2 metallothionein [Glycine max]	105	2.00E-21	1
ABQ44281.1	metallothionein type 2 [Sesbania drummondii]	93.6	4.00E-18	2
CAJ38394.1	cytochrome b5 reductase [Plantago major]	77.4	3.00E-13	1
Stress and defence response				
NP_188317.2	chitinase [Arabidopsis thaliana]	498	1.00E-139	2
CAO41879.1	leucine-rich repeat resistance protein-like protein	369	1.00E-100	1
BAD86819.1	hypersensitive-induced response protein [Lotus japonicus]	329	9.00E-89	1
BAB63949.1	pathogenesis-related 10 [Lupinus albus]	313	7.00E-84	7
AAF15296.2	lipoxygenase [Phaseolus vulgaris]	309	1.00E-82	2
P16148 PLZ12_LUPPO	Protein PPLZ12- Lupinus polyphyllus	236	1.00E-60	1
AAO33591.1	putative early light induced protein [Arachis hypogaea]	220	6.00E-56	1
AAT06600.2	dehydrin [Lupinus albus]	203	8.00E-51	3
AAD50376.1	ripening related protein [Glycine max]	203	1.00E-50	4
CAB44031.1	lectin [Glycine max]	191	4.00E-47	1
CAA03926.1	PR-10 protein [Lupinus albus]	158	1.00E-37	1
AAK73280.1	drought-induced protein [Retama raetam]	144	5.00E-33	5
AAB18970.2	lipoxygenase [Phaseolus vulgaris]	117	3.00E-25	2
AAP23944.1	leucine-rich repeat protein [x Citrofortunella mitis]	108	1.00E-22	1
ABB29467.1	salt-tolerance protein [Glycine max]	96.3	7.00E-19	1
NP_190693.1	senescence/dehydration-associated protein-related [Arabidopsis thaliana]	74.3	2.00E-12	1
AAZ85353.1	putative submergence induced protein 2-like [Solanum ochranthum]	75.1	3.00E-12	1
CAB85628.1	putative ripening-related protein [Vitis vinifera]	75.1	2.00E-12	1
BAE48663.1	Pm52 [Prunus mume]	71.2	4.00E-11	1
AAR26524.1	abscisic stress ripening-like protein [Glycine max]	71.2	8.00E-11	3
Nucleic acid binding				
ABN09109.1	Helicase, C-terminal [Medicago truncatula]	492	1.00E-137	1
NP_564150.1	F-box family protein [Arabidopsis thaliana]	475	1.00E-132	1

ABD32851.1	Helicase, C-terminal; Zinc finger, CCHC-type; GUCT [Medicago truncatula]	452	1.00E-125	1
AAG10600.1	MYB-related transcription factor PHAN1 [Pisum sativum]	384	1.00E-105	1
P48513	Transcription initiation factor IIB (General transcription factor TFIIB) [Glycine max]	382	1.00E-104	1
AAX13298.1	MADS box protein SEP3 [Lotus corniculatus var. japonicus]	327	4.00E-88	2
NP_172336.3	ATRX/CHR20; ATP binding / DNA binding / helicase [Arabidopsis thaliana]	286	8.00E-76	1
ABH02875.1	MYB transcription factor MYB123 [Glycine max]	247	8.00E-64	2
O49289	Putative DEAD-box ATP-dependent RNA helicase 29 [Arabidopsis thaliana]	246	1.00E-63	1
NP_001078676.1	RNA and export factor-binding protein, putative [Arabidopsis thaliana]	238	3.00E-61	1
ABS18448.1	WRKY55 [Glycine max]	221	6.00E-56	1
ABN06047.1	Zinc finger, RING-type; Transcription factor jumonji, jmjC; Zinc finger, C2H2-type [Medicago truncatula]	216	1.00E-54	1
NP_186796.1	ATHB-1 (Homeobox-leucine zipper protein HAT5); transcription factor [Arabidopsis thaliana]	211	6.00E-53	1
NP_180427.1	ATP binding / ATP-dependent helicase/ nucleic acid binding [Arabidopsis thaliana]	204	6.00E-51	1
ABI34666.1	bZIP transcription factor bZIP124 [Glycine max]	200	1.00E-49	1
CAL25353.1	ACBF-like dna binding protein [Platanus x acerifolia]	190	7.00E-47	1
AAA82062.1	eukaryotic release factor 3	189	1.00E-46	1
AAG13810.1	PSTVd RNA-binding protein Virp1a [Lycopersicon esculentum]	181	3.00E-44	1
BAE71188.1	BEL1-like homeodomain transcription factor [Trifolium pratense]	179	2.00E-43	1
P26585	HMG1/2-like protein (Protein SB11) [Glycine max]	164	5.00E-39	1
AAA88792.1	nucleosome assembly protein 1 [Glycine maxima]	117	4.00E-38	1
NP_974373.1	MIF2 (MINI ZINC FINGER 2); DNA binding [Arabidopsis thaliana]	130	4.00E-29	1
ABD28504.1	Nucleosome assembly protein (NAP) [Medicago truncatula]	117	8.00E-25	1
AAZ86071.1	MADS-box protein [Glycine max]	111	2.00E-23	1
AAQ96342.1	putative ethylene response factor ERF3b [Vitis aestivalis]	102	3.00E-20	1
NP_190149.1	RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	103	1.00E-20	2
NP_177360.1	PATL1 (PATELLIN 1); transporter [Arabidopsis thaliana]	90.9	9.00E-17	1
ABH02837.1	MYB transcription factor MYB81 [Glycine max]	79	2.00E-13	1
Transport				
AAL58570.1	vacuolar processing enzyme 2 [Glycine max]	483	1.00E-135	1
NP_200125.1	CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1) [Arabidopsis thaliana]	454	1.00E-126	1
CAA11025.1	aquaporin [Lupinus albus]	446	1.00E-123	3
AAL66293.1	phosphate transporter [Glycine max]	425	1.00E-117	1
Q9FY14	Probable aquaporin TIP-type (MtAQP1) [Medicago truncatula]	392	2.00E-107	2
NP_569004.1	nucleotide-sugar transporter family protein [Arabidopsis thaliana]	313	1.00E-100	1
ABB02396.1	temperature-induced lipocalin [Medicago truncatula]	339	1.00E-91	1
CAD56216.1	transportin-like protein [Cicer arietinum]	324	4.00E-87	1
CAA98170.1	RAB7C [Lotus japonicus]	313	6.00E-84	1
AAF21428.2 AF165422_1	salt-induced AAA-Type ATPase [Mesembryanthemum crystallinum]	298	4.00E-79	1
BAA25753.1	Ca2+/H+ exchanger [Vigna radiata]	258	2.00E-67	1
NP_177419.1	ATTIM23-2 (Arabidopsis thaliana translocase inner membrane subunit 23-2); protein translocase	158	3.00E-37	1
ABE68718.1	putative aquaporin [Arachis hypogaea]	149	1.00E-34	1

YP_001648758.1	ATP synthase subunit 6 [Mycosphaerella graminicola]	135	3.00E-30	1
ABD32809.1	Vacuolar (H ⁺)-ATPase G subunit; KH, prokaryotic type [Medicago truncatula]	121	3.00E-26	1
ABD33158.1	Syntaxin, N-terminal [Medicago truncatula]	102	1.00E-20	1
NP_182033.1	SEC61 BETA (suppressors of secretion-defective 61 Beta); protein transporter [Arabidopsis thaliana]	85.9	1.00E-15	1
Signalling				
BAA92699.1	type 2A protein phosphatase-3 [Vicia faba]	555	1.00E-157	1
ABC61505.1	AGO4-2 [Nicotiana benthamiana]	510	1.00E-143	3
AAU89742.1	serine/threonine protein kinase-like [Solanum tuberosum]	479	1.00E-134	1
Q9SWF9 ZFNL_PEA	Zinc finger CCCH domain-containing protein ZFN-like	475	1.00E-132	1
NP_190753.2	CPK13 (calcium-dependent protein kinase 13) [Arabidopsis thaliana]	461	1.00E-128	1
AAA53276.1	GTP-binding protein [Pisum sativum]	436	1.00E-121	1
NP_192169.1	ATMLO1/MLO1 (MILDEW RESISTANCE LOCUS O 1); calmodulin binding [Arabidopsis thaliana]	431	1.00E-119	1
Q39817	Calnexin homolog precursor [Glycine max]	413	1.00E-114	1
BAA02113.1	GTP-binding protein [Pisum sativum]	414	1.00E-114	1
P51139	Glycogen synthase kinase-3 homolog MsK-3 [Medicago sativa]	404	1.00E-111	1
AAQ72787.1	putative GTP-binding protein [Cucumis sativus]	398	1.00E-109	1
NP_179889.1	casein kinase II alpha chain, putative [Arabidopsis thaliana]	385	1.00E-105	1
NP_191645.1	guanine nucleotide exchange family protein [Arabidopsis thaliana]	366	1.00E-100	1
AAC33305.1	fiber annexin [Gossypium hirsutum]	344	2.00E-93	1
NP_195815.3	ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	319	1.00E-85	1
BAA92697.1	type 2A protein phosphatase-1 [Vicia faba]	313	4.00E-84	1
ABJ74170.1	histidine kinase 1 [Lupinus albus]	306	1.00E-81	1
NP_190767.1	protein kinase family protein [Arabidopsis thaliana]	303	1.00E-81	1
Q5J907	Translationally-controlled tumor protein homolog (TCTP) [Elaeis guineensis]	303	7.00E-81	4
AAM12880.1	GTP-binding protein [Helianthus annuus]	285	1.00E-75	1
AAO49473.1	putative serine/threonine kinase [Vitis vinifera]	274	4.00E-72	1
AAM83095.1	SOS2-like protein kinase [Glycine max]	253	8.00E-66	2
AAM65586.1	receptor protein kinase-like protein [Arabidopsis thaliana]	248	3.00E-64	1
AAG28503.1	hexokinase [Citrus sinensis]	246	2.00E-63	2
BAD01612.1	flowering locus T [Populus nigra]	228	3.00E-58	1
NP_174810.1	ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding [Arabidopsis thaliana]	206	1.00E-51	1
ABJ91228.1	CBL-interacting protein kinase 22 [Populus trichocarpa]	197	7.00E-49	1
CAC24474.1	GTP binding protein [Cichorium intybus x Cichorium endivia]	194	4.00E-48	1
AAP72282.2	calcium-dependent calmodulin-independent protein kinase isoform 2 [Cicer arietinum]	186	8.00E-46	1
P54766	GTP-binding nuclear protein Ran1B [Lotus japonicus]	147	2.00E-34	1
ABN08208.1	Remorin, C-terminal region [Medicago truncatula]	97.4	3.00E-19	1
BAA82130.1	acid phosphatase [Lupinus albus]	417	4.00E-115	1
Viral proteins				
AAB97459.1	nuclear inclusion B [bean yellow mosaic virus]	562	1.00E-159	4
P17765	Genome polyprotein [Bean yellow mosaic virus]	532	1.00E-150	2

AAF00522.1	polyprotein [bean yellow mosaic virus]	529	1.00E-148	3
AAB37237.1	polyprotein [Bean yellow mosaic virus]	513	1.00E-144	3
ABG33691.1	polyprotein [White lupin mosaic virus]	508	1.00E-142	6
BAE96599.1	polyprotein [Bean yellow mosaic virus]	491	1.00E-137	1
AAF00524.1	polyprotein [bean yellow mosaic virus]	487	1.00E-136	1
ABM69145.1	coat protein [Bean yellow mosaic virus]	371	1.00E-101	1
NP_734173.1	P1 protein [Bean yellow mosaic virus]	212	1.00E-53	1
CAO02584.2	polyprotein [Bean yellow mosaic virus]	106	4.00E-22	1
Unclassified				
CAE45585.1	coatomer alpha subunit-like protein [Lotus japonicus]	464	1.00E-129	1
NP_001062159.1	Os08g0500700 [Oryza sativa (japonica cultivar-group)]	355	2.00E-96	1
BAE71192.1	putative Asp1 [Trifolium pratense]	336	1.00E-90	1
NP_001046690.1	Os02g0321900 [Oryza sativa (japonica cultivar-group)]	322	2.00E-86	1
NP_001064799.1	Os10g0465800 [Oryza sativa (japonica cultivar-group)]	312	1.00E-83	2
CAA72315.1	putative 21kD protein precursor [Medicago sativa subsp. x varia]	281	3.00E-74	1
AAM21317.1 AF373100_1	auxin-regulated protein [Populus tremula x Populus tremuloides]	267	6.00E-70	2
NP_189128.2	SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana]	253	8.00E-66	1
NP_001046972.1	Os02g0519900 [Oryza sativa (japonica cultivar-group)]	251	3.00E-65	1
CAH66528.1	H0502B11.8 [Oryza sativa (indica cultivar-group)]	232	2.00E-59	1
NP_001065830.1	Os11g0163100 [Oryza sativa (japonica cultivar-group)]	217	6.00E-55	1
NP_172636.1	pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	214	5.00E-54	1
ABC70464.1	CASTOR protein [Glycine max]	212	2.00E-53	1
NP_001045723.1	Os02g0122000 [Oryza sativa (japonica cultivar-group)]	201	3.00E-50	1
BAB82450.1	PBng143 [Vigna radiata]	142	6.00E-33	1
AAM62421.1 AF515795_1	Drm3 [Pisum sativum]	126	8.00E-28	2
ABW74471.1	auxin-repressed protein [Paeonia suffruticosa]	81.3	6.00E-26	1
ABR25977.1	osiaa30-auxin-responsive aux/iaa gene family member [Oryza sativa (indica cultivar-group)]	114	2.00E-24	1
AAD32146.1 AF123508_1	Nt-iaa28 deduced protein [Nicotiana tabacum]	114	5.00E-24	1
ABN08340.1	ZIM [Medicago truncatula]	166	2.00E-39	1
AAD09514.1	GMFP5 [Glycine max]	159	3.00E-37	1
AAG33924.1	auxin-repressed protein [Robinia pseudoacacia]	66.6	5.00E-10	1
ABQ81923.1	aminotransferase 2 [Cucumis melo]	241	2.00E-62	1
ABC46708.1	chloroplast photosystem II 10 kDa protein [Arachis hypogaea]	196	7.00E-49	2
NP_198992.2	cell cycle control crn (crooked neck) protein-like [Arabidopsis]	168	4.00E-40	1
Q96453 1433D_SOYBN	14-3-3-like protein D (SGF14D)	459	1.00E-127	3
ABA54865.1	putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 3	413	1.00E-114	1
Unknown				
CAO44871.1	unnamed protein product [Vitis vinifera]	533	1.00E-150	1
CAO18187.1	unnamed protein product [Vitis vinifera]	528	1.00E-148	1
CAO66720.1	unnamed protein product [Vitis vinifera]	514	1.00E-144	1

CAO65935.1	unnamed protein product [Vitis vinifera]	503	1.00E-141	1
CAA10289.1	hypothetical protein [Cicer arietinum]	491	1.00E-137	2
CAO39286.1	unnamed protein product [Vitis vinifera]	471	1.00E-131	1
CAO44803.1	unnamed protein product [Vitis vinifera]	469	1.00E-130	1
CAO65211.1	unnamed protein product [Vitis vinifera]	458	1.00E-127	1
BAA88228.1	thiamin biosynthetic enzyme [Glycine max]	457	1.00E-127	1
CAO49304.1	unnamed protein product [Vitis vinifera]	451	1.00E-125	1
CAN63254.1	hypothetical protein [Vitis vinifera]	451	1.00E-125	1
CAO70618.1	unnamed protein product [Vitis vinifera]	425	1.00E-123	1
CAO21857.1	unnamed protein product [Vitis vinifera]	438	1.00E-121	1
CAO43786.1	unnamed protein product [Vitis vinifera]	437	1.00E-121	1
CAO40038.1	unnamed protein product [Vitis vinifera]	422	1.00E-116	1
CAO15636.1	unnamed protein product [Vitis vinifera]	409	1.00E-113	1
CAO43989.1	unnamed protein product [Vitis vinifera]	393	1.00E-108	1
CAO60892.1	unnamed protein product [Vitis vinifera]	387	1.00E-106	1
ABK96599.1	unknown [Populus trichocarpa x Populus deltoides]	386	1.00E-105	1
CAO65376.1	unnamed protein product [Vitis vinifera]	382	1.00E-104	1
CAN64994.1	hypothetical protein [Vitis vinifera]	381	1.00E-104	1
CAO15192.1	unnamed protein product [Vitis vinifera]	376	1.00E-103	1
CAO48194.1	unnamed protein product [Vitis vinifera]	373	1.00E-102	1
CAO61388.1	unnamed protein product [Vitis vinifera]	370	1.00E-101	1
ABD32814.1	hypothetical protein MtrDRAFT_AC148995g28v2 [Medicago truncatula]	366	1.00E-100	1
CAO23556.1	unnamed protein product [Vitis vinifera]	369	1.00E-100	1
ABK95228.1	unknown [Populus trichocarpa]	365	1.00E-99	1
CAO15903.1	unnamed protein product [Vitis vinifera]	355	2.00E-96	1
CAO45373.1	unnamed protein product [Vitis vinifera]	353	5.00E-96	1
CAO43035.1	unnamed protein product [Vitis vinifera]	351	3.00E-95	1
CAO71749.1	unnamed protein product [Vitis vinifera]	350	7.00E-95	2
CAO61488.1	unnamed protein product [Vitis vinifera]	298	9.00E-95	1
ABK96295.1	unknown [Populus trichocarpa x Populus deltoides]	343	8.00E-93	1
CAO71287.1	unnamed protein product [Vitis vinifera]	343	8.00E-93	1
CAO14950.1	unnamed protein product [Vitis vinifera]	342	1.00E-92	1
ABK93552.1	unknown [Populus trichocarpa]	339	1.00E-91	1
CAO66650.1	unnamed protein product [Vitis vinifera]	336	1.00E-90	1
CAO42343.1	unnamed protein product [Vitis vinifera]	334	4.00E-90	1
CAO41275.1	unnamed protein product [Vitis vinifera]	334	5.00E-90	1
ABK96203.1	unknown [Populus trichocarpa]	331	3.00E-89	1
CAO66272.1	unnamed protein product [Vitis vinifera]	329	1.00E-88	1
CAO64218.1	unnamed protein product [Vitis vinifera]	256	2.00E-88	1
CAO48327.1	unnamed protein product [Vitis vinifera]	326	1.00E-87	1

ABK96305.1	unknown [Populus trichocarpa x Populus deltoides]	324	3.00E-87	1
ABK95775.1	unknown [Populus trichocarpa]	324	4.00E-87	1
CAN60740.1	hypothetical protein [Vitis vinifera]	323	6.00E-87	1
CAO18297.1	unnamed protein product [Vitis vinifera]	323	6.00E-87	1
CAO44273.1	unnamed protein product [Vitis vinifera]	321	4.00E-86	1
CAN80762.1	hypothetical protein [Vitis vinifera]	319	1.00E-85	1
CAO24389.1	unnamed protein product [Vitis vinifera]	318	2.00E-85	1
CAN75443.1	hypothetical protein [Vitis vinifera]	317	5.00E-85	1
CAO42285.1	unnamed protein product [Vitis vinifera]	315	3.00E-84	1
CAO22996.1	unnamed protein product [Vitis vinifera]	308	3.00E-82	1
BAF01964.1	hypothetical protein [Arabidopsis thaliana]	274	4.00E-82	3
CAO21314.1	unnamed protein product [Vitis vinifera]	305	2.00E-81	1
CAO40176.1	unnamed protein product [Vitis vinifera]	298	3.00E-79	1
CAO39385.1	unnamed protein product [Vitis vinifera]	297	4.00E-79	1
CAO67339.1	unnamed protein product [Vitis vinifera]	297	5.00E-79	1
CAO44301.1	unnamed protein product [Vitis vinifera]	297	5.00E-79	1
BAF75825.1	hypothetical protein [Malus x domestica]	297	5.00E-79	1
CAN64894.1	hypothetical protein [Vitis vinifera]	296	1.00E-78	1
CAO24542.1	unnamed protein product [Vitis vinifera]	294	4.00E-78	1
CAO66868.1	unnamed protein product [Vitis vinifera]	293	8.00E-78	1
CAO22937.1	unnamed protein product [Vitis vinifera]	292	2.00E-77	1
ABK94929.1	unknown [Populus trichocarpa]	288	2.00E-76	1
ABK92884.1	unknown [Populus trichocarpa]	288	2.00E-76	1
CAO40339.1	unnamed protein product [Vitis vinifera]	288	3.00E-76	1
CAO47376.1	unnamed protein product [Vitis vinifera]	287	4.00E-76	1
CAN72172.1	hypothetical protein [Vitis vinifera]	287	7.00E-76	1
CAO61102.1	unnamed protein product [Vitis vinifera]	286	8.00E-76	1
CAO62087.1	unnamed protein product [Vitis vinifera]	285	2.00E-75	1
CAO65647.1	unnamed protein product [Vitis vinifera]	285	2.00E-75	1
CAN64937.1	hypothetical protein [Vitis vinifera]	283	7.00E-75	1
CAO68379.1	unnamed protein product [Vitis vinifera]	280	9.00E-74	2
CAB51659.1	putative protein [Arabidopsis thaliana]	277	4.00E-73	1
ABK94241.1	unknown [Populus trichocarpa]	276	8.00E-73	1
CAO18146.1	unnamed protein product [Vitis vinifera]	275	1.00E-72	1
CAO16914.1	unnamed protein product [Vitis vinifera]	274	4.00E-72	1
CAO39662.1	unnamed protein product [Vitis vinifera]	274	5.00E-72	1
ABN05794.1	hypothetical protein MtrDRAFT_AC148817g33v2 [Medicago truncatula]	274	6.00E-72	1
CAO68979.1	unnamed protein product [Vitis vinifera]	273	8.00E-72	1
CAO21699.1	unnamed protein product [Vitis vinifera]	273	1.00E-71	2
ABK93406.1	unknown [Populus trichocarpa]	270	6.00E-71	1

AAM63369.1	unknown [Arabidopsis thaliana]	270	6.00E-71	1
CAN79693.1	hypothetical protein [Vitis vinifera]	268	2.00E-70	1
CAO66747.1	unnamed protein product [Vitis vinifera]	267	4.00E-70	1
CAO44335.1	unnamed protein product [Vitis vinifera]	257	5.00E-67	1
CAO16621.1	unnamed protein product [Vitis vinifera]	257	7.00E-67	1
CAO23276.1	unnamed protein product [Vitis vinifera]	256	9.00E-67	1
CAO63407.1	unnamed protein product [Vitis vinifera]	256	1.00E-66	1
CAO23149.1	unnamed protein product [Vitis vinifera]	256	1.00E-66	1
CAO40354.1	unnamed protein product [Vitis vinifera]	255	2.00E-66	1
CAO63610.1	unnamed protein product [Vitis vinifera]	256	2.00E-66	1
CAN80823.1	hypothetical protein [Vitis vinifera]	249	8.00E-65	1
CAO69187.1	unnamed protein product [Vitis vinifera]	247	6.00E-64	1
ABK95200.1	unknown [Populus trichocarpa]	247	7.00E-64	1
CAO14701.1	unnamed protein product [Vitis vinifera]	242	2.00E-62	1
CAO41446.1	unnamed protein product [Vitis vinifera]	242	2.00E-62	1
CAO22537.1	unnamed protein product [Vitis vinifera]	239	1.00E-61	1
CAO44173.1	unnamed protein product [Vitis vinifera]	239	2.00E-61	1
CAB95830.1	hypothetical protein [Cicer arietinum]	238	3.00E-61	1
ABK95057.1	unknown [Populus trichocarpa]	235	3.00E-60	1
ABK94930.1	unknown [Populus trichocarpa]	233	5.00E-60	1
ABK95546.1	unknown [Populus trichocarpa]	233	9.00E-60	1
CAO66902.1	unnamed protein product [Vitis vinifera]	233	1.00E-59	1
CAO65442.1	unnamed protein product [Vitis vinifera]	231	2.00E-59	1
CAO14711.1	unnamed protein product [Vitis vinifera]	229	1.00E-58	1
CAA18194.1	putative protein [Arabidopsis thaliana]	228	4.00E-58	1
ABK92614.1	unknown [Populus trichocarpa]	226	7.00E-58	1
CAO43759.1	unnamed protein product [Vitis vinifera]	225	2.00E-57	1
CAO71132.1	unnamed protein product [Vitis vinifera]	222	1.00E-56	1
CAO40896.1	unnamed protein product [Vitis vinifera]	221	3.00E-56	1
ABK93477.1	unknown [Populus trichocarpa]	220	5.00E-56	1
CAB37492.1	putative protein [Arabidopsis thaliana]	218	4.00E-55	1
CAO17698.1	unnamed protein product [Vitis vinifera]	217	6.00E-55	1
ABK94675.1	unknown [Populus trichocarpa]	216	1.00E-54	1
NP_190603.1	unknown protein [Arabidopsis thaliana]	215	2.00E-54	1
CAN62024.1	hypothetical protein [Vitis vinifera]	214	6.00E-54	1
CAO15843.1	unnamed protein product [Vitis vinifera]	212	2.00E-53	1
CAO49409.1	unnamed protein product [Vitis vinifera]	210	7.00E-53	1
CAN81044.1	hypothetical protein [Vitis vinifera]	209	7.00E-53	1
CAN65779.1	hypothetical protein [Vitis vinifera]	207	3.00E-52	1
CAN61153.1	hypothetical protein [Vitis vinifera]	208	3.00E-52	1

CAO64505.1	unnamed protein product [Vitis vinifera]	207	6.00E-52	1
CAO21400.1	unnamed protein product [Vitis vinifera]	207	6.00E-52	1
CAO68222.1	unnamed protein product [Vitis vinifera]	204	2.00E-51	1
CAI84658.1	hypothetical protein [Nicotiana tabacum]	205	2.00E-51	1
CAO45214.1	unnamed protein product [Vitis vinifera]	204	4.00E-51	1
CAO39210.1	unnamed protein product [Vitis vinifera]	203	1.00E-50	1
CAO16473.1	unnamed protein product [Vitis vinifera]	201	1.00E-50	1
CAN67814.1	hypothetical protein [Vitis vinifera]	202	2.00E-50	2
CAO70908.1	unnamed protein product [Vitis vinifera]	201	4.00E-50	1
CAN77019.1	hypothetical protein [Vitis vinifera]	158	5.00E-50	1
CAO61780.1	unnamed protein product [Vitis vinifera]	200	6.00E-50	1
ABK94537.1	unknown [Populus trichocarpa]	198	3.00E-49	1
ABK95430.1	unknown [Populus trichocarpa]	196	6.00E-49	1
ABK95743.1	unknown [Populus trichocarpa]	197	6.00E-49	1
CAO15686.1	unnamed protein product [Vitis vinifera]	196	8.00E-49	1
CAO70074.1	unnamed protein product [Vitis vinifera]	196	1.00E-48	1
CAN64895.1	hypothetical protein [Vitis vinifera]	194	3.00E-48	1
CAO61631.1	unnamed protein product [Vitis vinifera]	193	4.00E-48	1
CAO47802.1	unnamed protein product [Vitis vinifera]	194	4.00E-48	1
ABK94218.1	unknown [Populus trichocarpa]	187	6.00E-46	1
CAN65949.1	hypothetical protein [Vitis vinifera]	187	1.00E-45	1
CAO61623.1	unnamed protein product [Vitis vinifera]	184	3.00E-45	1
ABK93574.1	unknown [Populus trichocarpa]	185	4.00E-45	1
CAN71308.1	hypothetical protein [Vitis vinifera]	183	8.00E-45	1
ABK96152.1	unknown [Populus trichocarpa]	181	4.00E-44	1
CAN63850.1	hypothetical protein [Vitis vinifera]	181	4.00E-44	1
CAO21917.1	unnamed protein product [Vitis vinifera]	181	5.00E-44	1
CAO67077.1	unnamed protein product [Vitis vinifera]	181	6.00E-44	1
CAN80873.1	hypothetical protein [Vitis vinifera]	179	1.00E-43	1
CAO44961.1	unnamed protein product [Vitis vinifera]	179	1.00E-43	1
ABK93457.1	unknown [Populus trichocarpa]	178	2.00E-43	1
CAO38954.1	unnamed protein product [Vitis vinifera]	176	9.00E-43	1
ABK94521.1	unknown [Populus trichocarpa]	175	2.00E-42	1
CAO45481.1	unnamed protein product [Vitis vinifera]	174	3.00E-42	1
ABK93219.1	unknown [Populus trichocarpa]	170	5.00E-41	1
CAN64864.1	hypothetical protein [Vitis vinifera]	123	3.00E-40	1
CAO16953.1	unnamed protein product [Vitis vinifera]	167	4.00E-40	1
CAO43985.1	unnamed protein product [Vitis vinifera]	166	5.00E-40	1
ABK93697.1	unknown [Populus trichocarpa]	167	6.00E-40	1
CAO45573.1	unnamed protein product [Vitis vinifera]	149	9.00E-39	1

ABK94884.1	unknown [Populus trichocarpa]	161	4.00E-38	1
ABK22743.1	unknown [Picea sitchensis]	160	1.00E-37	1
CAN66505.1	hypothetical protein [Vitis vinifera]	159	1.00E-37	1
ABK94836.1	unknown [Populus trichocarpa]	158	3.00E-37	1
YP_588403.1	hypothetical protein ZeamMp158 [Zea mays subsp. mays]	151	3.00E-37	1
CAO41469.1	unnamed protein product [Vitis vinifera]	157	4.00E-37	1
ABD28368.1	hypothetical protein MtrDRAFT_AC148289g12v2 [Medicago truncatula]	156	7.00E-37	1
CAO71550.1	unnamed protein product [Vitis vinifera]	156	1.00E-36	1
CAO45477.1	unnamed protein product [Vitis vinifera]	154	2.00E-36	1
CAO44286.1	unnamed protein product [Vitis vinifera]	155	2.00E-36	1
CAO15629.1	unnamed protein product [Vitis vinifera]	99.4	2.00E-36	1
CAO48579.1	unnamed protein product [Vitis vinifera]	152	1.00E-35	1
CAB96688.1	putative protein [Arabidopsis thaliana]	152	2.00E-35	1
CAO15090.1	unnamed protein product [Vitis vinifera]	152	2.00E-35	1
CAO42363.1	unnamed protein product [Vitis vinifera]	152	2.00E-35	1
ABK93674.1	unknown [Populus trichocarpa]	151	3.00E-35	1
ABK94193.1	unknown [Populus trichocarpa]	151	3.00E-35	1
CAN61119.1	hypothetical protein [Vitis vinifera]	130	3.00E-35	1
CAO68283.1	unnamed protein product [Vitis vinifera]	151	4.00E-35	1
CAN74819.1	hypothetical protein [Vitis vinifera]	151	5.00E-35	1
CAO15842.1	unnamed protein product [Vitis vinifera]	145	2.00E-33	1
CAN62217.1	hypothetical protein [Vitis vinifera]	144	2.00E-33	1
ABK96304.1	unknown [Populus trichocarpa x Populus deltoides]	138	1.00E-31	1
CAO23602.1	unnamed protein product [Vitis vinifera]	138	4.00E-31	1
ABK94210.1	unknown [Populus trichocarpa]	135	2.00E-30	1
CAO16712.1	unnamed protein product [Vitis vinifera]	135	3.00E-30	1
CAO42932.1	unnamed protein product [Vitis vinifera]	134	4.00E-30	1
CAO69966.1	unnamed protein product [Vitis vinifera]	134	5.00E-30	1
CAO64960.1	unnamed protein product [Vitis vinifera]	132	6.00E-30	1
ABK92973.1	unknown [Populus trichocarpa]	131	2.00E-29	1
CAN79760.1	hypothetical protein [Vitis vinifera]	131	6.00E-29	1
CAO17337.1	unnamed protein product [Vitis vinifera]	130	1.00E-28	1
CAO67112.1	unnamed protein product [Vitis vinifera]	128	3.00E-28	1
ABK93131.1	unknown [Populus trichocarpa]	127	4.00E-28	1
CAN62511.1	hypothetical protein [Vitis vinifera]	124	7.00E-27	1
CAO50031.1	unnamed protein product [Vitis vinifera]	124	8.00E-27	1
CAO66422.1	unnamed protein product [Vitis vinifera]	121	2.00E-26	1
CAO70557.1	unnamed protein product [Vitis vinifera]	120	8.00E-26	1
ABK92578.1	unknown [Populus trichocarpa]	118	1.00E-25	1
ABK94311.1	unknown [Populus trichocarpa]	117	2.00E-25	1

CAA10123.1	hypothetical protein [Cicer arietinum]	118	4.00E-25	1
ABK96690.1	unknown [Populus trichocarpa x Populus deltoides]	115	2.00E-24	1
CAO43566.1	unnamed protein product [Vitis vinifera]	115	4.00E-24	1
CAO24691.1	unnamed protein product [Vitis vinifera]	112	1.00E-23	1
CAO14801.1	unnamed protein product [Vitis vinifera]	107	2.00E-23	1
ABK96142.1	unknown [Populus trichocarpa]	112	2.00E-23	1
ABK93587.1	unknown [Populus trichocarpa]	110	4.00E-23	1
CAO70312.1	unnamed protein product [Vitis vinifera]	110	4.00E-23	1
CAB77598.1	putative protein [Arabidopsis thaliana]	108	2.00E-22	1
CAO67231.1	unnamed protein product [Vitis vinifera]	102	8.00E-21	1
CAO45301.1	unnamed protein product [Vitis vinifera]	102	9.00E-21	1
CAO68988.1	unnamed protein product [Vitis vinifera]	103	1.00E-20	1
CAO71442.1	unnamed protein product [Vitis vinifera]	102	3.00E-20	1
CAO43782.1	unnamed protein product [Vitis vinifera]	101	4.00E-20	1
NP_191358.1	unknown protein [Arabidopsis thaliana]	99.4	2.00E-19	1
ABK93164.1	unknown [Populus trichocarpa]	98.2	2.00E-19	1
CAN77855.1	hypothetical protein [Vitis vinifera]	98.6	4.00E-19	1
CAN82375.1	hypothetical protein [Vitis vinifera]	98.2	4.00E-19	1
CAN82126.1	hypothetical protein [Vitis vinifera]	95.1	1.00E-18	1
CAN70790.1	hypothetical protein [Vitis vinifera]	97.1	1.00E-18	1
AAM61659.1	unknown [Arabidopsis thaliana]	92	1.00E-17	1
CAO16187.1	unnamed protein product [Vitis vinifera]	90.9	2.00E-17	1
CAO42580.1	unnamed protein product [Vitis vinifera]	90.9	8.00E-17	1
ABK95674.1	unknown [Populus trichocarpa]	88.2	2.00E-16	1
CAO71849.1	unnamed protein product [Vitis vinifera]	89.7	2.00E-16	1
ABK93149.1	unknown [Populus trichocarpa]	88.2	3.00E-16	1
CAO14772.1	unnamed protein product [Vitis vinifera]	88.6	4.00E-16	1
CAO40090.1	unnamed protein product [Vitis vinifera]	88.2	6.00E-16	1
ZP_00874766.1	hypothetical protein SsuiDRAFT_1635 [Streptococcus suis 89/1591]	67.8	3.00E-15	1
CAO38914.1	unnamed protein product [Vitis vinifera]	82	1.00E-14	1
P26563 AATM_LUPAN	Aspartate aminotransferase P2, mitochondrial precursor (Transaminase A)	80.9	3.00E-14	1
CAO65372.1	unnamed protein product [Vitis vinifera]	80.9	3.00E-14	1
CAO47252.1	unnamed protein product [Vitis vinifera]	79.3	9.00E-14	1
CAO67977.1	unnamed protein product [Vitis vinifera]	78.2	3.00E-13	1
ABK23797.1	unknown [Picea sitchensis]	74.3	4.00E-12	1
CAO40846.1	unnamed protein product [Vitis vinifera]	59.7	8.00E-12	1
ABK93285.1	unknown [Populus trichocarpa]	72	1.00E-11	1
CAO45180.1	unnamed protein product [Vitis vinifera]	72.4	2.00E-11	1
CAO48073.1	unnamed protein product [Vitis vinifera]	70.9	6.00E-11	1
XP_001067213.1	PREDICTED: hypothetical protein [Rattus norvegicus]	68.9	4.00E-10	1

CAO68098.1	unnamed protein product [Vitis vinifera]	497	1.00E-139	1
CAO21841.1	unnamed protein product [Vitis vinifera]	479	1.00E-134	1
CAO23214.1	unnamed protein product [Vitis vinifera]	429	1.00E-118	1
ABK93489.1	unknown [Populus trichocarpa]	407	1.00E-112	1
CAO63600.1	unnamed protein product [Vitis vinifera]	397	1.00E-109	1
ABK93226.1	unknown [Populus trichocarpa]	378	1.00E-103	1
CAO63606.1	unnamed protein product [Vitis vinifera]	377	1.00E-103	1
CAO16101.1	unnamed protein product [Vitis vinifera]	372	1.00E-101	1
CAO69484.1	unnamed protein product [Vitis vinifera]	342	2.00E-92	1
NP_171983.2	unknown protein [Arabidopsis thaliana]	336	1.00E-90	1
ABK96759.1	unknown [Populus trichocarpa x Populus deltoides]	322	2.00E-86	1
CAN81221.1	hypothetical protein [Vitis vinifera]	316	1.00E-84	1
ABA46755.1	unknown [Solanum tuberosum]	292	2.00E-77	1
NP_568958.1	unknown protein [Arabidopsis thaliana]	159	5.00E-76	1
ABK93056.1	unknown [Populus trichocarpa]	219	1.00E-55	2
ABK96157.1	unknown [Populus trichocarpa]	202	6.00E-51	1
CAO42313.1	unnamed protein product [Vitis vinifera]	199	1.00E-49	1
ABK96772.1	unknown [Populus trichocarpa x Populus deltoides]	197	5.00E-49	1
CAO24297.1	unnamed protein product [Vitis vinifera]	151	3.00E-35	1
CAO14817.1	unnamed protein product [Vitis vinifera]	151	5.00E-35	1
CAO16964.1	unnamed protein product [Vitis vinifera]	150	8.00E-35	1
XP_001269594.1	hypothetical protein ACLA_028940 [Aspergillus clavatus NRRL 1]	73.6	1.00E-22	2
CAO41541.1	unnamed protein product [Vitis vinifera]	108	2.00E-22	1
NP_565728.1	unknown protein [Arabidopsis thaliana]	106	1.00E-21	1
EDP38581.1	hypothetical protein Bm1_05555 [Brugia malayi]	92	4.00E-17	1
ABK94233.1	unknown [Populus trichocarpa]	62	1.00E-08	1
ABN08062.1	Protein of unknown function DUF632 [Medicago truncatula]	52.8	1.00E-05	1
CAO40971.1	unnamed protein product [Vitis vinifera]	129	2.00E-28	1
CAO22611.1	unnamed protein product [Vitis vinifera]	183	9.00E-45	1